

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 22:26:00 ; Search time 44.2 Seconds
(without alignments)
88,680 Million cell updates/sec

Title: US-09-104-340-4
Perfect score: 1466
Sequence: 1 MDQQLSILLLLSCSYVDSFG.....VPIGKSCSNAGYERGFMCQ 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 143561 seqs, 14463640 residues

Total number of hits satisfying chosen parameters: 143561

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents, AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/PCRTUS.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/Backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1466	100.0	983	1	US-08-167-919A-10
2	1466	100.0	983	2	US-08-449-645A-21
3	1466	100.0	983	2	US-08-702-367A-21
4	1466	100.0	983	3	US-08-715-106-10
5	1466	100.0	983	4	PCT-US95-04681-21
6	1306	88.1	983	1	US-08-162-809-16
7	1302	88.8	982	2	US-08-673-789-4
8	1005	68.6	986	2	US-08-673-789-3
9	1003	68.4	948	2	US-08-469-537A-101
10	995	67.9	986	2	US-08-449-645A-15
11	995	67.9	986	2	US-08-702-367A-15
12	995	67.9	986	4	PCT-US95-04681-15
13	995	67.9	1104	4	US-08-222-616-36
14	995	67.9	1104	4	PCT-US95-04228-36
15	990	67.5	877	2	US-08-673-789-2
16	988	67.4	1005	2	US-08-469-537A-103
17	987	67.3	928	1	US-08-442-248-2
18	987	67.3	928	1	US-08-440-815-2
19	984	67.1	991	2	US-08-449-645A-13
20	984	67.1	991	2	US-08-702-367A-13
21	984	67.1	991	4	PCT-US95-04681-13
22	976.5	66.6	967	2	US-08-449-645A-30
23	976.5	66.6	967	2	US-08-702-367A-30
24	927.5	63.3	998	2	US-08-449-645A-17
25	927.5	63.3	998	4	PCT-US95-04681-17
26	927.5	63.3	998	4	PCT-US95-04681-17
27	926.5	63.2	610	4	PCT-US96-00419-3
28	926.5	63.2	626	4	PCT-US96-00419-5
29	926.5	63.2	998	4	PCT-US96-00419-2

30	774	52.8	995	2	US-08-673-789-5	Sequence 5, Appl
31	772	52.7	995	1	US-08-162-809-18	Sequence 18, Appl
32	772	52.7	1011	1	US-08-162-809-12	Sequence 12, Appl
33	767	52.3	970	2	US-08-449-645A-11	Sequence 11, Appl
34	767	52.3	970	2	US-08-702-367A-11	Sequence 11, Appl
35	767	52.3	970	4	PCT-US95-04681-11	Sequence 11, Appl
36	763.5	52.1	984	2	US-08-673-789-6	Sequence 6, Appl
37	692	47.2	998	2	US-08-449-645A-20	Sequence 20, Appl
38	692	47.2	998	4	US-08-702-367A-20	Sequence 20, Appl
39	692	47.2	998	2	PCT-US95-04681-20	Sequence 20, Appl
40	681.5	46.5	710	1	US-08-162-809-22	Sequence 22, Appl
41	681.5	46.5	722	1	US-08-162-809-4	Sequence 4, Appl
42	681.5	46.5	744	1	US-08-162-809-20	Sequence 20, Appl
43	679	46.3	973	1	US-08-162-809-10	Sequence 10, Appl
44	679	46.3	988	1	US-08-162-809-14	Sequence 14, Appl
45	679	46.3	993	1	US-08-348-143-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-167-919A-10
; Sequence 10, Application US/08167919A
; Patent No. 5674691
; GENERAL INFORMATION:
; APPLICANT: Boyd, Andrew W.
; APPLICANT: Simpson, Richard J.
; APPLICANT: Wicks, Ian
; APPLICANT: Ward, Larry D.
; APPLICANT: Wilkinson, David
; TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08167,919A
; FILING DATE: 18-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK6841 (AU)
; FILING DATE: 21-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK9992 (AU)
; FILING DATE: 12-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU92/00294
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELE: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-167-919A-10

Query Match 100.0%; Score 1466; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 5.2e-146;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCQLSILLLLSCVSDSGELIPQPSNEVNLDSKTIGELGWSIPSHGWEISGVDE 60
DB 1 MDCQLSILLLLSCVSDSGELIPQPSNEVNLDSKTIGELGWSIPSHGWEISGVDE 60
QY 61 HTPITRYOVNCNMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDONSIPVLGTCKEF 120
DB 61 HTPITRYOVNCNMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDONSIPVLGTCKEF 120
QY 121 NLYMESDDHGVKFRHEHFTKIDITIADESFQMDLGRILKLTETREVGVPVKKGFY 180
DB 121 NLYMESDDHGVKFRHEHFTKIDITIADESFQMDLGRILKLTETREVGVPVKKGFY 180
QY 181 LAFQDVACVALVSVRVYFKCPTVKNLAMPDTPVPMDSQSLVEYRGSCVNNKKEEDPP 240
DB 181 LAFQDVACVALVSVRVYFKCPTVKNLAMPDTPVPMDSQSLVEYRGSCVNNKKEEDPP 240
QY 241 RMYCSTEGEMLVPIGKSCNAGYEERGFMCQ 271
DB 241 RMYCSTEGEMLVPIGKSCNAGYEERGFMCQ 271

RESULT 2

US-08-449-645A-21

Sequence 21, Application US/08449645A

Patent No. 5981245

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,645A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 983 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-449-645A-21

Query Match 100.0%; Score 1466; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 5.2e-146;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCQLSILLLLSCVSDSGELIPQPSNEVNLDSKTIGELGWSIPSHGWEISGVDE 60
DB 1 MDCQLSILLLLSCVSDSGELIPQPSNEVNLDSKTIGELGWSIPSHGWEISGVDE 60

QY 61 HTPITRYOVNCNMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDONSIPVLGTCKEF 120
DB 61 HTPITRYOVNCNMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDONSIPVLGTCKEF 120
QY 121 NLYMESDDHGVKFRHEHFTKIDITIADESFQMDLGRILKLTETREVGVPVKKGFY 180
DB 121 NLYMESDDHGVKFRHEHFTKIDITIADESFQMDLGRILKLTETREVGVPVKKGFY 180
QY 181 LAFQDVACVALVSVRVYFKCPTVKNLAMPDTPVPMDSQSLVEYRGSCVNNKKEEDPP 240
DB 181 LAFQDVACVALVSVRVYFKCPTVKNLAMPDTPVPMDSQSLVEYRGSCVNNKKEEDPP 240
QY 241 RMYCSTEGEMLVPIGKSCNAGYEERGFMCQ 271
DB 241 RMYCSTEGEMLVPIGKSCNAGYEERGFMCQ 271

RESULT 3

US-08-702-367A-21

Sequence 21, Application US/08702367A

Patent No. 5981246

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,367A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 983 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-702-367A-21

Query Match 100.0%; Score 1466; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 5.2e-146;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCQLSILLLLSCVSDSGELIPQPSNEVNLDSKTIGELGWSIPSHGWEISGVDE 60
DB 1 MDCQLSILLLLSCVSDSGELIPQPSNEVNLDSKTIGELGWSIPSHGWEISGVDE 60
QY 61 HTPITRYOVNCNMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDONSIPVLGTCKEF 120
DB 61 HTPITRYOVNCNMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDONSIPVLGTCKEF 120
QY 121 NLYMESDDHGVKFRHEHFTKIDITIADESFQMDLGRILKLTETREVGVPVKKGFY 180
DB 121 NLYMESDDHGVKFRHEHFTKIDITIADESFQMDLGRILKLTETREVGVPVKKGFY 180
QY 181 LAFQDVACVALVSVRVYFKCPTVKNLAMPDTPVPMDSQSLVEYRGSCVNNKKEEDPP 240

Db 181 LAFOVGACVALSVRYVFKCPFTVKNLAMPDTPVPMDSOSLVEVRSGCVNNSKEEDPP 240
Qy 241 RMYCTEGEMLVPIGKCSGNAGYERGFMCQ 271
Db 241 RMYCTEGEMLVPIGKCSGNAGYERGFMCQ 271

RESULT 4

US-08-715-106-10
Sequence 10, Application US/08715106
Patent No. 6020306
GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGILIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-715-106-10

Query Match 100.0%; Score 1466; DB 3; Length 983;
Best Local Similarity 100.0%; Pred. No. 5.2e-146;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDCQSLILLSCSVLDSFGELIPQPSNEVNLDSKTIQGLGWTISYSHGWEIISGVDE 60
Db 1 MDCQSLILLSCSVLDSFGELIPQPSNEVNLDSKTIQGLGWTISYSHGWEIISGVDE 60

Qy 61 HTTPIRTYQVCNVMDHSONNMLRTNWVPRNSAQKIYVELKFTLRDCNSIPVLGCKETF 120
Db 61 HTTPIRTYQVCNVMDHSONNMLRTNWVPRNSAQKIYVELKFTLRDCNSIPVLGCKETF 120
Qy 121 NLYWESDDHGVKFRHQFTKIDITIADESFTQMDLGDRLIKLNTETIREVGPVKKGFY 180
Db 121 NLYWESDDHGVKFRHQFTKIDITIADESFTQMDLGDRLIKLNTETIREVGPVKKGFY 180
Qy 181 LAFOVGACVALSVRYVFKCPFTVKNLAMPDTPVPMDSOSLVEVRSGCVNNSKEEDPP 240
Db 181 LAFOVGACVALSVRYVFKCPFTVKNLAMPDTPVPMDSOSLVEVRSGCVNNSKEEDPP 240
Qy 241 RMYCTEGEMLVPIGKCSGNAGYERGFMCQ 271
Db 241 RMYCTEGEMLVPIGKCSGNAGYERGFMCQ 271

RESULT 5

PCT-US95-04681-21
Sequence 21, Application PC/TUS9504681
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-like Receptor Protein Tyrosine
KINASES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1640 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-21

Query Match 100.0%; Score 1466; DB 4; Length 983;
Best Local Similarity 100.0%; Pred. No. 5.2e-146;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDCQSLILLSCSVLDSFGELIPQPSNEVNLDSKTIQGLGWTISYSHGWEIISGVDE 60
Db 1 MDCQSLILLSCSVLDSFGELIPQPSNEVNLDSKTIQGLGWTISYSHGWEIISGVDE 60
Qy 61 HTTPIRTYQVCNVMDHSONNMLRTNWVPRNSAQKIYVELKFTLRDCNSIPVLGCKETF 120
Db 61 HTTPIRTYQVCNVMDHSONNMLRTNWVPRNSAQKIYVELKFTLRDCNSIPVLGCKETF 120
Qy 121 NLYWESDDHGVKFRHQFTKIDITIADESFTQMDLGDRLIKLNTETIREVGPVKKGFY 180
Db 121 NLYWESDDHGVKFRHQFTKIDITIADESFTQMDLGDRLIKLNTETIREVGPVKKGFY 180
Qy 181 LAFOVGACVALSVRYVFKCPFTVKNLAMPDTPVPMDSOSLVEVRSGCVNNSKEEDPP 240
Db 181 LAFOVGACVALSVRYVFKCPFTVKNLAMPDTPVPMDSOSLVEVRSGCVNNSKEEDPP 240

QY 241 RMYCSTEGEMLVPIGKSCNAGYERGFMCQ 271
DB 241 RMYCSTEGEMLVPIGKSCNAGYERGFMCQ 271

RESULT 6

US-08-162-809-16
; Sequence 16, Application US/08162809
; Patent No. 5457048
; GENERAL INFORMATION:
; APPLICANT: Pasquale, Elena B.
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162, 809
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-162-809-16

Query Match

Best Local Similarity 89.1%; Score 1306; DB 1; Length 983;
Best Local Similarity 91.3%; Pred. No. 4e-129;
Matches 240; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 9 LLLSCVLSDFGELLPOPSNEVNLDSKTIOGELGWTSPSHGMEISGVDEHYPIRTY 68
DB 8 LLLCALASAGLSARPGNEVNLDSKTIOGELGWTSPSHGMEISGVDEHYPIRTY 67
QY 69 QVCNVMDHSONMNLRTNWPVRNSAOKIYVELKFTLRDCNSIPVLVGTCKETFNLYMESD 128
DB 68 QESNVMDHSONMNLRTNWPVRNSAOKIYVELKFTLRDCNSIPVLVGTCKETFNLYMESD 127
QY 129 DDHGVAFREHOFTKIDTIADESFQMDLGDRIKLKLTREYGVNKKGFYLAFODVGA 188
DB 128 DDHIAFREHOFTKIDTIADESFQMDLGDRIKLKLTREYGVNKKGFYLAFODVGA 187
QY 189 CVALVSVRVYFKKCPFTVKNLAFPTVPMDQSILVEVSGCVNNSKEEDPPRYCSTEG 248
DB 188 CVALVSVRVYFKKCPFTVKNLAFPTVPMDQSILVEVSGCVNNSKEEDPPRYCSTEG 247
QY 249 EMLVPIGKSCNAGYERGFMCQ 271
DB 248 EMLVPIGKSCNAGYERGFMCQ 270

RESULT 7

US-08-673-789-4
; Sequence 4, Application US/08673789
; Patent No. 5814479
; GENERAL INFORMATION:
; APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS
; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
; TITLE OF INVENTION: BSK RECEPTOR LIKE
; TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
; TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,789
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/177,812
; FILING DATE: 04-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 982
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; US-08-673-789-4

Query Match

Best Local Similarity 88.8%; Score 1302; DB 2; Length 982;
Best Local Similarity 91.3%; Pred. No. 1e-128;
Matches 240; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 9 LLLSCVLSDFGELLPOPSNEVNLDSKTIOGELGWTSPSHGMEISGVDEHYPIRTY 68
DB 8 LLLCALASAGLSARPGNEVNLDSKTIOGELGWTSPSHGMEISGVDEHYPIRTY 67
QY 69 QVCNVMDHSONMNLRTNWPVRNSAOKIYVELKFTLRDCNSIPVLVGTCKETFNLYMESD 128
DB 68 QESNVMDHSONMNLRTNWPVRNSAOKIYVELKFTLRDCNSIPVLVGTCKETFNLYMESD 127
QY 129 DDHGVAFREHOFTKIDTIADESFQMDLGDRIKLKLTREYGVNKKGFYLAFODVGA 188
DB 128 DDHIAFREHOFTKIDTIADESFQMDLGDRIKLKLTREYGVNKKGFYLAFODVGA 187
QY 189 CVALVSVRVYFKKCPFTVKNLAFPTVPMDQSILVEVSGCVNNSKEEDPPRYCSTEG 248
DB 188 CVALVSVRVYFKKCPFTVKNLAFPTVPMDQSILVEVSGCVNNSKEEDPPRYCSTEG 247
QY 249 EMLVPIGKSCNAGYERGFMCQ 271
DB 248 EMLVPIGKSCNAGYERGFMCQ 270

[illegible]

Query Match	68.4%	Score 1003	DB 2	Length 948
Best Local Similarity	65.7%	Pred. No. 3.4e-97		
Matches 180	Conservative 39	Mismatches 37	Indels 18	Gaps 3

QY	3	COLSILLLLSCSVLDSFEGELIP-----QPSENVNLLDSKTIQOELGNIYSPSHGQ	52
Db	4	CEVEFEFLP-----QGFEPFLPLLTAWMGDCDSHNSNQVLLDITSTVMGELWKRTPLNGM	56
QY	53	ELISGVDEHYPIRTYOVCNMDHSONNWLTENVPRRSAKIYELKFTLLADCSIPLY	112
Db	57	DALTEMDHNPRIHTYOVCNMEPQNNWLTNWSRPAOKIYEMKFTLLDCNSIPWY	116
QY	113	LGTCKEFNLYMESDDDHGKFRBHOFTKIDTITAADESFQMDLGDRIKLINTEIREVG	172
Db	117	LGTCKEFNLYIIESDESHGTFKPSQYIKIDTITAADESFQMDLGDRIKLINTEIREVG	176
QY	173	PVNNKGFLIADODYGACALYSVRVYEFKGCFTYKNLAMEFDIYAP-MSQSILYEVKSGCY	231
Db	177	PIERKGFLIADODGACALYSVRVYEFKGCFTYKNLAMEFDIPIVSDSSILYEVKSGCY	236
QY	232	NNSKEEDPFRMYCSTEGEMLVPIGKCSGCAAYEE	265

DB 237 KSSERDTPKLYCAGDGMVLVPLGRCICCTGYEE 270

RESULT 10

US-08-449-645A-15
Sequence 15, Application US/08449645A
Patent No. 5981245

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-like Receptor Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,645A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 986 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-449-645A-15

Query Match 67.9%; Score 995; DB 2; Length 986;

Best Local Similarity 68.8%; Pred. No. 2.5e-96;

Matches 183; Conservative 37; Mismatches 42; Indels 4; Gaps 3;

DB 10 LISC--SVYDSFGELIPQPSNEVNLDSKTIQELGMIYSP-SHGWEISGVDEHYTPIR 66

DB 9 LFSCLFGICDVAATGSRVYFANEVTLIDSRVQELGMIASPLEGWEBSINDEKNTPIR 68

DB 67 TYQVCNVMDSQNNMLRTNMPNRSQKIYVELKFTLRDQNSIPVLGCKETFNLYME 126

DB 69 TYQVCNVMDSQNNMLRTNMPNRSQKIYVELKFTLRDQNSIPVLGCKETFNLYME 128

DB 127 SDDHGVKFRHQFTKIDITIADESFTQMDLGRILKLTETREYGVNKKGFYLAFOV 186

DB 129 SDDHGVKFRHQFTKIDITIADESFTQMDLGRILKLTETREYGVNKKGFYLAFOV 188

DB 187 GACVALSVRYEYFKCPTVKNLAMPPTVP-MDSQSLVEYRGSCVNNSEKEDVPKMYCS 245

DB 189 GACIALSVRYEYFKCPTVKNLAMPPTVP-MDSQSLVEYRGSCVNNSEKEDVPKMYCS 248

DB 246 TEGEWLVPIGKSCNAGYEERGFMCQ 271

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,367A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 986 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-702-367A-15

Query Match 67.9%; Score 995; DB 2; Length 986;

Best Local Similarity 68.8%; Pred. No. 2.5e-96;

Matches 183; Conservative 37; Mismatches 42; Indels 4; Gaps 3;

DB 10 LISC--SVYDSFGELIPQPSNEVNLDSKTIQELGMIYSP-SHGWEISGVDEHYTPIR 66

DB 9 LFSCLFGICDVAATGSRVYFANEVTLIDSRVQELGMIASPLEGWEBSINDEKNTPIR 68

DB 67 TYQVCNVMDSQNNMLRTNMPNRSQKIYVELKFTLRDQNSIPVLGCKETFNLYME 126

DB 69 TYQVCNVMDSQNNMLRTNMPNRSQKIYVELKFTLRDQNSIPVLGCKETFNLYME 128

DB 127 SDDHGVKFRHQFTKIDITIADESFTQMDLGRILKLTETREYGVNKKGFYLAFOV 186

DB 129 SDDHGVKFRHQFTKIDITIADESFTQMDLGRILKLTETREYGVNKKGFYLAFOV 188

DB 187 GACVALSVRYEYFKCPTVKNLAMPPTVP-MDSQSLVEYRGSCVNNSEKEDVPKMYCS 245

DB 189 GACIALSVRYEYFKCPTVKNLAMPPTVP-MDSQSLVEYRGSCVNNSEKEDVPKMYCS 248

DB 246 TEGEWLVPIGKSCNAGYEERGFMCQ 271

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

DB 249 ADGEWLVPIGKSCNAGYEERGFMCQ 274

APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-04228-36

Query Match 67.9%; Score 995; DB 4; Length 1104;
Best Local Similarity 68.8%; Pred. No. 3e-96;
Matches 183; Conservative 37; Mismatches 42; Indels 4; Gaps 3;

QY 10 LISC--SVLDSFGLIPOPSENEVNLDSKTIGELGMSYP-SHGWEISGVDEHYTPIR 66
DB 9 LKSCLEFGICDAVTSRVRVANEYTLTDSRSYOGELGMINASPLEGGEVYSINDEXTPIR 68
QY 67 TYQCVNMDHSONNMLRTNWPVPRNSAQKIYVELKFTLRDCNSIPLVLTCKETFNLYYME 126
DB 69 TYQCVNMDHSONNMLRTNWPVPRNSAQKIYVELKFTLRDCNSIPLVLTCKETFNLYYME 128
QY 127 SDDHGKFRERQFTIDITIADESFTQMDLGDRIKLNTREYGVPNKKGFTYLAFOV 186
DB 128 SDDHGKFRERQFTIDITIADESFTQMDLGDRIKLNTREYGVPNKKGFTYLAFOV 188
QY 187 GACVALSVRYEYFKKCPFTVKNLAMPDTPV-MDSQSLVEYVSGCVNNSKEEDPPRMYS 245
DB 189 GACIALSVRYEYFKKCPFTVKNLAMPDTPV-MDSQSLVEYVSGCVNNSKEEDPPRMYS 248
QY 246 TEGEWLVPIGKCSNAGYEERGFMCQ 271
DB 249 ADGEWLVPIGKCSNAGYEERGFMCQ 274

RESULT 15
US-08-673-789-2
Sequence 2, Application US/08673789
Patent No. 5814479
GENERAL INFORMATION:
APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/673,789
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 877
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
US-08-673-789-2

Query Match 67.5%; Score 990; DB 2; Length 877;
Best Local Similarity 66.2%; Pred. No. 7.2e-96;
Matches 174; Conservative 44; Mismatches 41; Indels 4; Gaps 2;

QY 10 LISC--SVLDSFGLIPOPSENEVNLDSKTIGELGMSYP-SHGWEISGVDEHYTPIR 69
DB 46 LILCALRT--LSPSPNEVNLDSRTYMGDLGIAFPKNWEISGVDEHYTPIR 102
QY 70 VCVNMDHSONNMLRTNWPVPRNSAQKIYVELKFTLRDCNSIPLVLTCKETFNLYYME 129
DB 103 VCVNMDHSONNMLRTNWPVPRNSAQKIYVELKFTLRDCNSIPLVLTCKETFNLYYME 162
QY 130 DHCYVFRERQFTIDITIADESFTQMDLGDRIKLNTREYGVPNKKGFTYLAFOV 189
DB 163 ENGSRILEKQYIKIDITIADESFTQMDLGDRIKLNTREYGVPNKKGFTYLAFOV 222
QY 190 VALSVRYEYFKKCPFTVKNLAMPDTPV-MDSQSLVEYVSGCVNNSKEEDPPRMYS 248
DB 223 TALSVRYEYFKKCPFTVKNLAMPDTPV-MDSQSLVEYVSGCVNNSKEEDPPRMYS 282
QY 249 EWLVPPIGKCSNAGYEERGFMCQ 271
DB 283 EWLVPPIGKCSNAGYEERGFMCQ 305

Search completed: May 9, 2000, 22:26:02
Job time: 4151 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 21:52:05 ; Search time 50.71 Seconds
(without alignments)
126.581 Million cell updates/sec

Title: US-09-104-340-4
Perfect score: 1466
Sequence: 1 MCOLSILLILSCSVLDSFG.....VPIKGCSCNAGYERGFMCQ 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq.36.*
Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	1466	100.0	983	1 R31466	HEK polypeptide. R
2	1306	89.1	983	1 R75711	Eph-related PTK Ce
3	1003	68.4	948	1 W63148	Rat receptor tyros
4	995	67.9	986	1 R85936	Protein tyrosine-k
5	995	67.9	986	1 R85091	Eph-1ike receptor
6	990	67.5	877	1 W71628	Mouse Bsk receptor
7	988	67.4	1005	1 W63147	Rat receptor tyros
8	987	67.3	928	1 R71853	Rat REK7 eph-relat
9	984	67.1	991	1 R85090	Eph-1ike receptor
10	927.5	63.3	998	1 R85092	Eph-1ike receptor
11	926.5	63.2	610	1 W03422	Mouse developmenta
12	926.5	63.2	626	1 W03423	Mouse developmenta
13	926.5	63.2	626	1 W03421	Mouse developmenta
14	772	52.7	995	1 R75712	Eph-related PTK Ce
15	772	52.7	1011	1 R75709	Eph-related PTK Ce
16	767	52.3	970	1 R85089	Eph-1ike receptor
17	767	52.3	994	1 R87018	Receptor tyrosine
18	767	52.3	994	1 W26365	Mouse Nuk tyrosine
19	761.5	51.9	984	1 R4513	ELK. Expression of
20	692	47.2	990	1 R51899	Human embryonal ki
21	681.5	46.5	710	1 R75714	Eph-related PTK Ce
22	681.5	46.5	722	1 R75705	Eph-related PTK Ce
23	681.5	46.5	744	1 R75713	Eph-related PTK Ce
24	679	46.3	973	1 R75708	Eph-related PTK Ce
25	679	46.3	988	1 R75710	Eph-related PTK Ce
26	679	46.3	993	1 R75843	Protein p140 CDNA
27	679	46.3	993	1 R75844	Eph-related PTK Ce
28	622	42.4	973	1 R75707	Embryonic stem cel
29	616	42.0	977	1 W19258	Embryonic stem cel
30	588	40.1	951	1 R75704	Eph-related CK6.
31	569.5	38.8	849	1 R75706	Eph-related PTK Ce
32	528.5	36.1	1006	1 W72256	Human receptor typ
33	528.5	36.1	1006	1 W70525	Human thymus recep
34	528.5	36.1	1021	1 W70526	Human thymus recep

35	493	33.6	522	1 R76466	Non-differentiated
36	493	33.6	522	1 R94653	Receptor type tyro
37	493	33.6	522	1 W06330	Receptor type tyro
38	493	33.6	522	1 W11303	Receptor-type tyro
39	493	33.6	972	1 R76468	Mature non-differe
40	493	33.6	972	1 W06331	Full-length recept
41	493	33.6	987	1 R85930	Protein tyrosine-k
42	493	33.6	987	1 R89263	Human non-differe
43	493	33.6	987	1 R94652	Receptor type tyro
44	493	33.6	987	1 W06335	Full length recept
45	493	33.6	987	1 W11304	Receptor-type tyro

ALIGNMENTS

RESULT	ID	Description	Location/Qualifiers
1	R31466	HEK polypeptide. R	1..20
	R31466	Eph-related PTK Ce	/note= "Signal peptide"
	R31466	Rat receptor tyros	21..39
	R31466	Protein tyrosine-k	/note= "Purified HEK protein #1"
	R31466	Eph-1ike receptor	840..860
	R31466	Mouse Bsk receptor	/note= "Purified HEK protein #2"
	R31466	Rat receptor tyros	232..234
	R31466	Rat REK7 eph-relat	/note= "N-link glycosylation"
	R31466	Eph-1ike receptor	337..339
	R31466	Eph-1ike receptor	/note= "N-link glycosylation"
	R31466	Mouse developmenta	391..393
	R31466	Mouse developmenta	/note= "N-link glycosylation"
	R31466	Mouse developmenta	404..406
	R31466	Mouse developmenta	/note= "N-link glycosylation"
	R31466	Mouse developmenta	493..495
	R31466	Mouse developmenta	/note= "N-link glycosylation"
	R31466	Mouse developmenta	542..565
	R31466	Mouse developmenta	/note= "Transmembrane domain"
	R31466	Mouse developmenta	628
	R31466	Mouse developmenta	/note= "Arp binding site"
	R31466	Mouse developmenta	630
	R31466	Mouse developmenta	/note= "Arp binding site"
	R31466	Mouse developmenta	633
	R31466	Mouse developmenta	/note= "Arp binding site"
	R31466	Mouse developmenta	779
	R31466	Mouse developmenta	/note= "Putative autophosphorylation site"
	R31466	Mouse developmenta	W09300425-A.
	R31466	Mouse developmenta	07-JAN-1993.
	R31466	Mouse developmenta	19-JUN-1992; AU0294.
	R31466	Mouse developmenta	21-JUN-1991; AU-006841.
	R31466	Mouse developmenta	12-DEC-1991; AU-009992.
	R31466	Mouse developmenta	(HALT-) HALT INST MEDICAL RES WALTER & ELIZ.
	R31466	Mouse developmenta	Boyd AD, Simpson R, Ward LD, Wicks I, Wilkinson D;
	R31466	Mouse developmenta	WPI. 93-036373/04.
	R31466	Mouse developmenta	P-ESDB; R31466.
	R31466	Mouse developmenta	Receptor-type tyrosine kinase reactive with monoclonal antibody
	R31466	Mouse developmenta	III-A4 - is Eph-ELK-like kinase, useful for phosphorylating
	R31466	Mouse developmenta	proteins in modulating pre-B, B and T cell function, in cancer
	R31466	Mouse developmenta	therapy etc.
	R31466	Mouse developmenta	Claim 6, Fig 1, 58pp. English.
	R31466	Mouse developmenta	This sequence represents human eph/elk-like kinase (HEK). HEK is
	R31466	Mouse developmenta	expressed in both pre-B cells and T cell lines and in a number of
	R31466	Mouse developmenta	tumours of human origin, eg. lymphoid tumours LK63, Lila-1 and JM,
	R31466	Mouse developmenta	and the epithelial tumour Hela. This receptor-type thymidine kinase
	R31466	Mouse developmenta	(TK) and/or its ligands are useful as agents in modulation of the

CC production and/or function of pre-B, B and T cells. The TK and its
 CC analogues have activity in transducing signals or in stimulating
 CC cellular responses such as growth and/or differentiation.
 SQ Sequence 983 AA;

Query Match 100.0%; Score 1466; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 6.5e-143;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCQSLILLLSCSVDSFGEILPQPSNEVNLDSKTIGELGWIISPSHGMEISGYDE 60
 DB 1 MDCQSLILLLSCSVDSFGEILPQPSNEVNLDSKTIGELGWIISPSHGMEISGYDE 60
 QY 61 HXTPRTTYQVCNVMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDQNSIPVLGCTKETP 120
 DB 61 HXTPRTTYQVCNVMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDQNSIPVLGCTKETP 120
 QY 121 NLIYMSDDDHGKFKREHQTIDITIAADESFQMDLGRILKLTNLEIREVGPVNRKGFY 180
 DB 121 NLIYMSDDDHGKFKREHQTIDITIAADESFQMDLGRILKLTNLEIREVGPVNRKGFY 180
 QY 181 LAFQDVACVALYSVRVYFKKCPFTVKNLAMPDTPVPMDSQSLVEYRGSCVNSKEDPP 240
 DB 181 LAFQDVACVALYSVRVYFKKCPFTVKNLAMPDTPVPMDSQSLVEYRGSCVNSKEDPP 240
 QY 241 RMYCSTEGEMLVPIGKSCNAGYEERGFMCQ 271
 DB 241 RMYCSTEGEMLVPIGKSCNAGYEERGFMCQ 271

RESULT 2

ID R75711 standard; Protein: 983 AA.
 AC R75711;
 DT 11-NOV-1995 (first entry)
 DE Eph-related PK Cdk4
 KW Cdk4; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
 KM prognosis.
 OS Gallus sp.
 PN WO9515375-A.
 PD 08-JUN-1995.
 PF 07-SEP-1994; U10140.
 PR 03-DEC-1993; US-162809.
 PA (LJOL-) LA JOLIA CANCER RES FOUND.
 PI Pasquale EB, Sajjadi FG;
 DR WPI: 95-215256/28.
 DR N-PSDB: 090659.
 PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
 PI cancer.
 PS Disclosure: Page 85-89; 129pp; English.
 CC Probes derived from the Eph-related PKs Cdk4 (090659) and Cdk5
 CC (090660) were used to isolate novel cDNA clones (090652-58,
 CC 090661-62) from chicken embryo and embryonic brain libraries.
 CC Cdk4 is highly expressed in the chicken developing brain and
 CC embryonic tissues and also in the adult brain and retina.
 SQ Sequence 983 AA;

Query Match 89.1%; Score 1306; DB 1; Length 983;
 Best Local Similarity 91.3%; Pred. No. 2.3e-126;
 Matches 240; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 9 LLLSCSVLDSFGEILPQPSNEVNLDSKTIGELGWIISPSHGMEISGYDEHYTPRTY 68
 DB 8 LLLSCSVLDSFGEILPQPSNEVNLDSKTIGELGWIISPSHGMEISGYDEHYTPRTY 68
 QY 69 QVCNVMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDQNSIPVLGCTKETPFLYMEED 128
 DB 69 QVCNVMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDQNSIPVLGCTKETPFLYMEED 128
 QY 129 DDHGVFREHQTIDITIAADESFQMDLGRILKLTNLEIREVGPVNRKGFYLAEDVGA 188
 DB 129 DDHGVFREHQTIDITIAADESFQMDLGRILKLTNLEIREVGPVNRKGFYLAEDVGA 188

DB 128 DDHGVFREHQTIDITIAADESFQMDLGRILKLTNLEIREVGPVNRKGFYLAEDVGA 187
 QY 189 CVALYSVRVYFKKCPFTVKNLAMPDTPVPMDSQSLVEYRGSCVNSKEDPPRMKCTEG 248
 DB 188 CVALYSVRVYFKKCPFTVKNLAMPDTPVPMDSQSLVEYRGSCVNSKEDPPRMKCTEG 247

QY 249 EMLVPIGKSCNAGYEERGFMCQ 271
 DB 248 EMLVPIGKSCNAGYEERGFMCQ 270

RESULT 3

ID W83148 standard; Protein: 948 AA.
 AC W83148;
 DT 11-FEB-1999 (first entry)
 DE Rat receptor tyrosine kinase Eph-2.
 KW Receptor tyrosine kinase; Ror-1; Ror-2; Eph-1; Eph-2; detection;
 KW neurotrophin activity; TrkB; proto-oncogene; tyrosine kinase receptor;
 KM binding protein; BDNF; NT-3; diagnosis.
 OS Rattus sp.
 PN US5843749-A.
 PD 01-DEC-1998.
 PF 06-JUN-1995; 469537.
 PR 17-MAR-1995; US-406247.
 PR 26-JUL-1991; US-736559.
 PR 28-OCT-1993; US-144952.
 PR 06-JUN-1995; US-469537.
 PA (REGE-) REGENERON PHARM INC.
 PI Maisondierre FC, Mastakowski P, Yancopoulos GD;
 DR WPI: 99-044584/04.
 DR N-PSDB: V70208.
 PT DNA encoding receptor tyrosine kinase proteins - and corresponding
 PT proteins
 PS Example: Fig 21; 194pp; English.
 CC The present invention describes nucleic acid molecules for ror-1,
 CC ror-2, eph-1 and eph-2. Also described are the corresponding proteins:
 CC Ror-1; Ror-2; Eph-1; and Eph-2. The proteins are orphan receptor
 CC tyrosine kinases. The present sequence represents rat Eph-2.
 SQ Sequence 948 AA;

Query Match 68.4%; Score 1003; DB 1; Length 948;
 Best Local Similarity 65.7%; Pred. No. 4.6e-95;
 Matches 180; Conservative 39; Mismatches 37; Indels 18; Gaps 3;

QY 3 COLSILLILSCSVDSFGEILP-----QPSNEVNLDSKTIGELGWIISPSHG 52
 DB 4 CEVREFLL-----QFGEFLPLTAWTGDCSHVSNOVLLDTSTVMGELGRTYPLMGW 56
 QY 53 EISGVDEHYTPRTYQVCNVMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDQNSIPV 112
 DB 57 DATTEDEHNRRIHYTYQVCNVMDSQNNMLRTNMVPRNSAQKIYVELKFTLRDQNSIPV 116
 QY 113 LGCTKETPFLYMEEDDHGKFKREHQTIDITIAADESFQMDLGRILKLTNLEIREV 172
 DB 117 LGCTKETPFLYMEEDDHGKFKREHQTIDITIAADESFQMDLGRILKLTNLEIREV 176
 QY 173 PYNRKGFYLAEDVACVALYSVRVYFKKCPFTVKNLAMPDTPV-MDSQSLVEYRGSCV 231
 DB 177 PIERKGFYLAEDVACVALYSVRVYFKKCPFTVKNLAMPDTPV-MDSQSLVEYRGSCV 236
 QY 232 NNSKEDPPRMKCTEGEMLVPIGKSCNAGYE 265
 DB 237 KSEERDTPKTLGADGDLVPLGRCICTGTGEE 270

RESULT 4

ID R85936 standard; Protein: 986 AA.
 AC R85936;
 DT 14-FEB-1996 (first entry)
 DE Protein tyrosine-kinase bprk7.

[illegible]

QY 127 SDDHGKVFREHQFTKIDTIADESEFTQMDIGDRILKINTEIREVGVNKKGGFYLAPOV 186

QY	187	GACALVALSVRRFYKCPPTVYNKLAMFPDYV-MQSLSLVEVRGSCVNNSKKEDDPPRMICS	245
		: : : : :	
Db	189	GACIALVASVFRRFKCPLTVRNLAQFPPTINGADTSLSLVEVRGSCVNNSKEKDVPKMYCG	248
QY	246	TEGEWLVPIGRKCSNAGYEERGFMCQ	271
		:	
Db	249	ADGEMLVPIGCNLGNAGHERSGECQ	274
RESULT	6		
W71628			
ID	W71628	standard; Protein; 877 AA.	
AC	W71628:		
DT	25-NOV-1998	(first entry)	
DE	Mouse Bsk receptor-like tyrosine kinase.		
KM	Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neoplasm;		
FW	neurodegenerative disease; limbic system neuron regeneration;		
RN	chromosomal abnormality; degenerative growth; development disorder:		

OS Mus SP.
PN US814479-A.
PD 29-SEP-1998.
PF 11-JUN-1996; 673789.
PR 04-JAN-1994; US-177812.
PR 11-JUN-1996; US-673789.
PA (KROM/) KROMER L F.
PA (SCHU/) SCHULZ N T.
PA (MOUD/) WOUDE G F V.
PA (ZHOU/) ZHOU R.
PI Kromer LF, Schulz NT, Woude GFV, Zhou R;
DR WPI; 98-541751/46.
DR N-PSDB; V58192.

Isolate nucleic acid sequence encoding protein - used in Bsk
nucleic acid probes, used in detecting alterations in level of Bsk
messenger-RNA in biological samples isolated from mammal afflicted
with disease
Claim 1; Fig 2; 72pp: English.
The present sequence represents mouse Bsk, which is a receptor-like
tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in
Bsk nucleic acid probes, which can be used in detecting alterations in
the level of Bsk messenger-RNA (mRNA) in biological samples isolated
from a mammal afflicted with a disease, such as neurodegenerative
diseases or disorders and neoplasms. The nucleic acid sequence can also
be delivered into the limbic system of patients with limbic system
neurodegenerative disease, disorder or injury, to promote or enhance
limbic system neuron regeneration or growth. Such neurodegenerative
diseases include: chromosomal abnormalities, degenerative growth and
development disorders, viral infections, bacterial infections, brain
injuries, neoplastic conditions, Alzheimer's disease, epilepsy,
schizophrenia, or stroke and cerebral ischemia.
Sequence 877 MA;

Query Match	67.5%	Score	990	DB	1	Length	877
Best Local Similarity	66.28%	Pred. No.	9e-94				
Matches 1/4; Conservative	44;	Mismatches	41;	Indels		Gaps	2;

Qy	10	ILISCVLDSFGBLLPOPEENVLNLSDKRIOELGMIWSPHSGMEISGVEHNTPTRTYQ	69
Db	46	ILICCAALT-----LASPENEVLNLSDKRYMGDLWLAPKKGWEEIEVDENAPLHTTYQ	102
Qy	70	VCNVADHSQNMWLRITNWPRNSAOKIYVELFTLRDNCNSIPLYLGTCKETFNLYMESDD	129
Db	103	VCKVMEQNMWMLLTISNIGASRIFFELKFLTRDNCNSLPGLGATCKEKFNNYIESDD	162
Qy	130	DHGVEFEHQTKIDTIAADSEFFQMDLGDHLLNLNFIIRVGVYNNKKGYLAFQDYGAC	189
Db	163	ENGSRKIKENQIKIDTIAADSEFFELDGDHVMKLNIEVRVGYPLSKKGYLAFQDYGAC	222
Qy	190	VALVSVRYYEKKCFEPTVNLAMFDTVP--MDSQSLVEYRSGCVNNSKEEPPRNYCSTEG	248
Db	223	IALVSVRYYEKKCPVYVHNLAIFFDTIIGDSSQLLEYSQSCVNHSTYDDPPKHCASAG	282
Qy	249	EWLYPIGKCSNAGTEERGFNCQ 271	
Db	283	EWLYPIGKCMCKAGTEERKNGTCQ 305	

RESULT	7	
ID	W83147	
AC	W83147;	
DT	11-FEB-1999	(first entry)
DE	Ret receptor tyrosine kinase Ehk-1.	
KW	Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection;	
KW	neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor	
KW	binding protein; BDNF; Nt-3; diagnosis.	
OS	Rattus sp.	
PN	US5843749-A.	
PD	01-DEC-1998.	
PE	06-JUN-1995; 469537.	
PR	17-MAR-1995; US-406247.	
PR	26-JUL-1991; US-736559.	
PR	28-OCT-1993; US-144932.	
PR	06-JUN-1995; US-469537.	
PI	(REGGE-) REGENERON PHARM INC.	
PI	Malsompierre PC, Mastakowski P, Yancopoulos GD;	
DR	WPI: 99-044584/04.	
PT	DNA encoding receptor tyrosine kinase proteins - and corresponding	
PT	proteins	
PS	Example: Fig 22; 194pp; English.	
CC	The present invention describes nucleic acid molecules for ror-1,	
CC	ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins	
CC	Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor	

CC tyrosine kinases. The present sequence represents rat Etk-1.
SQ Sequence 1005 AA;

Query Match	67.4%	Score 988	DB 1	Length 1005
Best Local Similarity	66.2%	Pred. No. 1.8e-93		
Matches 1/4; Conservative	44;	Mismatches	41;	Indels 4; Gaps 2;

[illegible]

```

RESULT      8
ID          R97853 standard; Protein: 928 AA.
AC          R97853;
DE          05-JAN-1997 (first entry)
KW          Rat REK7 eph-related tyrosine kinase receptor; AL-1; ligand;
OS          neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis
FH          Rattus sp.
FT          Key
FT          Location/Qualifiers
FT          peptide
FT          1..57
FT          /label= Sig_peptide
FT          58..928
FT          /label= Mat_protein
FT          58..462
FT          domain
FT          /label= Extracellular_domain
PN          M09613518-A1.
PD          09-MAY-1996.
PE          26-OCT-1995; U14016.
PR          27-OCT-1994; US-330128.
PR          07-JUN-1995; US-486449.
PA          (GENTH ) GENENTECH INC.
PI          Caras IM, Winslow JW;
DR          WPI: 96-239448/24.
DR          NP-PSDB: T18893.
PT          AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in
PT          treatment and diagnosis of neuronal disorders and
PT          angiogenesis-related conditions.
PS          Example 1; Page 50-53; 75pp; English.
CC          Rat REK7 (R97853) is an eph-related tyrosine kinase receptor, for
CC          which AL-1 (see also M97854) is a ligand. Its amino acid sequence
CC          was deduced from a cDNA clone (T18893) isolated from a hippocampus
CC          cDNA library. An REK-1g6 fusion was used to screen cultured cell
CC          lines for tyrosine expression of REK-binding activity. Primers
CC          (see also T4332-83) based on peptide sequences (R97856-59) of
CC          isolated ligands were used to amplify human breast carcinoma BT20
CC          cell cDNA, and an amplified fragment was used to screen a human
CC          foetal brain cDNA library, leading to the isolation of AL-1 cDNA
CC          (T18897).
SC          Sequence      928 AA:

```

Query Match	67.3%;	Score 987;	DB 1;	Length 928
Best Local Similarity	66.2%;	Pred. No. 2e-93;		

Matches 174; Conservative 44; Mismatches 41; Indels 4; Gaps 2;

```
QY 10 LLSGSLVDSFGELIPQPSNEVNLDSKTIQGEIGWISYPSHGHEEISGDEHTPIRTYO 69
DB 46 LLLCALALRT---LLASPSNEVNLDSRTVLGDDGWIAPFRKNGWEEIGEVDENTPPIHTYQ 102
QY 70 VCNVMDHSONNMLRTNWPBRNSAQKIYVELKFTLRDCNSIPVLATGCKETFNLYMESDD 129
DB 103 VCKVMEQNNMNLTLWSINEGASRIFIELKFTLRDCNSLPGGLGCKETFNMYIESDD 162
QY 130 DHGVCFREHQFTKIDTIADESFTQMDLDRILKLTETIREVGPVKKGFYLAFOGVAC 189
DB 163 ENGRNIKEQYIKIDTIADESFTLEDLDRVAKLTETVRYDVGPILSKRGFYLAFOGVAC 222
QY 190 VALVSRYVEFKCPFTVKNLAMPDTPV--MDSQSLVEVSGSCVNNKDEDPNRYCSTEG 248
DB 223 IALVSRYVYKKCPSVYRLALAFPPDTITGADSSQLLEVSGSCVNSHVTDPDMHCSAEG 282
QY 249 EWLVPVIGKCMCAGYEERGFMCQ 271
DB 283 EWLVPVIGKCMCAGYEERKNGTCQ 305
RESULT 9
R85090
ID R85090 standard; Protein: 991 AA.
AC R85090:
DT 16-APR-1996 (first entry)
DE EPH-like receptor protein tyrosine kinase HEK7.
KW EPH-like receptor protein tyrosine kinase; PTK; HEK7;
KM human eph-like kinase; therapy; diagnosis; vector; antibody.
OS Homo sapiens.
PN MO9528484-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04681.
PR 15-APR-1994; US-229509.
PA (AMGE-) AMGEN INC.
PI Fox GM, Jing S, Welcher AA;
DR WPI: 95-373799/48.
DR N-PSDB: T02947.
PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -
PT and related vectors, host cells, proteins, antibodies etc., used
PT diagnostically and therapeutically to modulate receptor activation
PT or prodn.
PS Claim 18: Page 54-57; 133pp; English.
CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
CC HEK8 and HEK11 (R85089-92), respectively, were identified following
CC isolation of their encoding cDNAs (T02946-49) from a human foetal brain
CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8.
CC HEK11 shows no homology to any known EPH-like receptor. Recombinant
CC HEK receptors (or their soluble extracellular domains) are produced by
CC expression of encoding sequences in procarvotic or eucaryotic host
CC cells, and are used to produce antibodies (utilised in diagnostic
CC assays), or to identify and purify ligands for HEK receptors, or
CC therapeutically to modulate the activation of cell-associated
CC receptors. Soluble HEK7 receptor may primarily affect
CC proliferation and/or differentiation of brain cells.
CC pancreatic cells.
SQ Sequence 991 AA;
```

```
QY 130 DHGVCFREHQFTKIDTIADESFTQMDLDRILKLTETIREVGPVKKGFYLAFOGVAC 189
DB 137 QNGRNIKENQYIKIDTIADESFTLEDLDRVAKLTETVRYDVGPILSKRGFYLAFOGVAC 196
QY 190 VALVSRYVEFKCPFTVKNLAMPDTPV--MDSQSLVEVSGSCVNNKDEDPNRYCSTEG 248
DB 197 IALVSRYVYKKCPSVYRLALAFPPDTITGADSSQLLEVSGSCVNSHVTDPDMHCSAEG 256
QY 249 EWLVPVIGKCMCAGYEERGFMCQ 271
DB 257 EWLVPVIGKCMCAGYEERKNGTCQ 279
RESULT 10
R85092
ID R85092 standard; Protein: 998 AA.
AC R85092:
DT 16-APR-1996 (first entry)
DE EPH-like receptor protein tyrosine kinase HEK11.
KW EPH-like receptor protein tyrosine kinase; PTK; HEK11;
KM human eph-like kinase; therapy; diagnosis; antibody; vector.
OS Homo sapiens.
PN MO9528484-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04681.
PR 15-APR-1994; US-229509.
PA (AMGE-) AMGEN INC.
PI Fox GM, Jing S, Welcher AA;
DR WPI: 95-373799/48.
DR N-PSDB: T02949.
PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -
PT and related vectors, host cells, proteins, antibodies etc., used
PT diagnostically and therapeutically to modulate receptor activation
PT or prodn.
PS Claim 18: Page 71-75; 133pp; English.
CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
CC HEK8 and HEK11 (R85089-92), respectively, were identified following
CC isolation of their encoding cDNAs (T02946-49) from a human foetal brain
CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8.
CC HEK11 shows no homology to any known EPH-like receptor. Recombinant
CC HEK receptors (or their soluble extracellular domains) are produced by
CC expression of encoding sequences in procarvotic or eucaryotic host
CC cells, and are used to produce antibodies (utilised in diagnostic
CC assays), or to identify and purify ligands for HEK receptors, or
CC therapeutically to modulate the activation of cell-associated
CC receptors.
SQ Sequence 998 AA;
```

Query Match 63.3%; Score 927.5; DB 1; Length 998;
Best Local Similarity 68.4%; Pred. No. 3.2e-87;
Matches 171; Conservative 39; Mismatches 37; Indels 3; Gaps 2;

```
QY 25 QPSNEVNLDSKTIQGEIGWISYPSHGHEEISGDEHTPIRTYOVCNVMHSONNMLRT 84
DB 28 QAKAEVLLDSKRAQOTELEMISSPPNGWEEISGLDENHTPIRTYOVCVMEPNQNNMLT 87
QY 85 NNVPBRNSAQKIYVELKFTLRDCNSIPVLATGCKETFNLYMESDDDHGKPFREHOFTRKD 144
DB 88 NWISKGNMQRIVELKFTLRDCNSLPGVLGCKETFNLYTETDVTGNNIRENNLYVKID 147
QY 145 TIADESFTQMDLDRILKLTETIREVGPVKKGFYLAFOGVACVALVSRYVEFKCPF 204
DB 148 TIADESFTQMDLGRKKMLKLTETVREIGPLSKRGFYLAFOGVACIALVSRYVYKKCMS 207
QY 205 TYKNLAMPDTPV--MDSQSLVEVSGSCVNNKKE--EDPPRYCSTEGEVLVPIGKSCNA 261
DB 208 ILENLALFPDVTGSEFSLVEVGTGVSADEEENAPRMHCSAEGEVLVPIGKICKCA 267
QY 262 GYEEERGFMCQ 271
```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 21:51:35 ; Search time 71.69 seconds
(without alignments)
212.770 Million cell updates/sec

Title: US-09-104-340-1

Perfect score: 1200
Sequence: 1 WEISGVDEHYTPIRTYQC.....VPIKCSNAGYEERGFMCQ 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

SPTREMBL_12.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	884.5	74.5	985	13	Q91694 xenopus lae
2	894.5	74.5	986	13	Q91845 xenopus lae
3	862.5	71.9	993	13	Q42422 gallus gall
4	838.5	69.9	880	13	Q73879 brachydanio
5	755.5	63.0	981	13	Q13146 brachydanio
6	708	59.0	1055	4	Q43477 homo sapien
7	691.5	57.6	985	13	Q91571 xenopus lae
8	676.5	56.4	943	4	Q43569 homo sapien
9	676.5	56.4	973	4	Q95143 homo sapien
10	676.5	56.4	984	4	Q95142 homo sapien
11	663	55.2	974	13	Q91735 xenopus lae
12	644	53.7	988	11	Q07498 gallus gall
13	589	49.1	938	11	Q60659 mus musculu
14	563.5	47.0	902	13	Q91736 xenopus lae
15	541.5	45.1	952	13	Q07494 gallus gall
16	509	42.4	976	13	Q73878 brachydanio
17	464	38.7	1014	11	Q08644 mus musculu
18	460	38.3	1006	4	Q15197 homo sapien
19	379.5	31.6	1035	5	Q9XZL6 drosophila
20	379.5	31.6	1080	5	Q9Y1J0 drosophila

21	369.5	30.8	1019	5	Q96435 drosophila.
22	333.5	27.8	871	13	Q73875 brachydanio
23	280	23.3	815	13	Q57458 xenopus lae
24	241	20.1	1122	5	Q61460 caenorhabdi
25	194.5	16.2	773	13	Q91626 xenopus lae
26	194	16.2	893	5	Q9Y1X3 ephydaria f
27	89.5	7.5	668	10	Q65616 arabidopsis
28	88.5	7.4	413	2	Q05989 staphylococ
29	87.5	7.3	788	13	Q07012 xenopus lae
30	86.5	7.2	305	2	Q32378 methylobacti
31	86	7.2	919	5	Q21477 caenorhabdi
32	85.5	7.1	347	5	Q18395 caenorhabdi
33	84.5	7.0	865	10	Q23617 arabidopsis
34	84.5	7.0	3110	4	Q93022 homo sapien
35	82.5	6.9	369	2	Q50966 borrelia bu
36	81.5	6.8	630	5	Q16366 caenorhabdi
37	81	6.8	573	2	Q23431 helicobacte
38	80.5	6.7	684	6	P79101 bos taurus
39	80	6.7	1436	3	Q07527 saccharomyc
40	79.5	6.6	570	5	Q17698 caenorhabdi
41	78.5	6.5	1419	5	Q9Y1L5 plasmodium
42	78	6.5	1321	4	Q75129 homo sapien
43	77	6.4	324	5	Q97397 phaeton coc
44	77	6.4	806	2	Q9ZJ63 helicobacte
45	76.5	6.4	336	2	Q66912 aquilex aeo

ALIGNMENTS

RESULT 1
ID Q91694 PRELIMINARY; PRT; 985 AA.
AC Q91694; 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-NOV-1999 (TRENBLREL. 12, Last annotation update)
DE TYROSINE-PROTEIN KINASE RECEPTOR PAC PRECURSOR (EC 2.7.1.112)
DE (PAGLIACCIO).
GN PAC.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidoae; Pipidae; Xenopodinae;
CC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NEURAL CREST;
RX MEDLINE; 95001564.
RA WINNING R.S., SARGENT T.D.;
RT "Pagliaccio, a member of the Eph family of receptor tyrosine kinase genes, has localized expression in a subset of neural crest and neural tissues in Xenopus laevis embryos."
RT Mech. Dev. 46:219-229(1994).
RL -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY (BY SIMILARITY). MAY PLAY A ROLE IN THE DIFFERENTIATION OF CRANIAL NEURAL CREST AND OTHER TISSUES.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: LOCALIZED EXPRESSION IN A SUBSET OF NEURAL CREST AND NEURAL TISSUES IN EMBRYOS.
CC -1- DEVELOPMENTAL STAGE: PRESENT TRANSDIENTLY IN VISCERAL ARCH 3. ALSO EXPRESSED IN THE PREBRAIN, RHOMERES R3 AND R5 OF THE HINDBRAIN AND IN THE PROMPHOS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPH FAMILY.
DR EMBL; I26069; AAA64464.1; -.
DR HSSP; P00523; 2PTK.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE EPH-LIKE RECEPTOR TYROSINE KINASE PRECURSOR (EC 2.7.1.112) (TYROSINE-
GN CEPHA7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
RN Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RP [1]
RC SEQUENCE FROM N.A.
RX TISSUE-EMBRYO;
MEDLINE: 98092111.
RA ARABUO M., NIETO M.A.;
RT "The expression of chick EphA7 during segmentation of the central and
RT peripheral nervous system.";
RL Mech. Dev. 68:173-177(1997).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN FAMILY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM, EXPRESSION IS
CC RESTRICTED TO PROSOMERES 1 AND 2 IN THE DIENCEPHALON AND ALL THE
CC RHOMBOMERES IN THE HINDRAIN DURING SEGMENTATION STAGES. LATER ON,
CC A SUPERIMPOSED PATTERN APPEARS THAT CORRELATES WITH THE FORMATION
CC OF SEVERAL AXONAL TRACTS. IN THE SOMITIC MESODERM, THE EXPRESSION
CC CORRELATES WITH SEGMENTATION AND THE GUIDANCE OF BOTH NEURAL CREST
CC AND MOTOR AXONS THROUGH THE SCLEROTOMES.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC EMBL: Y14211; CAA4643.1; -.
DR HSSP: P00523; 2PTK.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; pkinase; 1.
DR PFAM: PF00536; SAM; 1.
DR PFAM: PF01404; EPH_Lbd; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRINTS: PR00014; FNTYPEIT1.
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain.
FT SIGNAL 1 30
FT CHAIN 31 993
FT DOMAIN 31 551
FT TRANSMEM 552 572
FT DOMAIN 573 993
FT DOMAIN 67 116
FT DOMAIN 192 328
FT DOMAIN 329 438
FT DOMAIN 439 536
FT DOMAIN 536 889
FT DOMAIN 628 889
FT NP_BIND 634 642
FT DISULFID 74 109
FT BINDING 660 660
FT ACT_SITE 753 753
FT MOD_RES 786 786
FT CARBOHYD 343 343
FT POTENTIAL 410 410
SQ SEQUENCE 993 AA; 111366 MW; 656BBD17 CRC32;

Query Match 71.9%; Score 862.5; DB 13; Length 993;
Best Local Similarity 69.5%; Pred. No. 2,6e-76;
Matches 155; Conservative 39; Mismatches 26; Indels 3; Gaps 2;

QY 1 WEISGVDEHYTPIRTYOVCNVMDHSONNMLRTNWVPRNSAQKIYELKFTLRDCNSIPLV 60
DB 55 WEISGLDENITPIRTYOVCQWESNOMNKLRTNWLAKSNAQKIFVELKFTLRDCNSLPG 114
QY 61 VLTCKETENLYMESDDHGVKFRHQPFTKIDTIADESFTQMDLGRILKINTEIREV 120

DB 115 VLTCKETENLYXYEDYDTGRNIRENOYVKIDTIADESFTQDGERMKINTEIREV 174
QY 121 GPVNRKGFYAFODVACALVSVRVYFKKCPFTYVNLMEPDTPV -MOSQSLVEVRGSC 179
DB 175 GPUSKRGFYAFODVACALVSVKVYKRCWSIENLAFPUTVYGSEPSLSVEVRGTC 234
QY 180 VNNSKE -EDPPRMKSTEGEWLVPIGKSCSNAGYERGFMCQ 220
DB 235 VSSAEAEANSPRMKCSAGEWLVPIGKICICRAGYQOKDITCE 277
RESULT 4
ID 073879 PRELIMINARY; PRT; 880 AA.
AC 073879;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE EPH-LIKE RECEPTOR TYROSINE KINASE RTK4 (FRAGMENT).
GN RTK4.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprininae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RA COOKE J.E.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA COOKE J.E.; XU Q.; WILSON S.W.; HOLDER N.;
RL Dev. Genes Evol. 206:515-531(1997).
DR EMBL: AJ005030; CAA06303.1; -.
DR HSSP: P00523; 2PTK.
DR ZFIN: ZDB-GENE-990415-61; rtk4.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PFAM: PF01404; EPH_Lbd; 1.
DR PFAM: PF00069; pkinase; 1.
DR PFAM: PF00041; fn3; 2.
DR NON_TER 1 1
FT NON_TER 880 880
SQ SEQUENCE 880 AA; 98862 MW; 7C139606 CRC32;

Query Match 69.9%; Score 838.5; DB 13; Length 880;
Best Local Similarity 68.0%; Pred. No. 5e-74;
Matches 149; Conservative 36; Mismatches 33; Indels 1; Gaps 1;

QY 3 EISGVDEHYTPIRTYOVCNVMDHSONNMLRTNWVPRNSAQKIYELKFTLRDCNSIPLV 62
DB 1 EVSIMDEKINPIRTYOVCNVMDHSONNMLRTNWVPRNSAQKIYELKFTLRDCNSIPLV 60
QY 63 GTCKEFTNLYMESDDHGVKFRHQPFTKIDTIADESFTQMDLGRILKINTEIREV 122
DB 61 GTCKEFTNLYMESDDHGVKFRHQPFTKIDTIADESFTQMDLGRILKINTEIREV 120
QY 123 VNKRGFYAFODVACALVSVRVYFKKCPFTYVNLMEPDTPV -MDSQSLVEVRGSCV 181
DB 121 LSRAGFYAFODVACALVSVRVYFKKCPFTYVNLMEPDTPV -MDSQSLVEVRGSCV 180
QY 182 NSKEEDPPRMKSTEGEWLVPIGKSCSNAGYERGFMCQ 220
DB 181 HSBEQEVPRMKCGADGEWLVPIGKICICRAGYQOKDITCE 219
RESULT 5
ID 013146 PRELIMINARY; PRT; 981 AA.
AC 013146;

DT	01-JUL-1997 (TREMblrel. 04, Created)	
DT	01-JUL-1997 (TREMblrel. 04, Last sequence update)	
DT	01-NOV-1999 (TREMblrel. 12, Last annotation update)	
DE	EPH-LIKE KINASE 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ZEK1).	
GN	ZEK1.	
OS	Brachydanio rerio (zebrafish) (zebra danio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Cypriniformes; Cyprinidae; Cyprinidae; Rasbora; Danio.	
RA	BOVENKAMP D.E., GREER P.;	
RT	"Novel Eph-family receptor tyrosine kinase is widely expressed in the developing zebrafish nervous system.";	
RL	Dev. Dyn. 209:166-181(1997).	
CC	-1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. MAY PLAY A ROLE IN EARLY PATTERN FORMATION WITHIN THE DEVELOPING NERVOUS SYSTEM.	
CC	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.	
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE DEVELOPING ZEBRAFISH NERVOUS SYSTEM.	
CC	-1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.	
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.	
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.	
DR	EMBL; U89295; AAC60220.1; -.	
DR	HSSP; P00523; 2PTK.	
DR	ZFIN; ZDB-GENE-990415-58; zek1.	
DR	PROSITE; PS00107; PROTEIN KINASE.ATP; 1.	
DR	PROSITE; PS00109; PROTEIN KINASE.TYR; 1.	
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.	
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FALSE_NEG.	
DR	PFAM; PF00069; KINASE. 1.	
DR	PFAM; PF00536; SAM. 1.	
DR	PFAM; PF01404; EPH_Lbd. 1.	
DR	PFAM; PF00041; fn3. 2.	
DR	PRINTS; PR00109; TYRKINASE.	
DR	PRINTS; PR00014; FMYPEIII.	
KW	Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain.	
KW	Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain.	
ET	SIGNAL	1
ET	CHAIN	21
ET	DOMAIN	21
ET	TRANSMEM	546
ET	DOMAIN	567
ET	DOMAIN	64
ET	DOMAIN	192
ET	DOMAIN	326
ET	DOMAIN	438
ET	DOMAIN	439
ET	DOMAIN	626
ET	NP_BIND	632
ET	DISULFID	71
ET	BINDING	658
ET	ACT_SITE	751
ET	MOD_RES	784
ET	CARBOHYD	340
ET	CARBOHYD	410
ET	CARBOHYD	435
ET	CARBOHYD	485
ET	VARIANT	141
EQ	SEQUENCE	981 AA; 109654 MW; 10D38182 CRC32; S -> N.

```
Query Match      63.0%; Score 755.5; DB 13; Length 981;
Best Local Similarity 61.4%; Pred. No. 8e-66;
Matches 137; Conservative 37; Mismatches 46; Indels 3; Gaps 1

QY    1 WEISGVDEHYPIRFRYYQCVMNMDHSDQNMMWLRPNRSAGKIIVELFTLIDCSIPL 60
||||| :|| :|||||:::||||| : | ||:::||:|||||:::
```

```

Db 52 WEELSYVNDERINIPARTYOVCVMEANQNMRLTSLIQRGAQRYYVEIKFTFLDQNSLP6 111
Qy 61 VLGTCKEFTENLYWESDDHGV--KREHOFTKIDTIAADESFTOMDLCDRLIKLNTET 117
Db 112 VPGCKEFTENLYWESDDHGV--KREHOFTKIDTIAADESFTOMDLCDRLIKLNTET 117
Qy 118 REYGVNKKGGYLAFFQYDGVCAVLAIVSYRVYFKKPPFYKULAMPDPTVYPMDSQSLVEYRG 177
Db 172 RDISGLSRGYYLAFFQDGVCAVLAIVSYRVYFKKPPFLVNLAMPDPTVYTGDSALVEYRG 231
Qy 178 SCVNNKREDDPRMYCSTEGEWLPIKQSCQNAQYEEGRFMCQ 220
Db 232 TCVEADEELBGPRIKFCSDADGGWLVPIGCVACRPFEEYDGHQ 274

```

RESULT	6			
043477				
ID	043477	PRELIMINARY:	PRT:	1055 AA.
AC	043477;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	PROTEIN-TYROSINE KINASE EPHB2V.			
GN	EPHB2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homnidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 96154673.			
RA	IREGAKI N., TANG X.X., LIU X.G., BIEGEL J.A., ALLEN C., YOSHIOKA A			
RA	SULMAN E.P., BRODEUR G.M., PLEASURE D.E.;			
RT	"Molecular characterization and chromosomal localization of DRT			
RT	(EPH3) a developmentally regulated human protein-tyrosine kinases			
RT	gene of the EPH family.";			
RL	Hum. Mol. genet. 4:2033-2045(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	TANG X.X., PLEASURE D.E., IREGAKI N.;			
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF025304; AAB94602.1; .			
DR	HSSP; P00523; 2PTR.			
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR. 1.			
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V.1; 1.			
DR	PROSITE; PS00791; RECEPTOR_TYR_KIN_V.2; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP. 1.			
DR	PFAM; PF01404; EPH_1bd; 1.			
DR	PFAM; PF00041; fn3; 2.			
DR	PFAM; PF00069; pkinase; 1.			
DR	PFAM; PF00536; SAM; 1.			
DR	PRINTS; PR00014; ENTPEPIT.			
DR	PRINTS; PR00109; TYRKINASE.			
KW	Tyrosine-protein kinase			
SO	SEQUENCE 1055 AA; 117492 MW; EAF28155 CRC32;			

Query Match	Similarity	59.0%	Score 708	DB 4	Length 1055
Best Local	Similarity	55.7%	Pred. No. 4e-61		
Matches	127	Conservative	49	Mismatches	44
				Indels	8
				Gaps	4
QY	1	WEEISGVDEHYPIRTYOVCNVMDSNNMWTNTMVPNRSQAKIYELKFTLRDCNSIPL	60		
DB	43	WEEVSQYGDENMNTIRTYOVCNVESSQNNMLTKFIRRGARIRIHVKMFVSVRDCSSIS	102		
QY	61	VLTGKEKFEINLYMSSDDDHGK----FHROFTIIDIADDESTQMDLGRILKATTE	116		
DB	103	YPSGSKETEFNLYYADAFDSATKEPPNMENMWPVVDITADDESSQYDLGRVKNINTE	162		
QY	117	IREVVPVNNKGFYLFADPDGACVALVSVRYVYKCPFTKYNLAMPDPVP--MDSSIVLEV	175		
DB	163	VASFQPVASGSLYLFQDYGGCMSLAAKVFTRKCPRIIONGAIQETIOLSGAESTLVAA	222		
QY	176	RGSVCNNKNEEDP--RMYCSTEGEWLVPIGKSCSNAGYE--ERGFMCQ	220		

DB	223	RGSCIANAEVDYPRKLYCNGDGEMLVPIGRCKMCKAGFEAVENGTCYR	270
RESULT	7		
ID	091571	PRELIMINARY;	PRT; 985 AA.
AC	091571;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)		
DE	EPHRIN TYPE-B RECEPTOR XEK PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR XEK).		
GN	XEK.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;		
OC	Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; Xenopodinae;		
OC	Xenopus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 95215070.		
RA	JONES T.L., KARAVANOVA I., MAENO M., ONG R.C., KUNG H.-F., DARR I.O.;		
RT	"Expression of an amphibian homolog of the Eph family of receptor tyrosine kinases is developmentally regulated."		
RL	Oncogene 10:1111-1117(1995).		
CC	-1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. MAY PLAY A ROLE IN THE DEVELOPMENT OR FUNCTION OF THE CENTRAL NERVOUS SYSTEM.		
CC	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	-1- DEVELOPMENTAL STAGE: MATERNALLY EXPRESSED, IT DECREASES AT MID BLASTULA TRANSITION AND REAPPEARS AT LATE NEURULATION. EXPRESSED AT HIGHER LEVELS IN THE ANTERIOR AND DORSAL REGIONS OF EMBRYONIC STAGES 16, 24 AND 37. IN ADULT IT APPEARS TO BE UBQUITOUSLY EXPRESSED WITH HIGHER EXPRESSION IN BRAIN AND OVARY. EXPRESSION IN THE BRAIN, BRACHIAL ARCHES, TRIGEMINAL FACIAL GANGLION, AND THE RETINA OF SWIMMING TADPOLE STAGE OF DEVELOPMENT.		
CC	-1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.		
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.		
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.		
DR	EMBL; U14164; AAA74888.1; -.		
DR	HSSP; P00523; 2PTK.		
DR	PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.		
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; FALSE_NEG.		
DR	PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.		
DR	PFAM; PF00041; fn3; 2.		
DR	PFAM; PF00069; pkinase; 1.		
DR	PFAM; PF00536; SAM; 1.		
DR	PFAM; PF01404; EPH_1bd; 1.		
DR	PRINTS; PR00109; TYRKINASE.		
FW	Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain.		
FT	SIGNAL	1	19
FT	CHAIN	20	985
FT	DOMAIN	6	12
FT	DOMAIN	20	542
FT	TRANSMEM	543	563
FT	DOMAIN	564	985
FT	DOMAIN	56	105
FT	DOMAIN	185	321
FT	DOMAIN	322	431
FT	DOMAIN	432	529
FT	DOMAIN	620	883
FT	NP_BIND	626	634
FT	DISULFID	63	98
FT	BINDING	652	745
FT	ACG_SITE	745	779
FT	MOD_RES	779	779
FT	CARBOHYD	336	336
FT	CARBOHYD	428	428
FT	POTENTIAL.		

FT	CARBOND	482	482	POTENTIAL.
SO	SEQUENCE	985 AA;	110104 MM;	2416A8E9 CRC32;
	Query Match	57.6%;	Score 691.5;	DB 13; Length 985;
	Best Local Similarity	55.1%;	Pred. No. 1.5e-59;	
	Matches 125;	Conservative 47;	Mismatches 48;	Indels 7; Gaps 4;
OY	1 WEISGVDEHYTPRTIYOVYCVNMDHSONWMLRTMWPVPRNSAQKIYVELKFTLRDCNSIPL 60			
Db	44 WEEVSYGDEINLTIRTYOVYCVNVEFGKQNMWLTFTFIPRGHRYVEKRFYRDCSSLPN 103			
OY	61 VLGCTKEPFLNYEYSDDDHGVK---FREQHFKIDPIADSEFTQMDLGRILKLTNTE 116			
Db	104 VPGSCKEFTFNLYIETDSDVIAITKKSAPFSEAPYLKVDITADESFSOVDGRGLMKVNTTE 163			
OY	117 IREVPVARKKGFYLAFOYGVACVALVSYRYVEFKKCPFTVKMLIAFPDTPV-MDSQSLVEY 175			
Db	164 VRSFEPFLRSGFYLAFOYGVACMSLTSRYVFFKEMPSVYQULVYFPEIMGAEESTSLVIA 223			
OY	176 RGSVYNNKSEDDPP-RMYCSTEGEMLVPIGKSCNAGYE-ERGFMCQ 220			
Db	224 RGTCTPNAEYVDVPIKLYCNGDGEWMPVIGKCTCKAGYEPEPNHYVCK 270			
RESULT	8			
O43569	PRELIMINARY;	PRT;	943 AA.	
ID	O43569			
AC	O43569;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	EPH-LIKE RECEPTOR TYROSINE KINASE HEPHB1C			
DE	(EPH-LIKE RECEPTOR TYROSINE KINASE HEPHB1D).			
GN	EPHB1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-KIDNEY;			
RA	STEIN E., SCHOECKMANN H.O., DANIEL T.O.;			
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF037333; AAB94627.1;			
DR	EMBL; AF037334; AAB94628.1;			
DR	HSSP; P08631; 2HKC.			
DR	PFAM; PF00041; fn3. 2.			
DR	PFAM; PF00069; kinase; 2.			
DR	PFAM; PF00536; SAM; 1.			
DR	PFAM; PF01404; EPH_1bd; 1.			
DR	PRINTS; PR00109; TYRKINASE.			
DR	PRINTS; PR00014; FNTYPEIIT.			
SO	SEQUENCE 943 AA; 105291 MM; C4C78A21 CRC32;			
	Query Match	56.4%;	Score 676.5;	DB 4; Length 943;
	Best Local Similarity	54.2%;	Pred. No. 4.3e-58;	
	Matches 123;	Conservative 45;	Mismatches 52;	Indels 7; Gaps 4;
OY	1 WEISGVDEHYTPRTIYOVYCVNMDHSONWMLRTMWPVPRNSAQKIYVELKFTLRDCNSIPL 60			
Db	42 WEEVSYGDEINLTIRTYOVYCVNVEFGKQNMWLTFTFIPRGHRYVEKRFYRDCSSLPN 101			
OY	61 VLGCTKEPFLNYEYSDDDHGVK---FREQHFKIDPIADSEFTQMDLGRILKLTNTE 116			
Db	102 VPGSCKEFTFNLYIETDSDVIAITKKSAPFSEAPYLKVDITADESFSOVDGRGLMKVNTTE 161			
OY	117 IREVPVARKKGFYLAFOYGVACVALVSYRYVEFKKCPFTVKMLIAFPDTPV-MDSQSLVEY 175			
Db	162 VRSFEPFLRSGFYLAFOYGVACMSLTSRYVFFKEMPSVYQULVYFPEIMGAEESTSLVIA 221			
OY	176 RGSVYNNKSEDDPP-RMYCSTEGEMLVPIGKSCNAGYE-ERGFMCQ 220			

DB 222 RGTCTPNAEEVDVPIKLYCNGDGMVPIGRCTCKRGPYEPNSVACK 268

RESULT 9
095143 PRELIMINARY; PRT; 973 AA.

AC 095143: 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE EPH-LIKE RECEPTOR TYROSINE KINASE HEPH1B.
GN EPH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP TISSUE=KIDNEY;
RC STEIN E., SCHOCKLMANN H.O., DANIEL T.O.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR HSSP; P00523; 2PTK.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor; Kinase.

Query Match 56.4%; Score 676.5; DB 4; Length 973;
Best Local Similarity 54.2%; Pred. No. 4.5e-58;
Matches 123; Conservative 45; Mismatches 52; Indels 7; Gaps 4;

QY 1 WEISGVDEHYPIRTYQVCNVDHSONMNLRTNVPNRSACKIYELKFTLRDCNSIPL 60
DB 31 WEVSQYDENLNTIRTYQVCNVEPNQNMWMLTFTINRGAHRIYSEMRFTYRDCSSLPN 90
QY 61 VLGCTKEFTNLYMESDDDHGK----FRHOFTKIDITIADESFQMDLGDRIKLNT 116
DB 91 VPGSCKEFTNLYYETDVIATKKSAPFSEAPLKYDTIADESFQVDFRGRLEKVNTE 150
QY 117 IREVGPNKGFYLAFOADGACVALSVRYVFEKCFPTVKNLAMPDPTP-NDOSLVEV 175
DB 151 VRSFGPLTRNGEYLAFOADGACMILSVRYVFEKCFPSIYNFAVEFTMGASTSLVIA 210
QY 176 RSCVNSKEDDP-RLMYCSTEGEWLVPIGKCSNAGYE-ERGFMCQ 220
DB 211 RGTCTPNAEEVDVPIKLYCNGDGMVPIGRCTCKRGPYEPNSVACK 257

RESULT 10
095142 PRELIMINARY; PRT; 984 AA.

AC 095142: 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE EPH-LIKE RECEPTOR TYROSINE KINASE HEPH1.
GN EPH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA STEIN E., HUYNH-DO U., LANE A., CERRETTI D.P., DANIEL T.O.;
RT "Nck recruitment to Eph receptor, Eph1/BLK, couples ligand activation to c-Jun kinase.";
RL J. Biol. Chem. 0:0-0(1997).
DR HSSP; P00523; 2PTK.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor; Kinase.

SQ SEQUENCE 984 AA; 110041 MW; DF5CBED3 CRC32;

Query Match 56.4%; Score 676.5; DB 4; Length 984;
Best Local Similarity 54.2%; Pred. No. 4.6e-58;
Matches 123; Conservative 45; Mismatches 52; Indels 7; Gaps 4;

QY 1 WEISGVDEHYPIRTYQVCNVDHSONMNLRTNVPNRSACKIYELKFTLRDCNSIPL 60
DB 42 WEVSQYDENLNTIRTYQVCNVEPNQNMWMLTFTINRGAHRIYSEMRFTYRDCSSLPN 101
QY 61 VLGCTKEFTNLYMESDDDHGK----FRHOFTKIDITIADESFQMDLGDRIKLNT 116
DB 102 VPGSCKEFTNLYYETDVIATKKSAPFSEAPLKYDTIADESFQVDFRGRLEKVNTE 161
QY 117 IREVGPNKGFYLAFOADGACVALSVRYVFEKCFPTVKNLAMPDPTP-NDOSLVEV 175
DB 162 VRSFGPLTRNGEYLAFOADGACMILSVRYVFEKCFPSIYNFAVEFTMGASTSLVIA 221
QY 176 RSCVNSKEDDP-RLMYCSTEGEWLVPIGKCSNAGYE-ERGFMCQ 220
DB 222 RGTCTPNAEEVDVPIKLYCNGDGMVPIGRCTCKRGPYEPNSVACK 268

RESULT 11
091735 PRELIMINARY; PRT; 974 AA.

AC 091735: 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR) (TCK).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96069901.
RA SCALES J.B., WINNING R.S., RENAUD C.S., SHEA L.J., SARGENT T.D.;
RT "Novel members of the eph receptor tyrosine kinase subfamily expressed during Xenopus development.";
RL Oncogene 11:1745-1752(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY (BY SIMILARITY).
CC -1- CARLYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN PRE-SOMITIC MESODERM, CAUDAL SOMITES, MIDBRAIN, AND CEMENT GLAND. MOST ABUNDANT IN ADULT BRAIN, EYE, HEART, LUNG AND OVARY. LOWER LEVELS IN INTESTINE, KIDNEY, OVIDUCT AND PHARYNX.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR EMBL; I43620; AA93526.1; -.
DR HSSP; P00523; 2PTK.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00069; pkinase; 1.
DR PFAM; PF00536; SAM; 1.
DR PFAM; PF01404; EPH_lbd; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR00014; ENTRYPELTI.
DR Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain; SIGNAL 1 16 POTENTIAL.

```
FT CHAIN 17 974 EPHRIN TYPE-B RECEPTOR.
FT DOMAIN 17 534 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 535 555 POTENTIAL.
FT DOMAIN 556 974 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 53 102 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 178 315 CY8-RICH.
FT DOMAIN 316 423 FIBRONECTIN TYPE-III.
FT DOMAIN 424 520 FIBRONECTIN TYPE-III.
FT DOMAIN 609 872 PROTEIN KINASE.
FT NP_BIND 615 623 ATP (BY SIMILARITY).
FT DISULFID 60 95 BY SIMILARITY.
FT BINDING 641 641 ATP (BY SIMILARITY).
FT ACT_SITE 734 734 BY SIMILARITY.
FT MOD_RES 768 768 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CARBOHYD 330 330 POTENTIAL.
SQ SEQUENCE 420 420 POTENTIAL.
FT CARBOHYD 420 420 POTENTIAL.
SQ SEQUENCE 974 AA; 108263 MW; BD419F6D CRC32;

Query Match 55.2%; Score 663; DB 13; Length 974;
Best Local Similarity 53.5%; Pred. No. 9.5e-57;
Matches 122; Conservative 41; Mismatches 53; Indels 12; Gaps 5;

QY 1 WEISGVDEHYTPIRTYQVCNVMDSQNNMLRTMWPVNSAQKIYVELKFTLRDCNSIPL 60
DB 41 WEISGVDEANPRTITRYQVCNVRBNSQNNMLRTGFIHQDQVQRYVELKFTVRDCNSIPLN 100
QY 61 VLGTCKEFTNLYMESDDHGVK---FHQFTKIDITIADESFQMDLGRILKLTTE 116
DB 101 LRGCKEFTNLYMESDDHGVK---FHQFTKIDITIADESFQMDLGRILKLTTE 116
QY 117 IREGVPNKKGFYLAFOQVACALVSVRYEKKCFPTVKNLAMPDTPV-MDSQSLVEV 175
DB 157 IREGVPNKKGFYLAFOQVACALVSVRYEKKCFPTVKNLAMPDTPV-MDSQSLVEV 175
QY 176 RGSQVNSKEEDPP-RMYCSTEGEMVLVIGKCSNAGYEERG--FMQ 220
DB 217 PGTCIPNAVEYVPLKLCNGDGMVVPVGACTCAAGIEPAMKDTQCO 264

RESULT 12
Q07498 PRELIMINARY; PRT; 988 AA.
AC 007498;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1999 (Tremblrel. 01, Last sequence update)
DE TYROSINE KINASE CERK10 RECEPTOR (EC 2.7.1.112) (FRAGMENT).
GN CER10.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYO;
RX MEDLINE; 93288394.
RA SALJADI F.G., PASOUBLE E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed.";
RL Oncogene 8:1807-1813(1993).
DR EMBL; Z19061; CA79511.1; -.
DR HSSP; P00523; 2PTK.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PFAM; PF01404; EPH_Lbd; 1.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00536; SAM; 1.
DR PFAM; PF00069; PKinase; 1.
FT TRANSFERASE.
FT NON_TER 1
SQ SEQUENCE 988 AA; 109578 MW; C5CA9B7B CRC32;
```

```
Query Match 53.7%; Score 644; DB 13; Length 988;
Best Local Similarity 51.3%; Pred. No. 7.1e-55;
Matches 117; Conservative 48; Mismatches 51; Indels 12; Gaps 5;

QY 1 WEISGVDEHYTPIRTYQVCNVMDSQNNMLRTMWPVNSAQKIYVELKFTLRDCNSIPL 60
DB 34 WEISGVDEANPRTITRYQVCNVRBNSQNNMLRTGFIHQDQVQRYVELKFTVRDCNSIPLN 93
QY 61 VLGTCKEFTNLYMESDDHGVK---FHQFTKIDITIADESFQMDLGRILKLTTE 116
DB 94 LRGCKEFTNLYMESDDHGVK---FHQFTKIDITIADESFQMDLGRILKLTTE 116
QY 117 IREGVPNKKGFYLAFOQVACALVSVRYEKKCFPTVKNLAMPDTPV-MDSQSLVEV 175
DB 150 IREGVPNKKGFYLAFOQVACALVSVRYEKKCFPTVKNLAMPDTPV-MDSQSLVEV 175
QY 176 RGSQVNSKEEDPP-RMYCSTEGEMVLVIGKCSNAGYEER--FMQ 220
DB 210 PGTCIPNAVEYVPLKLCNGDGMVVPVGACTCAAGIEPAMKDTQCO 257

RESULT 13
Q06069 PRELIMINARY; PRT; 938 AA.
AC 06069;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1999 (Tremblrel. 01, Last sequence update)
DE TYROSINE KINASE CERK10 RECEPTOR (EC 2.7.1.112) (FRAGMENT).
GN CERK10 OR ETK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 95200798.
RA RUTZ J.C., CONLON F.L., ROBERTSON E.J.;
RT "Identification of novel protein kinases expressed in the myocardium
RT of the developing mouse heart.";
RL Mech. Dev. 48:153-164(1994).
DR EMBL; U11493; AA67925.1; -.
DR HSSP; P00523; 2PTK.
DR MSD; MG1:104770; Ephb3.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PFAM; PF01404; EPH_Lbd; 1.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00536; SAM; 1.
DR PFAM; PF00069; PKinase; 1.
FT NON_TER 1
SQ SEQUENCE 938 AA; 103996 MW; 2B01D2A0 CRC32;

Query Match 49.1%; Score 589; DB 11; Length 938;
Best Local Similarity 49.8%; Pred. No. 1.7e-49;
Matches 108; Conservative 45; Mismatches 54; Indels 10; Gaps 4;

QY 3 EISGVDEHYTPIRTYQVCNVMDSQNNMLRTMWPVNSAQKIYVELKFTLRDCNSIPL 62
DB 1 EISGVDEANPRTITRYQVCNVRBNSQNNMLRTGFIHQDQVQRYVELKFTVRDCNSIPLN 60
QY 63 GCKEFTNLYMESDDHGVK---FHQFTKIDITIADESFQMDLGRILKLTTE 118
DB 61 GCKEFTNLYMESDDHGVK---FHQFTKIDITIADESFQMDLGRILKLTTE 118
QY 119 EGVPNKKGFYLAFOQVACALVSVRYEKKCFPTVKNLAMPDTPV-MDSQSLVEV 177
DB 117 SFGLSKAGFYLAFOQVACALVSVRYEKKCFPTVKNLAMPDTPV-MDSQSLVEV 176
```

QY 178 SCVNSKEDPP-RMYCSTEGEWLPVIGKSCNAGYE 213
DB 177 ACIANAWEVSVPLKLYCNGDGEWMPVAGCATCATGHE 213

RESULT 14
QY1736 PRELIMINARY; PRT; 902 AA.

AC QY1736;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
DE EPH RECEPTOR TYROSINE KINASE (XELK) (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidoes; Pipidae; Xenopodinae;
OC Xenopus.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 96068901.
RA SCALES J.B., WINNING R.S., RENAUD C.S., SHEA L.J., SARGENT T.D.;
RT "Novel members of the eph receptor tyrosine kinase subfamily expressed
during Xenopus development.";
RL Oncogene 11:1745-1752(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY (BY
SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP + PROTEIN
TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRIO IN THE BRAIN AND
SPINAL CORD AND IN THE FIRST AND FOURTH VISCERAL ARCHES. MOST
ABUNDANT IN ADULT BRAIN, WITH LOWER LEVELS IN EYE, HEART, OVARY,
OVIDUCT, LUNG AND PHARYNX.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR EMBL; L43621; AAA93527.1; -.
DR HSSP; P00523; 2PTRK.
DR PROSITE; PS00107; PROTEIN KINASE_ATP. 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR. 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00069; pkinase; 1.
DR PFAM; PF00536; SAM; 1.
DR PFAM; PF01404; EPH_lbd; 1.
KW Receptor; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN <1 459 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 460 480 POTENTIAL.
FT DOMAIN 481 902 CYTOPLASMIC (POTENTIAL).
FT DOMAIN <1 21 IG-LIKE C2-TYPE DOMAIN (BY SIMILARITY).
FT DOMAIN 101 237 CYS-RICH.
FT DOMAIN 238 347 FIBRONECTIN TYPE-III.
FT DOMAIN 348 445 FIBRONECTIN TYPE-III.
FT DOMAIN 537 800 PROTEIN KINASE.
FT NP_BIND 543 551 ATP (BY SIMILARITY).
FT DISULFID ? 14 BY SIMILARITY.
FT BINDING 569 569 ATP (BY SIMILARITY).
FT ACT_SITE 662 662 BY SIMILARITY.
FT MOD_RES 696 696 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CARBOHYD 252 252 POTENTIAL.
FT CARBOHYD 344 344 POTENTIAL.
FT CARBOHYD 398 398 POTENTIAL.
SQ SEQUENCE 902 AA; 100850 MW; C096D006 CRC32;

Query Match 47.0%; Score 563.5; DB 13; Length 902;
Best Local Similarity 55.1%; Pred. No. Se-47; 34; Indels 7; Gaps 4;
Matches 102; Conservative 42; Mismatches 34; Indels 7; Gaps 4;

QY 43 KIYVELKFTLRDNCNSIPVLGTCKETFNLYMESPDDHGVK----FREHOFTKIDITIAAD 98
DB 2 RYIVEMRTVVDNCSSLRPVPGSKETFNLYYEIDNSINDNKISTFWMNSPLKADITIAAD 61

QY 99 ESFTOMDLDRIKILNTEIREVGVNKKGYFLAFODVAGVALVSVRYEKKCEPTVKNL 158
DB 62 ESFSQVDGGRIMKYNTEVRSFGPLTRSGFYLAFODYGACSKLSLVRFKKCPVYQNF 121

QY 159 AMEPTVP-MDSQSLVEVRSQVNSKEDPP-RMYCSTEGEWLPVIGKSCNAGYE-ER 215
DB 122 AVEFTMTGAESTLVIANGCITPNAEEVDVPIKLYCNGDEWMPVIGKCTCKAGYEEN 181

QY 216 GEMCO 220
DB 182 HVCCK 186

RESULT 15
QY07494 PRELIMINARY; PRT; 952 AA.

AC QY07494;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
DE CER6 PROTEIN (FRAGMENT).
GN CER6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN SEQUENCE FROM N.A.
RX TISSUE-BRAIN:
RX MEDLINE; 93288394.
RA SAUTAD F.G., PASQUALE E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
expressed.";
RL Oncogene 8:1807-1813(1993).
DR EMBL; Z19110; CA879526.1; -.
DR HSSP; P00523; 2PTRK.
DR PROSITE; PS00107; PROTEIN KINASE_ATP. 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR. 1.
DR PFAM; PF00536; SAM; 1.
DR PFAM; PF00069; pkinase; 1.
DR PFAM; PF01404; EPH_lbd; 1.
DR PFAM; PF00041; fn3; 2.
FT NON_TER 1
SQ SEQUENCE 952 AA; 105994 MW; D939D7D0 CRC32;

Query Match 45.1%; Score 541.5; DB 13; Length 952;
Best Local Similarity 45.4%; Pred. No. 7.7e-45;
Matches 103; Conservative 39; Mismatches 46; Indels 39; Gaps 5;

QY 1 WEISGVDEHYTPRTFYVCNVMDSQNNMLRTMVPNNSAQIKYVELKFTLRDNCNSIPL 60
DB 23 WEVSGYDENLMTIRTYOVCVNEEENQNNMLLTETINRGARHRITEKRFVYRDCSSLPN 82

QY 61 VLGTKEKFNLYMSSDDHGVK---FREHOFTKIDITIAADESTOMDLDRIKILNTE 116
DB 83 VPGSKETFNLYYTDVIAITKSAFTETAPYIKLVDTIADESPSQVDFGRIMK---- 139

QY 117 IREVPVNNKKGYFLAFODVAGVALVSVRYEKKCEPTVKNLAMEPDPVP-MDSQSLVEY 175
DB 139 -----GAEFFKCPVYQNFALFPEMTGAESTLVTA 170

QY 176 RQSVNSKEDPP-RMYCSTEGEWLPVIGKSCNAGYE-ERGFMCQ 220
DB 171 RGTCTPNAEEVDVPIKLYCNGDGEWMPVIGKCTCKAGYEENNAACR 217

Search completed: May 9, 2000, 22:31.07

Job time: 2372 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 21:52:09 ; Search time 49.21 Seconds

(without alignments)
136.153 Million cell updates/sec

Title: US-09-104-340-1

Perfect score: 1200
Sequence: 1 WEISGVDEHYTPIRRYQVC.....VPIKGCNAGYERGFMCQ 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	983	1	EPB3_HUMAN
2	1186	98.0	984	1	EPB3_RAT
3	1176.5	98.0	983	1	EPB3_MOUSE
4	1139	94.9	983	1	EPB3_CHICK
5	914.5	76.2	948	1	EPB6_RAT
6	914.5	76.2	1035	1	EPB6_MOUSE
7	910.5	75.9	986	1	EPB4_CHICK
8	905.5	75.5	986	1	EPB4_HUMAN
9	882.5	74.4	986	1	EPB4_MOUSE
10	866.5	72.4	877	1	EPB5_MOUSE
11	863.5	72.0	1005	1	EPB5_RAT
12	860.5	71.7	1037	1	EPB5_HUMAN
13	857.5	71.5	998	1	EPB7_MOUSE
14	856.5	71.4	998	1	EPB7_HUMAN
15	856.5	71.4	998	1	EPB7_RAT
16	831.5	69.3	1004	1	EPB8_MOUSE
17	825.5	68.8	1013	1	EPB8_CHICK
18	713	59.4	988	1	EPB2_CHICK
19	708	59.0	986	1	EPB2_HUMAN
20	706	58.8	993	1	EPB2_MOUSE
21	693.5	57.8	984	1	EPB1_RAT
22	688.5	57.4	984	1	EPB1_HUMAN
23	681	56.8	987	1	EPB2_COTUJA
24	637.5	53.1	977	1	EPB2_MOUSE
25	632	52.7	998	1	EPB3_HUMAN
26	627	52.2	976	1	EPB3_MOUSE
27	620	51.7	993	1	EPB3_HUMAN
28	574	47.8	1002	1	EPB5_CHICK
29	539	44.9	976	1	EPB1_HUMAN
30	478	39.8	987	1	EPB4_MOUSE
31	465	38.8	987	1	EPB4_HUMAN
32	460	38.3	1006	1	EPB6_HUMAN
33	88.5	7.4	982	1	MSHM_SAKEL
34	84.5	7.0	3110	1	IMA2_HUMAN

35	82.5	6.9	461	1	HMC5_ARATH
36	80	6.7	819	1	EPG2_YEAST
37	79.5	6.6	3106	1	IMA2_MOUSE
38	78.5	6.5	158	1	KRP5_KLULA
39	77.5	6.5	1634	1	DPOL_METUJA
40	77	6.4	806	1	SYL_HELPJ
41	76.5	6.4	1360	1	MSH6_HUMAN
42	75.5	6.3	1046	1	CHID_VIBFNU
43	74.5	6.2	427	1	CG23_YEAST
44	74.5	6.2	769	1	ITB2_PIG
45	74.5	6.2	771	1	ITB2_MOUSE

ALIGNMENTS

RESULT 1
EPB3_HUMAN STANDARD; PRT; 983 AA.
AC P29320:
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETKI) (HEK).
GN EPB3 OR ETK1 OR ETK OR HEK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RX MEDLINE: 92179233.
RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.,
RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed by human lymphoid tumor cell lines".
RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
RP [2]
RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
RX MEDLINE: 92147681.
RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A.,
RT "Isolation and characterization of a novel receptor-type protein tyrosine kinase (hek) from a human pre-B cell line".
RL J. Biol. Chem. 267:3262-3267(1992).
CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID FUNCTION.
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: RESTRICTED TO LYMPHOID TUMOR CELL LINES.
CC -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@sib-sib.ch).
CC -----
DR EMBL: M83941; AA58633.1; -;
DR EMBL: A28003; CA01906.1; -;
DR PIR: A38224; A38224.
DR HSSP: P00523; PPTK.
DR MIM: 179611; -;
DR PRINTS: PR00014; ENTYPITL.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.

DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00069; pkinase; 1.
 DR PFAM: PF00536; SAM; 1.
 DR PFAM: PF01404; EPH_1bd; 1.
 DR Transferrase; tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 983 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 21 541 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 542 565 POTENTIAL.
 FT DOMAIN 566 983 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 21 320 CYS-RICH.
 FT DOMAIN 321 431 FIBONECTIN TYPE-III.
 FT DOMAIN 432 528 FIBONECTIN TYPE-III.
 FT DOMAIN 529 882 PROTEIN KINASE.
 FT NP_BIND 621 635 ATP (BY SIMILARITY).
 FT BINDING 636 653 ATP (BY SIMILARITY).
 FT ACT_SITE 746 746 BY SIMILARITY.
 FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 232 232 POTENTIAL.
 FT CARBOHYD 337 337 POTENTIAL.
 FT CARBOHYD 381 381 POTENTIAL.
 FT CARBOHYD 404 404 POTENTIAL.
 FT CARBOHYD 493 493 POTENTIAL.
 FT CONFLICT 507 507 F -> L (IN CAA01906).
 FT CONFLICT 724 724 V -> L (IN CAA01906).
 SO SEQUENCE 983 AA; 110086 MW; B8D900FA80F5121 CMC64;

Query Match 100.0%; Score 1200; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 5.6e-103;
 Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEISGVDEHYPIRIRYQVCNWDHSONNWLRTNWPFRNSAOKIYVELKFTLRDCNSIPL 60
 DB 52 WEISGVDEHYPIRIRYQVCNWDHSONNWLRTNWPFRNSAOKIYVELKFTLRDCNSIPL 111
 QY 61 VLGTCKETFNLYMESDDHGVKFRHOFTKIDITIADESFOTMDGDRILKLTNTEIRREV 120
 DB 112 VLGTCKETFNLYMESDDHGVKFRHOFTKIDITIADESFOTMDGDRILKLTNTEIRREV 171
 QY 121 GPNVKKGFYLAQDVACVALSVRVYFKKCPFTYKNLAMPDTPVMDQSLSVEVNGSCV 180
 DB 172 GPNVKKGFYLAQDVACVALSVRVYFKKCPFTYKNLAMPDTPVMDQSLSVEVNGSCV 231
 QY 181 NNSKEDPPRMVCTSGEMLVPIGKCSNAGYBERGFMCQ 220
 DB 232 NNSKEDPPRMVCTSGEMLVPIGKCSNAGYBERGFMCQ 271

RESULT 2
 EPH3_RAT
 ID EPH3_RAT STANDARD; PRT; 984 AA.
 AC 008680;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 KINASE RECEPTOR REK4).
 GN EPH3 OR REK4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE; 98120505.
 RA Li Y.Y., McTiernan C.F., Feldman A.M.;
 RT "IL-1 beta alters the expression of the receptor tyrosine kinase gene
 r-Eph3 in neonatal rat cardiomyocytes";

RL Am. J. Physiol. 274:H331-H341(1998).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE ~ ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBONECTIN TYPE III-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; U69278; AAC06273.1; -.
 DR HSSP; P16109; 1FSB.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE: PS00111; PROTEIN KINASE_DOM; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00069; pkinase; 1.
 DR PFAM: PF00536; SAM; 1.
 DR PFAM: PF01404; EPH_1bd; 1.
 DR Transferrase; tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 984 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 21 541 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 542 565 POTENTIAL.
 FT DOMAIN 566 984 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 21 321 CYS-RICH.
 FT DOMAIN 322 432 FIBONECTIN TYPE-III.
 FT DOMAIN 433 529 FIBONECTIN TYPE-III.
 FT DOMAIN 529 883 PROTEIN KINASE.
 FT NP_BIND 628 636 ATP (BY SIMILARITY).
 FT BINDING 636 654 ATP (BY SIMILARITY).
 FT ACT_SITE 747 747 BY SIMILARITY.
 FT MOD_RES 780 780 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 232 232 POTENTIAL.
 FT CARBOHYD 337 337 POTENTIAL.
 FT CARBOHYD 391 391 POTENTIAL.
 FT CARBOHYD 404 404 POTENTIAL.
 FT CARBOHYD 493 493 POTENTIAL.
 SO SEQUENCE 984 AA; 110227 MW; F170C49312F7A0AB CMC64;

Query Match 98.8%; Score 1186; DB 1; Length 984;
 Best Local Similarity 98.6%; Pred. No. 1.1e-101;
 Matches 217; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEISGVDEHYPIRIRYQVCNWDHSONNWLRTNWPFRNSAOKIYVELKFTLRDCNSIPL 60
 DB 52 WEISGVDEHYPIRIRYQVCNWDHSONNWLRTNWPFRNSAOKIYVELKFTLRDCNSIPL 111
 QY 61 VLGTCKETFNLYMESDDHGVKFRHOFTKIDITIADESFOTMDGDRILKLTNTEIRREV 120
 DB 112 VLGTCKETFNLYMESDDHGVKFRHOFTKIDITIADESFOTMDGDRILKLTNTEIRREV 171
 QY 121 GPNVKKGFYLAQDVACVALSVRVYFKKCPFTYKNLAMPDTPVMDQSLSVEVNGSCV 180
 DB 172 GPNVKKGFYLAQDVACVALSVRVYFKKCPFTYKNLAMPDTPVMDQSLSVEVNGSCV 231
 QY 181 NNSKEDPPRMVCTSGEMLVPIGKCSNAGYBERGFMCQ 220
 DB 232 NNSKEDPPRMVCTSGEMLVPIGKCSNAGYBERGFMCQ 271

Db 232 NNSKEEDPPRMVSTGEWLVPIGKCTCNAGYERGFICQ 271

RESULT 3

EP3_MOUSE STANDARD; PRT; 983 AA.

AC P29319;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (ME44).

GN EPHA3 OR ETK1 OR MEK4 OR MEK4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-ICR X SWISS WEBSTER; TISSUE-EMBRYO;

RX MEDLINE: 92031278.

RA Sajjadi F.G., Pasquale E.B., Subramani S.;

RT Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor.;

RL New Biol. 3:769-778(1991).

CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: A SECRETED VARIANT WITHOUT THE TRANSMEMBRANE REGION AND THE KINASE DOMAIN IS PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.

CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE BRAIN.

CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

CC -----

DR EMBL: M68513; AAA39521.1; -.

DR EMBL: M68515; AAA39522.1; ALT_SEQ.

DR PIR: A45583; A45583.

DR HSSP: P16109; 1FSB.

DR MGD: MGI:9612; EPHA3.

DR PRINTS: PRO0014; EPHYB11.

DR PRINTS: PRO0109; TYRKINASE.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.

DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.

DR PROSITE: PS01186; EGF_2; UNKNOWN_1.

DR PFAM: PF00041; fn3; 2.

DR PFAM: PF00069; kinase; 1.

DR PFAM: PF00536; SAM; 1.

DR PFAM: PF01404; EPH_Lbd; 1.

KM Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.

KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.

FT SIGNAL 1 20

FT CHAIN 21 983

FT DOMAIN 21 540

FT TRANSMEM 541 564

FT DOMAIN 565 983

FT DOMAIN 21 320

FT DOMAIN 321 431

CC CYTOSOLASMIC (POTENTIAL).

CC CYS-RICH.

CC FIBRONECTIN TYPE-III.

FT DOMAIN 432 528 FIBRONECTIN TYPE-III.

FT DOMAIN 621 882 PROTEIN KINASE.

FT NP_BIND 627 635 ATP (BY SIMILARITY).

FT BINDING 653 653 ATP (BY SIMILARITY).

FT ACT_SITE 746 746 BY SIMILARITY.

FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT CARBOHYD 231 231 POTENTIAL.

FT CARBOHYD 336 336 POTENTIAL.

FT CARBOHYD 390 390 POTENTIAL.

FT CARBOHYD 403 403 POTENTIAL.

FT CARBOHYD 492 492 POTENTIAL.

FT VARSP_LIC 530 983 MISSING (IN SHORT ISOFORM).

SO SEQUENCE 983 AA; 109955 MW; BE44A655D8107A2 CRC64;

Query Match 98.0%; Score 1176.5; DB 1; Length 983;

Best Local Similarity 98.6%; Pred. No. 8,3e-101;

Matches 217; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Qy 1 WEISGVDEHYTPRTYQVGNVMDHSONMLRTNWPVRSNOKIYVELKFTLDGNSIPL 60

Db 52 WEISGVDEHYTPRTYQVGNVMDHSONMLRTNWPVRSNOKIYVELKFTLDGNSIPL 111

Qy 61 VLGTCKETFNLYMESDDHGVAFREHQFTKIDTIADESFTQMDLGRILKLTETIREV 120

Db 112 VLGTCKETFNLYMES-DDHGVAFREHQFTKIDTIADESFTQMDLGRILKLTETIREV 170

Qy 121 GPVKKGFYLAFDVGCVALSVRYFFKCPFTVKLAMPDPTVPMDOSLVEVRSQV 180

Db 171 GPVKKGFYLAFDVGCVALSVRYFFKCPFTVKLAMPDPTVPMDOSLVEVRSQV 230

Qy 181 NNSKEEDPPRMVSTGEWLVPIGKCTCNAGYERGFICQ 220

Db 231 NNSKEEDPPRMVSTGEWLVPIGKCTCNAGYERGFICQ 270

RESULT 4

EP3_CHICK STANDARD; PRT; 983 AA.

AC P29318;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (CEK4).

GN EPHA3 OR ETK1 OR CEK4.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 92031278.

RA Sajjadi F.G., Pasquale E.B., Subramani S.;

RT Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor.;

RL New Biol. 3:769-778(1991).

CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE BRAIN.

CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial


```

DT 01-NOV-1997 (Rel. 35, last annotation update)
DE EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
GN EPHA6 OR EHK2 OR EHK-2) (EPH HOMOMLOGY KINASE-2).
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C.
RX MEDLINE: 97047913.
RA Lee A.M., Navaratnam D., Ichimaya S., Greene M.I., Davis J.G.;
RT "Cloning of m-ehk2 from the murine inner ear, an eph family receptor
RT tyrosine kinase expressed in the developing and adult cochlea.";
RL DNA Cell Biol. 15:817-825(1996).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN, BELONGS TO THE EPHRIN RECEPTOR FAMILY
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U58332; AAB53836.1; -.
DR HSSP: P00523; 2PTRK.
DR MCD: MGI:108034; EPHA6.
DR PRINTS: PR00014; FNTYPEIIT.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR. 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM. 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1. 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2. 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; PKINASE. 1.
DR PFAM: PF00536; SAM; 1.
DR PFAM: PF01404; EPH_1bd; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 1035
FT DOMAIN 23 549
FT TRANSMEM 550 570
FT DOMAIN 571 1035
FT DOMAIN 630 943
FT NP_BIND 636 644
FT BINDING 662 662
FT ACT_SITE 797 797
FT CARBOHYD 342 342
FT CARBOHYD 396 396
FT CARBOHYD 409 409
FT SEQUENCE 1035 AA; 116137 MW; 560B264194A5EF74 CRC64;

```

Query Match 76.2%; Score 914.5; DB 1; Length 1035;
 Best Local Similarity 74.0%; Pred. No. 1.3e-76;
 Matches 159; Conservative 33; Mismatches 22; Indels 1; Gaps 1;

```

OY 1 WEISGVDEHYVPIRTYOVCMVDSNNWMLRTNWPNSAKIYVEKFTLDCNSTL 60
DB 56 WDAITEDEHNPPIHTYOVCMVDSNNWMLRTNWPNSAKIYVEKFTLDCNSTL 115
OY 61 VLGCKETFTNLYMESDDHGKVFREHOFTKIDTIADESFTOMDLGRILKLTREIRV 120

```

```

DB 116 VLGCKETFTNLYMESDDHGKVFREHOFTKIDTIADESFTOMDLGRILKLTREIRV 175
OY 121 GPNVKKGFILAFODVGCALYVAVYRKPCFTYKNTLAMPDIYV-MDSGLVYRSC 179
DB 176 GPIERKGFILAFODVGCALYVAVYRKPCFTYKNTLAMPDIYVDSGLVYRSC 235
OY 180 VNSKREDEPPRMVCSLEGMLVPIKSCSNAGYEE 214
DB 236 VNSAERDTPKLYCGADGMDLVPLGRICISGYEE 270

```

RESULT 7
 EPHA4_CHICK STANDARD. PRT; 986 AA.

```

ID EPHA4_CHICK STANDARD. PRT; 986 AA.
AC 007496; Q080772;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR CER8).
GN EPHA4 OR CER8.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPINAL CORD;
RX MEDLINE: 96404128.
RA Ohta K., Nakamura M., Hirokawa K., Tanaka S., Iwama A., Suda T.,
RA Ando M., Tanaka H.;
RT "The receptor tyrosine kinase, Cer8, is transiently expressed on
RT subtypes of motoneurons in the spinal cord during development.";
RL Mechn. Dev. 54:59-69(1996).
RN [2]
RP SEQUENCE OF 138-986 FROM N.A.
RC TISSUE-EMBRYO;
RX MEDLINE: 93288394.
RA Sajjadi F.G., Pasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed.";
RL Oncogene 8:1807-1813(1993).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 AND A-3.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC DOMAIN, BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D38174; BAA07373.1; -.
DR EMBL: Z19059; CAA79509.1; -.
DR HSSP: P00523; 2PTRK.
DR PRINTS: PR00014; FNTYPEIIT.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR. 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM. 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1. 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2. 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; PKINASE. 1.
DR PFAM: PF00536; SAM; 1.

```

DR PFAM: PF01404; EPH_Lbd; 1.
 KM Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 FT SIGNAL 1 19
 FT CHAIN 20 986
 FT DOMAIN 20 547
 FT TRANSMEM 548 569
 FT DOMAIN 570 586
 FT DOMAIN 335 435
 FT DOMAIN 436 532
 FT NP_BIND 621 635
 FT BINDING 633 653
 FT ACT_SITE 746 746
 FT MOD_RES 779 779
 FT CARBOHYD 235 235
 FT CARBOHYD 340 340
 FT CARBOHYD 408 408
 FT CONFLICT 138 138
 FT CONFLICT 487 487
 SQ SEQUENCE 986 AA; 109482 MW; BD88C2A5BD840A0F CRC64;

Query Match 75.9%; Score 910.5; DB 1; Length 986;
 Best Local Similarity 73.3%; Pred. No. 2.9e-76;
 Matches 162; Conservative 30; Mismatches 28; Indels 1; Gaps 1;

QY 1 WEISGVDEHYTPRTYQVCNMDHSONNWLRTNVPNRSAGKIYELKFTLDCNSIPL 60
 DB 54 WEVSIMDEKNPIRTYQVCNMEPSQNNWLTWDWIPRGAQRYVIEIKFTLDCNSLPG 113
 QY 61 VGTCKEFTNLYMESDDHGVKFRHQFTKIDTIADESFQMDLGRILKLTREIV 120
 DB 114 VGTCKEFTNLYMESDDHGVKFRHQFTKIDTIADESFQMDLGRILKLTREIV 173
 QY 121 GPVNRKGFYLAQDVGACALVSRYFRKCPFTYKNLAMPDTPV-MDSQSLVVRGSC 179
 DB 174 GPVNRKGFYLAQDVGACALVSRYFRKCPFTYKNLAMPDTPV-MDSQSLVVRGSC 233
 QY 180 VNNSKEEDPPRMVSTEGEMLVPICGSCNAGYEERGFMCQ 220
 DB 234 VNNSKEEDPPRMVSTEGEMLVPICGSCNAGYEERGFMCQ 274

RESULT 8
 EPHA4_HUMAN STANDARD: PRT: 986 AA.
 ID EPHA4_HUMAN
 AC P54764;
 DT 01-OCT-1996 (rel. 34, Created)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 15-OUL-1998 (rel. 36, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR SEK) (RECEPTOR PROTEIN-TYROSINE KINASE HEK8).
 GN EPHA4 OR SEK OR HEK8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 95206782.
 RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M., Basu R., Welcher A.A.;
 RT "CDNA cloning and tissue distribution of five human EPH-like receptor protein-tyrosine kinases";
 RL Oncogene 10:897-905(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 AND A-3.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----

DR HSRP: I36645; AAA74246.1; -
 DR HSRP: P00523; 2PTK.
 DR MIM: 602188; -
 DR PRINTS: PR00014; FNTYPEP11.
 DR PRINTS: PR00109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM_1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00069; pkinase; 1.
 DR PFAM: PF00536; SAM; 1.
 DR PFAM: PF01404; EPH_Lbd; 1.
 KM Transferase; Tyrosine-protein kinase; ATP-binding; phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 986
 FT DOMAIN 20 547
 FT TRANSMEM 548 569
 FT DOMAIN 570 586
 FT DOMAIN 325 435
 FT DOMAIN 436 532
 FT DOMAIN 621 882
 FT NP_BIND 627 635
 FT BINDING 633 653
 FT ACT_SITE 746 746
 FT MOD_RES 779 779
 FT CARBOHYD 235 235
 FT CARBOHYD 340 340
 FT CARBOHYD 408 408
 FT CARBOHYD 545 545
 SQ SEQUENCE 986 AA; 109859 MW; 0C39C1152EDD46F CRC64;

Query Match 75.5%; Score 905.5; DB 1; Length 986;
 Best Local Similarity 73.3%; Pred. No. 8.2e-76;
 Matches 162; Conservative 30; Mismatches 28; Indels 1; Gaps 1;

QY 1 WEISGVDEHYTPRTYQVCNMDHSONNWLRTNVPNRSAGKIYELKFTLDCNSIPL 60
 DB 54 WEVSIMDEKNPIRTYQVCNMEPSQNNWLTWDWIPRGAQRYVIEIKFTLDCNSLPG 113
 QY 61 VGTCKEFTNLYMESDDHGVKFRHQFTKIDTIADESFQMDLGRILKLTREIV 120
 DB 114 VGTCKEFTNLYMESDDHGVKFRHQFTKIDTIADESFQMDLGRILKLTREIV 173
 QY 121 GPVNRKGFYLAQDVGACALVSRYFRKCPFTYKNLAMPDTPV-MDSQSLVVRGSC 179
 DB 174 GPVNRKGFYLAQDVGACALVSRYFRKCPFTYKNLAMPDTPV-MDSQSLVVRGSC 233
 QY 180 VNNSKEEDPPRMVSTEGEMLVPICGSCNAGYEERGFMCQ 220
 DB 234 VNNSKEEDPPRMVSTEGEMLVPICGSCNAGYEERGFMCQ 274

RESULT 9
 EPHA4_MOUSE STANDARD: PRT: 986 AA.
 ID EPHA4_MOUSE
 AC 003137;
 DT 01-OCT-1994 (rel. 30, Created)
 DT 01-OCT-1994 (rel. 30, Last sequence update)
 DT 01-NOV-1997 (rel. 35, Last annotation update)

DE EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (BC 2.7.1.112) (TYROSINE-PROTEIN
 GN KINASE RECEPTOR SEK) (MFK-3).
 DE EPHA4 OR SEK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-C57BL; TISSUE-EMBRYONIC BRAIN;
 RX MEDLINE: 93096484.
 RA Giliardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G.,
 RA Chetlier A., Wilkinson D.G., Charney P.;
 RT "An Epi-related receptor protein tyrosine kinase gene segmentally
 RT expressed in the developing mouse hindbrain.";
 RL Oncogene 7:2499-2506(1992).
 RN [2]
 RN ERRATUM.
 RX MEDLINE: 93205393.
 RA Giliardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G.,
 RA Chetlier A., Wilkinson D.G., Charney P.;
 RL Oncogene 8:1103-1103(1993).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 AND A-3.
 CC MAY PLAY A ROLE IN A SIGNAL TRANSDUCTION PROCESS INVOLVED IN
 CC HINDRAIN PATTERN FORMATION.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM WITH A DELETION OF 49
 CC AMINO ACIDS ALTERING THE CATALYTIC SITE MAY BE GENERATED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN THE BRAIN, LOWER LEVELS
 CC IN THE HEART, LUNG AND KIDNEY. IT IS SEGMENTALLY EXPRESSED
 CC IN THE EMBRYONIC BRAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X65138; CAA46268.1; -;
 DR EMBL: X57241; CAA40517.1; -;
 DR EMBL: S57168; AAB25836.1; -;
 DR HSSP: P00523; 2PTR.
 DR MGD: MGI:98277; EPHA4.
 DR PRINTS: PR000104; FNTPELIT.
 DR PRINTS: PR00109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PFM: PF00041; fn3; 2.
 DR PFM: PF00069; PKINASE; 1.
 DR PFM: PF00536; SAM; 1.
 DR PFM: PF01404; EPH_lbd; 1.
 DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 986
 FT DOMAIN 20 547
 FT TRAMSMEM 548 569
 FT DOMAIN 570 986
 FT DOMAIN 325 435
 FT DOMAIN 436 532
 FT DOMAIN 621 882
 FT NP_BIND 627 635
 FT ATP (BY SIMILARITY).

FT BINDING 653 653 ATP (BY SIMILARITY).
 FT ACT_SITE 746 746 BY SIMILARITY.
 FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 235 235 POTENTIAL.
 FT CARBOHYD 340 340 POTENTIAL.
 FT CARBOHYD 408 408 POTENTIAL.
 FT CARBOHYD 423 423 POTENTIAL.
 FT VARSPIC 783 832 MISSING (IN SHORT ISOFORM).
 SO SEQUENCE 986 AA; 109801 MW; D16AD8B85668C80E CRC64;
 Query Match 74.4%; Score 892.5; DB 1; Length 986;
 Best Local Similarity 72.4%; Pred. No. 1.3e-74;
 Matches 160; Conservative 30; Mismatches 30; Indels 1; Gaps 1;
 QY 1 WEISGVDEHYPTPIRYQVCNVMDSQNNWLTNVPNSAKIYELKFLRDCNSIDL 60
 DB 54 WEVSIMDEKNTPIRTYQVCNVMASQNNWLTMTDITREGARVYIEIKFLRDCNSLPG 113
 QY 61 YGTGKEPTFLYMSDDHGKFRFHOTKIDTIADESFTOMLGRILKLTNTEIRV 120
 DB 114 YGTGKEPTFLYMSDDHGKFRFHOTKIDTIADESFTOMLGRILKLTNTEIRV 173
 QY 121 GPVNRKGFYLAQDYACALYSVRYEKKCPFTYKNLAFPDYV-MDSQSLAVEYRGSC 179
 DB 174 GPLSKRGFLAQDYACALYSVRYEKKCPFTYKNLAFPDYV-MDSQSLAVEYRGSC 233
 QY 180 VNNSKEDEPPMYCSTEGEMLVPICKSCNAGYEERGFQ 220
 DB 234 VNNSKEDEPPMYCSTEGEMLVPICKSCNAGYEERGFQ 274
 RESULT 10
 EPHA_MOUSE STANDARD: PRT; 877 AA.
 ID EPHA_MOUSE
 AC Q60629;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (BC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR EHK-1) (EPH HOMOLOG KINASE-1) (BRAIN-SPECIFIC KINASE)
 DE (CEK-7).
 GN EPHA5 OR EHK1 OR CEK7 OR BSK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE: 94194581.
 RA Zhou R., Copeland T.D., Kromer L.F., Schulz N.T.;
 RT "Isolation and characterization of Bsk, a growth factor receptor-like
 RT tyrosine kinase associated with the limbic system.";
 RL J. Neurosci. Res. 37:129-143(1994).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U07357; AAA17038.1; -;

DR HSDP; P00523; 2PTR.
 DR MGD; MGI:99654; EPHAS.
 DR PRINTS; PRO0014; ENTPEI1.
 DR PRINTS; PRO0109; TYRKINASE.
 DR PROSITE; P500107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; P500109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; P500111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; P500790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; P500791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; P501186; EGF_2; UNKNOWN_1.
 DR PFAM; PF00041; fn3; 1.
 DR PFAM; PF00069; kinase; 1.
 DR PFAM; PF00366; SAM; 1.
 DR PFAM; PF01404; EPH_Lbd; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 877
 FT DOMAIN 27 412
 FT TRANSMEM 413 433
 FT DOMAIN 434 877
 FT DOMAIN 305 399
 FT DOMAIN 514 775
 FT NP_BIND 520 528
 FT BINDING 546 546
 FT ACT_SITE 639 639
 FT CARBOHYD 266 266
 FT CARBOHYD 301 301
 FT SEQUENCE 877 AA; 97115 MW; 54AD2DC64178214 CRC64;

Query Match 72.2%; Score 866.5; DB 1; Length 877;
 Best Local Similarity 68.3%; Pred. No. 2.8e-72;
 Matches 151; Conservative 35; Mismatches 34; Indels 1; Gaps 1;

OY 1 WEISGVDEHYTIRTYQYCNVNDHSONNMLRTNWPFRNSAQIYVEIKFTLDCNSIP 60
 DB 85 WEISGVDEHYTIRTYQYCNVNDHSONNMLRTNWPFRNSAQIYVEIKFTLDCNSIP 144
 OY 61 VLGCTKETFNLYMESDDHGVKFRHOFKTIIDTIADESFOTMDIGDRILKINTEIREY 120
 DB 145 GLGCTKETFNLYMESDDHGVKFRHOFKTIIDTIADESFOTMDIGDRILKINTEIREY 204
 OY 121 GPVNNKGFILAFODVACALVSVRYEKKCPFTVNNLAFPTVPV-MDSQSLVEVSGSC 179
 DB 205 GPVNNKGFILAFODVACALVSVRYEKKCPFTVNNLAFPTVPV-MDSQSLVEVSGSC 264
 OY 180 VNNKREDDPRMVCSTGEGLVPIGKSCNAGYEERGFMOQ 220
 DB 265 VNNKREDDPRMVCSTGEGLVPIGKSCNAGYEERGFMOQ 305

RESULT 11
 EPHAS_RAT STANDARD; PRT; 1005 AA.
 AC P54757;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR EHK-1) (EPH HOMOLOG KINASE-1).
 GN EPHAS OR EKH1 OR EHK-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 94067777.
 RA Maisonneuve P.C., Barrezaeta N.X., Yancopoulos G.D.;
 RT "Ehk-1 and Ekh-2: two novel members of the Eph receptor-like tyrosine
 RT kinase family with distinctive structures and neuronal expression."
 RL Oncogene 8:3277-3288(1995).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 95206467.
 RA Taylor V., Pfaff S., Mescher G.C., Honegger P., Breitschopf H.,
 RA Lassmann H., Steck A.J.;
 RT "Expression and developmental regulation of Ekh-1, a neuronal
 RT Etk-like receptor tyrosine kinase in brain."
 RL Neuroscience 63:163-178(1994).
 CC -1 FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1 ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1 TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
 CC SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
 CC -1 SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1 SIMILARITY: CONTRAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-slb.ch/announce/>
 CC or send an email to license@isb-slb.ch).

CC EMBL; X78689; CAA55357.1; -.
 DR HSDP; P00523; 2PTR.
 DR PRINTS; PRO0014; ENTPEI1.
 DR PRINTS; PRO0109; TYRKINASE.
 DR PROSITE; P500107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; P500109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; P500111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; P500790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; P500791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; P501186; EGF_2; UNKNOWN_1.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00069; kinase; 1.
 DR PFAM; PF01404; EPH_Lbd; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
 FT SIGNAL 1 26
 FT CHAIN 27 877
 FT DOMAIN 27 412
 FT TRANSMEM 413 433
 FT DOMAIN 434 877
 FT DOMAIN 305 399
 FT DOMAIN 514 775
 FT NP_BIND 520 528
 FT BINDING 546 546
 FT ACT_SITE 639 639
 FT CARBOHYD 266 266
 FT CARBOHYD 301 301
 FT CARBOHYD 371 371
 FT CARBOHYD 425 425
 FT CARBOHYD 438 438
 FT CARBOHYD 463 463
 FT CARBOHYD 10 20
 FT VARSPLIC 306 358
 FT VARSPLIC 358 470
 FT VARSPLIC 597 621
 FT CONFLICT 170 170
 FT CONFLICT 566 566
 FT CONFLICT 578 578
 CC -1 SIMILARITY: CONTRAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-slb.ch/announce/>
 CC or send an email to license@isb-slb.ch).

OS Mus musculus (Mouse) .
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE: 95134729.
 RA Ciossek T., Millauner B., Ullrich A.;
 RA Fletcher F.A., Ziegler S.F., Rogers J.H.;
 RT "Embryo brain kinase: a novel gene of the eph/erb receptor tyrosine
 RT MDK1, a novel receptor tyrosine kinase expressed in the murine
 RT nervous system.";
 RL Oncogene 10:97-108(1995).
 RN [2]
 RP SEQUENCE OF 431-998 FROM N.A. (ISOFORM MDK1).
 RC TISSUE-BRAIN;
 RX MEDLINE: 96081374.
 RA Ellis J., Liu Q., Breilman M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Tempest H.V., Warren S., Muir E., Schalling H.,
 RA Fletcher F.A., Ziegler S.F., Rogers J.H.;
 RT "Embryo brain kinase: a novel gene of the eph/erb receptor tyrosine
 RT MDK1, a novel receptor tyrosine kinase expressed in the murine
 RT nervous system.";
 RL Mech. Dev. 52:319-341(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN (MDK1, MDK1-1,
 CC MDK1-2, MDK1-T1 AND MDK1-T2) ARE PRODUCED BY ALTERNATIVE
 CC SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF
 CC MDK1.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN EMBRYO. IN ADULT,
 CC EXPRESSION RESTRICTED TO HIPPOCAMPUS, TESTIS AND SPLEEN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on ways
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X79082; CAAS5687.1; -;
 DR EMBL: X79083; CAAS5688.1; -;
 DR EMBL: X79084; CAAS5689.1; -;
 DR EMBL: X81466; CAAS7224.1; -;
 DR HSSP: P00523; 2PTK.
 DR WGD: MGI:95276; EPHA7.
 DR PRINTS: PRO0014; FNTYPEIII.
 DR PRINTS: PRO0109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V.1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V.2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PFM: PFO0041; fn3; 2.
 DR PFM: PFO0069; Pkinase; 1.
 DR PFM: PFO0536; SAM; 1.
 DR PFM: PFO1404; EPH_Lbd; 1.
 KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
 FT SIGNAL 1 29
 FT CHAIN 30 998 EPHRIN TYPE-A RECEPTOR 7.
 FT DOMAIN 30 556 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 557 577 POTENTIAL.
 FT DOMAIN 578 998 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 329 438 FIBRONECTIN TYPE-III.
 FT DOMAIN 439 537 FIBRONECTIN TYPE-III.
 FT DOMAIN 633 894 PROTEIN KINASE.

FT	NP_BIND	639	647	APP (BY SIMILARITY).
FT	BINDING	665	665	AAP (BY SIMILARITY).
FT	ACT_SITE	758	758	BY SIMILARITY.
FT	MOD_RES	791	791	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	CARBOHYD	64	64	POTENTIAL.
FT	CARBOHYD	343	343	POTENTIAL.
FT	CARBOHYD	410	410	POTENTIAL.
FT	VARSPLIC	540	544	MISSING (IN ISOFORM MDK1-1).
FT	VARSPLIC	601	604	MISSING (IN ISOFORM MDK1-2).
FT	VARSPLIC	600	610	FERRECKTYID -> SLVYNELSLVL (IN ISOFORM MDK1-T1).
FT	VARSPLIC	611	998	MISSING (IN ISOFORM MDK1-T1).
FT	VARSPLIC	600	626	KFFPGKTYIDETDENRAVHCFAR -> SLVRENDDGN
FT	VARSPLIC	627	998	ETQHNKMMKIMISCSSL (IN ISOFORM MDK1-T2).
FT	CONFLICT	480	480	MISSING (IN ISOFORM MDK1-T2).
SO	SEQUENCE	998 AA;	111874 MW;	Y -> H (IN REF. 2).
				81C5538E15A8A28A CRC64;

Query Match	71.5%	Score 857.5	DB 1	Length 998
Best Local Similarity	70.0%	Pred. No. 2.2e-71		
Matches 156	Conservative 36	Mismatches 28	Indels 3	Gaps 2

```

0Y 1 WEESGVDEHTPRTRTOVCVMHDSNNMRTWVRNRSOKRYVLEKTLBDCNSIPL 60
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 55 WEESGIDENTPRTTRTOVCVMHDSNNMRTWVRNRSOKRYVLEKTLBDCNSIPL 114
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
0Y 61 VLGTCKETFNLYMESDDHVKFREHOFTKIDTIADESFQWDLDRILKLTETREY 120
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 115 VLGTCKETFNLYETDYDGRNTRREMLYKIDTIADESFQWDLDRILKLTETREI 174
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
0Y 121 GPVNRKGEYLAFOGVGACVALSVRYVEFKKCPFTYKMLAFPTDVP- MDSQSLVEYVGC 179
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 175 GPLSKRGYLAFOGVGACIALSVRYVKKCKMTIVENLAIFPPDYVTSSESSLVEYVGC 234
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

```

QY 180 VNNSKE--EDPPRYCSTEGEWLVPIGKCSNAGYEERGFMCQ 220
|:::| : ||||| | | | | | | | | | | | | | | | | |
Db 235 VSSAEFEAENSPRMHCSAGEWLVPIGKCICKAGYQQKDTC E 277

RESULT	14
EPA7_HUMAN	
ID	
EPA7_HUMAN	
STANDARD;	
PRT;	998 AA

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EHK-3) (EPH HOMOLOG KINASE-3) (RECEPTOR PROTEIN-
DE TYROSINE KINASE HEK11).
GN EPHA7 OR EHK3 OR HEK11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE-BRAIN.
RX MEDLINE: 95206782.
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA Basu R., Welcher A.A.;
RT "CDNA Cloning and tissue distribution of five human EPH-like receptor
RT protein-tyrosine kinases.";
RL Oncogene 10:897-905(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collabor

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).

DR EMBL; L36642; AAA74243.1; -
DR HSSP; P00523; 2PTK.
DR MIM; 602190; -
DR PRINTS; PRO0014; FNTYPEIIT.
DR PRINTS; PRO0109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00069; pkinase; 1.
DR PFAM; PF00536; SAM; 1.
DR PFAM; PF01404; EPH_1bd; 1.
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 998
FT DOMAIN 25 556
FT TRANSMEM 557 577
FT DOMAIN 578 998
FT DOMAIN 329 998
FT DOMAIN 439 537
FT NP_BIND 633 894
FT NP_BIND 639 647
FT BINDING 665 665
FT ACT_SITE 758 758
FT MOD_RES 791 791
FT CARBOHYD 343 343
FT CARBOHYD 410 410
SQ SEQUENCE 998 AA; 112096 MW; 479B9CAD02BB06EB CRC64;

Query Match 71.4%; Score 856.5; DB 1; Length 998;
Best Local Similarity 69.5%; Pred. No. 2.8e-71;
Matches 155; Conservative 37; Mismatches 28; Indels 3; Gaps 2;

QY 1 WEISGVDEHTPIRTYOVCMNDHSONNMLRTNVPNSAKIYELKFTLRDCNSIDL 60
DB 55 WEISGIDENLPIRTYOVCMNDHSONNMLRTNVPNSAKIYELKFTLRDCNSIDL 114
QY 61 VLGTCKETFNLYYMESEDDHGVKFEHOFKIDITIADESFQMDLGRILKLTNIREV 120
DB 115 VLGTCKETFNLYYETDIDTGNIRENLVKIDITIADESFQMDLGRILKLTNIREV 174
QY 121 GPNVKGFFLYAFQDVACVALSVREYERKCPFTVKNLAMPDTPV-MDSQSLAVEVRS 179
DB 175 GPLSKRGFFLYAFQDVACVALSVREYERKCPFTVKNLAMPDTPV-MDSQSLAVEVRS 234
QY 180 VNNSEK--EDPPRMVCSBGEMLVPIGKSCNAGYERGFMCQ 220
DB 235 VSSAEAEENAPRMHCSAGEMLVPIGKSCNAGYERGFMCQ 277

RESULT 15
ID EPH7_RAT STANDARD; PRT; 998 AA.
AC P54759;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (BC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EHK-3) (EPH HOMOLOG YOKOJCE 277).
GN EPH7 OR EHK3 OR EHK-3.
OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95249272.
RA Valenzuela D.M., Rojas E., Griffiths J.A., Compton D.L., Gieser M.,
RA Ip N.Y., Goldfarb M., Yancopoulos G.D.;
RT "Identification of full-length and truncated forms of EHK-3, a novel
RT member of the Eph receptor tyrosine kinase family.";
RL Oncogene 10:1573-1580(1995).
CC EPHRIN-A1, -A2, -A3, -A4 and -A5.
CC CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1 SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.
CC -1 ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING. THE TRUNCATED FORM LACKS THE KINASE DOMAIN. THE LONG
CC FORM IS MORE WIDELY EXPRESSED IN THE EMBRYO.
CC -1 TISSUE SPECIFICITY: RESTRICTED TO THE NERVOUS SYSTEM.
CC -1 SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).

DR EMBL; U21954; AAA86830.1; -
DR EMBL; U21955; AAA86831.1; -
DR HSSP; P00523; 2PTK.
DR PRINTS; PRO0014; FNTYPEIIT.
DR PRINTS; PRO0109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00069; pkinase; 1.
DR PFAM; PF00536; SAM; 1.
DR PFAM; PF01404; EPH_1bd; 1.
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 998
FT DOMAIN 25 556
FT TRANSMEM 557 577
FT DOMAIN 578 998
FT DOMAIN 329 998
FT DOMAIN 439 537
FT NP_BIND 633 894
FT NP_BIND 639 647
FT BINDING 665 665
FT ACT_SITE 758 758
FT MOD_RES 791 791
FT CARBOHYD 343 343
FT CARBOHYD 410 410
FT VARSPLIC 600 610
SQ SEQUENCE 998 AA; 111953 MW; A7A82A698924876C CRC64;

Query Match 71.4%; Score 856.5; DB 1; Length 998;
Best Local Similarity 69.5%; Pred. No. 2.8e-71;
Matches 155; Conservative 37; Mismatches 28; Indels 3; Gaps 2;

QY 1 WEISGVDEHTPIRTYOVCMNDHSONNMLRTNVPNSAKIYELKFTLRDCNSIDL 60
DB 55 WEISGIDENLPIRTYOVCMNDHSONNMLRTNVPNSAKIYELKFTLRDCNSIDL 114

Db 55 WEISGLDENYTPIRTYQCVMEPNQNNWMLRTNWISKNAQRIFVELKFTLRDCNSLPg 114
QY 61 VLGTCKETNLIYMESDDHGKFKREHQFTKIDTIADESFTQMDLGDRILKINTEIREV 120
Db 115 VLGTCKETNLIYXYETDYDGRNIRENLYKIDTIADESFTQDGERRMLKINTEIREI 174
QY 121 GPVNRKGFYLAFODVACVALSVRYRFFKCPPTYKNLAMPDTPV-MDSQSLVEYRGSC 179
Db 175 GPLSKRGFYLAFODVACIALVSVKYRKCSIIENLAVFPDPTVGSSESSLVEYRGTC 234
QY 180 VNNSKE--EDPPRMVCTEGEMLVPIGKCSNAGYEERGFMCQ 220
Db 235 VSSAEEREAENSPRMHCSAEGEMLVPIGKCIKAGYQKGDTC 277

Search completed: May 9, 2000, 22:32:06
Job time: 2397 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 21:18:01 ; Search time 64.29 Seconds
(without alignments)
200.631 Million cell updates/sec

Title: US-09-104-340-1
Perfect score: 1200
Sequence: 1 WEISGVDEHYTPRTYQVC.....VPGRKSCNAGYERGMQ 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1200	100.0	983	2 A38224	protein-tyrosine k
2	1176.5	98.0	983	2 A45583	receptor tyrosine
3	1139	94.9	983	2 B45583	receptor tyrosine
4	914.5	76.2	948	2 S51605	receptor-like tyro
5	905.5	75.5	986	2 I78844	receptor protein-t
6	894.5	74.5	985	2 I51549	receptor tyrosine
7	892.5	74.4	986	2 S78059	protein-tyrosine k
8	866.5	72.2	877	2 I48967	brain-specific kin
9	866.5	72.2	898	2 S47489	receptor tyrosine
10	863.5	72.0	893	2 S51603	receptor-like tyro
11	863.5	72.0	981	2 S51604	receptor-like tyro
12	863.5	72.0	1005	2 S49015	receptor tyrosine
13	860.5	71.7	991	2 I78843	receptor protein-t
14	857.5	71.5	605	2 JCS673	receptor tyrosine
15	857.5	71.5	610	2 I48612	developmental kina
16	857.5	71.5	626	2 I48614	receptor tyrosine
17	857.5	71.5	998	2 JCS672	receptor tyrosine
18	856.5	71.4	998	2 I58351	receptor protein-t
19	825.5	68.8	1013	2 I50615	receptor-type prot
20	713	59.4	995	2 A56599	embryo kinase 5 -
21	708	59.0	970	2 I78842	receptor protein-t
22	693.5	57.8	984	2 A39753	protein-tyrosine k
23	691.5	57.6	985	2 I51672	receptor tyrosine
24	644	53.7	988	2 I50611	protein-tyrosine k
25	637.5	53.1	977	2 S49004	tyrosine kinase Mp
26	632	52.7	998	2 S37627	protein-tyrosine k
27	627	52.2	976	2 A36355	protein-tyrosine k
28	620	51.7	993	2 I48653	mouse developmenta
29	601	50.1	975	2 I48974	receptor-protein t
30	589	49.1	938	2 I49071	protein kinase - m

31	569.5	47.5	849	2 I50617	protein-tyrosine k
32	541.5	45.1	952	2 I50612	protein-tyrosine k
33	539	44.9	984	1 A34076	protein-tyrosine k
34	478	39.8	987	2 I48953	eph-related recept
35	478	39.8	987	2 I48652	mouse developmenta
36	466	38.8	987	2 A54092	protein-tyrosine k
37	460	38.3	1006	2 JCS526	kinase-defective E
38	369.5	30.8	1019	2 T13039	tyrosine kinase re
39	241	20.1	1122	2 T42400	Eph receptor tyros
40	89.5	7.5	668	2 T05803	hypothetical prote
41	87.5	7.3	788	2 I51530	integrin beta-3 su
42	86	7.2	919	2 T29581	hypothetical prote
43	85.5	7.1	347	2 T34131	hypothetical prote
44	84.5	7.0	865	2 H71447	trehalose-6-phosph
45	82.5	6.9	369	2 B70220	conserved hypothet

ALIGNMENTS

RESULT 1
A38224
protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C:Accession: A38224; B38224
R:Wicks, I.P.; Wilkinson, D.; Salvaris, E.; Boyd, A.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
A:Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expe
A:Reference number: A38224; MUID:92179233
A:Accession: A38224
A:Molecule type: mRNA
A:Residues: 1983 <WIC>
A:Cross-references: GB:W83941; NID:q183931; PIDN:AA58633.1; PID:q183932
A:Experimental source: pre-B-cell leukemia cell line LK63
A:Note: sequence extracted from NCBI backbone (NCBIP:86627)
A:Accession: B38224
A:Molecule type: protein
A:Residues: 21-39/810-860 <WIC>
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: AMP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferas
F:1-20/Domain: signal sequence #status predicted <Sig>
F:21-983/Product: protein-tyrosine kinase hek #status experimental <TM>
F:542-565/Domain: transmembrane #status predicted <TM>
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif
F:232,337,391,404,493/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1200; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.3e+101;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEISGVDEHYTPRTYQVCNVMDSQNMVLRFWVRNSAQRTYVLTFRDNCNIP 60
|||||
Db 52 WEISGVDEHYTPRTYQVCNVMDSQNMVLRFWVRNSAQRTYVLTFRDNCNIP 111
|||||

QY 61 VLGTCKETFNLYWESDDHGVKFRHQFTKIDTIAADESFQWDLGDRILKNTETREV 120
|||||
Db 112 VLGTCKETFNLYWESDDHGVKFRHQFTKIDTIAADESFQWDLGDRILKNTETREV 171
|||||

QY 121 GPVNRKGFYLAQDVGVCAVLAVSRYVFKKCPFTVKYLAEPDTPVDSQSLVEVRSCV 180
|||||
Db 172 GPVNRKGFYLAQDVGVCAVLAVSRYVFKKCPFTVKYLAEPDTPVDSQSLVEVRSCV 231
|||||

QY 181 NNSKEEDPPRYCSTEGEWLVPIGKSCNAGYERGMQ 220
|||||
Db 232 NNSKEEDPPRYCSTEGEWLVPIGKSCNAGYERGMQ 271
|||||

RESULT 2
A45583
receptor tyrosine kinase Mek4 - mouse

C:Species: Mus musculus (house mouse)
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: A45583
R:Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
A:Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
A:Reference number: A45583; MUID:92031278
A:Accession: A45583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-983 <SAB>
A:Cross-references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C:Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif

Query Match 98.0%; Score 1176.5; DB 2; Length 983;
Best Local Similarity 98.6%; Pred. No. 3.2e-99;
Matches 217; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 WEISGVDEHTPIRTYOVNCNMDSQNNMLRTNVPNRSACKIYELKFTLRDQNSIPL 60
|||||
DB 52 WEISGVDEHTPIRTYOVNCNMDSQNNMLRTNVPNRSACKIYELKFTLRDQNSIPL 111
|||||

QY 61 VLGTCKEFTNLYMESDDDHGKVFREHOFTRKIDTIAADESFQMDLGRILKLTNTEIREV 120
|||||
DB 112 VLGTCKEFTNLYYMS-DDHGKVFREHOFTRKIDTIAADESFQMDLGRILKLTNTEIREV 170
|||||

QY 121 GPVKKGGTYLAFQDVGACVALSVRYFRKCCPTVYKNLAMPDYVPMDSQSLVEYRGSCV 180
|||||
DB 171 GPVKKGGTYLAFQDVGACVALSVRYFRKCCPTVYKNLAMPDYVPMDSQSLVEYRGSCV 230
|||||

QY 181 NNSKEEDPRMYCSTEGEMLVPIGKSCNAGYEENGFCQ 220
|||||
DB 231 NNSKEEDPRMYCSTEGEMLVPIGKCTCNAGYEENGFCQ 270
|||||

RESULT 3
B45583
receptor tyrosine kinase Cerk4 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: B45583
R:Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
A:Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
A:Reference number: A45583; MUID:92031278
A:Accession: B45583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-983 <SAB>
A:Cross-references: GB:M68514; NID:g454809; PIDN:AAA48666.1; PID:g211447
A:Note: sequence extracted from NCBI backbone (NCBIN:62405, NCBIR:62411)
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C:Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif

Query Match 94.9%; Score 1139; DB 2; Length 983;
Best Local Similarity 94.5%; Pred. No. 8.4e-96;
Matches 208; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEISGVDEHTPIRTYOVNCNMDSQNNMLRTNVPNRSACKIYELKFTLRDQNSIPL 60
|||||
DB 51 WEISGVDEHTPIRTYOVNCNMDSQNNMLRTNVPNRSACKIYELKFTLRDQNSIPL 110
|||||

QY 61 VLGTCKEFTNLYMESDDDHGKVFREHOFTRKIDTIAADESFQMDLGRILKLTNTEIREV 120
|||||
DB 111 VLGTCKEFTNLYYMSDDDHGKVFREHOFTRKIDTIAADESFQMDLGRILKLTNTEIREV 170
|||||

QY	121	GP	KK	KG	GY	LA	FO	VG	CA	LV	SV	RY	EF	KC	PE	YV	KI	LA	PD	IV	PD	SD	SL	VE	RS	CV	168
Db	171	GP	VS	KK	GY	LA <td>FO <td>VG <td>CA <td>LV <td>SV <td>RY <td>EF <td>KC <td>PE <td>YV <td>KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	FO <td>VG <td>CA <td>LV <td>SV <td>RY <td>EF <td>KC <td>PE <td>YV <td>KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	VG <td>CA <td>LV <td>SV <td>RY <td>EF <td>KC <td>PE <td>YV <td>KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	CA <td>LV <td>SV <td>RY <td>EF <td>KC <td>PE <td>YV <td>KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	LV <td>SV <td>RY <td>EF <td>KC <td>PE <td>YV <td>KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	SV <td>RY <td>EF <td>KC <td>PE <td>YV <td>KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	RY <td>EF <td>KC <td>PE <td>YV <td>KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td>	EF <td>KC <td>PE <td>YV <td>KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td></td></td></td></td>	KC <td>PE <td>YV <td>KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td></td></td></td>	PE <td>YV <td>KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td></td></td>	YV <td>KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td></td>	KI <td>LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td></td>	LA <td>PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td></td>	PD <td>IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td></td>	IV <td>PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td></td>	PD <td>SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td></td>	SD <td>SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td></td>	SL <td>VE <td>RS <td>CV <td>230</td> </td></td></td>	VE <td>RS <td>CV <td>230</td> </td></td>	RS <td>CV <td>230</td> </td>	CV <td>230</td>	230
QY	181	NN	SK	ED	PD	PR	MY	CS	TE	GE	EM	LV	PI	CK	SC	NN	NG	YE	RG	FM	QC	220					
Db	231	NN	SK	ED	PD	PR	MY	CS	TE	GE	EM	LV	PI	CK	SC	NN	NG	YE	RG	FM	QC	270					

RESULT 4

receptor-like tyrosine kinase Etk-2 - rat

c;species: Rattus norvegicus (Norway rat)
c;Date: 07-May-1995 #sequence revision 21-Jul-1995 #covt change 20-May-1998

C;Accession: S51605

Oncogene 8, 3277-3288, 1993

A:Reference number: S49015: MUID:9406777777

A:Accession: 551605
A:Status: preliminary

A;Molecule type: mRNA

A;Cross-references: EMBL:S68030

C:Keywords: ATP; transmembrane protein

E:6336-644/Region: protein kinase homology <KIN>
F:628-956/Domain: protein kinase homology <KIN>

Query Match	76.28;	Score 914.5;	DB 2;	Length 948;
-------------	--------	--------------	-------	-------------

```

Matches      159: Conservative    31: Mismatches   24: Indels       1: Gaps        1:
2008-2009-2010-2011-2012-2013-2014-2015-2016-2017-2018-2019-2020-2021-2022-2023-2024-2025-2026-2027-2028-2029-2030-2031-2032-2033-2034-2035-2036-2037-2038-2039-2040-2041-2042-2043-2044-2045-2046-2047-2048-2049-2050-2051-2052-2053-2054-2055-2056-2057-2058-2059-2060-2061-2062-2063-2064-2065-2066-2067-2068-2069-2070-2071-2072-2073-2074-2075-2076-2077-2078-2079-2080-2081-2082-2083-2084-2085-2086-2087-2088-2089-2090-2091-2092-2093-2094-2095-2096-2097-2098-2099-2100-2101-2102-2103-2104-2105-2106-2107-2108-2109-2110-2111-2112-2113-2114-2115-2116-2117-2118-2119-2120-2121-2122-2123-2124-2125-2126-2127-2128-2129-2130-2131-2132-2133-2134-2135-2136-2137-2138-2139-2140-2141-2142-2143-2144-2145-2146-2147-2148-2149-2150-2151-2152-2153-2154-2155-2156-2157-2158-2159-2160-2161-2162-2163-2164-2165-2166-2167-2168-2169-2170-2171-2172-2173-2174-2175-2176-2177-2178-2179-2180-2181-2182-2183-2184-2185-2186-2187-2188-2189-2190-2191-2192-2193-2194-2195-2196-2197-2198-2199-2200-2201-2202-2203-2204-2205-2206-2207-2208-2209-2210-2211-2212-2213-2214-2215-2216-2217-2218-2219-2220-2221-2222-2223-2224-2225-2226-2227-2228-2229-2230-2231-2232-2233-2234-2235-2236-2237-2238-2239-2240-2241-2242-2243-2244-2245-2246-2247-2248-2249-2250-2251-2252-2253-2254-2255-2256-2257-2258-2259-2260-2261-2262-2263-2264-2265-2266-2267-2268-2269-2270-2271-2272-2273-2274-2275-2276-2277-2278-2279-2280-2281-2282-2283-2284-2285-2286-2287-2288-2289-2290-2291-2292-2293-2294-2295-2296-2297-2298-2299-2300-2301-2302-2303-2304-2305-2306-2307-2308-2309-2310-2311-2312-2313-2314-2315-2316-2317-2318-2319-2320-2321-2322-2323-2324-2325-2326-2327-2328-2329-2330-2331-2332-2333-2334-2335-2336-2337-2338-2339-2340-2341-2342-2343-2344-2345-2346-2347-2348-2349-2350-2351-2352-2353-2354-2355-2356-2357-2358-2359-2360-2361-2362-2363-2364-2365-2366-2367-2368-2369-2370-2371-2372-2373-2374-2375-2376-2377-2378-2379-2380-2381-2382-2383-2384-2385-2386-2387-2388-2389-2390-2391-2392-2393-2394-2395-2396-2397-2398-2399-2400-2401-2402-2403-2404-2405-2406-2407-2408-2409-2410-2411-2412-2413-2414-2415-2416-2417-2418-2419-2420-2421-2422-2423-2424-2425-2426-2427-2428-2429-2430-2431-2432-2433-2434-2435-2436-2437-2438-2439-2440-2441-2442-2443-2444-2445-2446-2447-2448-2449-2450-2451-2452-2453-2454-2455-2456-2457-2458-2459-2460-2461-2462-2463-2464-2465-2466-2467-2468-2469-2470-2471-2472-2473-2474-2475-2476-2477-2478-2479-2480-2481-2482-2483-2484-2485-2486-2487-2488-2489-2490-2491-2492-2493-2494-2495-2496-2497-2498-2499-2500-2501-2502-2503-2504-2505-2506-2507-2508-2509-2510-2511-2512-2513-2514-2515-2516-2517-2518-2519-2520-2521-2522-2523-2524-2525-2526-2527-2528-2529-2530-2531-2532-2533-2534-2535-2536-2537-2538-2539-2540-2541-2542-2543-2544-2545-2546-2547-2548-2549-2550-2551-2552-2553-2554-2555-2556-2557-2558-2559-2560-2561-2562-2563-2564-2565-2566-2567-2568-2569-2570-2571-2572-2573-2574-2575-2576-2577-2578-2579-2580-2581-2582-2583-2584-2585-2586-2587-2588-2589-2590-2591-2592-2593-2594-2595-2596-2597-2598-2599-2600-2601-2602-2603-2604-2605-2606-2607-2608-2609-2610-2611-2612-2613-2614-2615-2616-2617-2618-2619-2620-2621-2622-2623-2624-2625-2626-2627-2628-2629-2630-2631-2632-2633-2634-2635-2636-2637-2638-2639-2640-2641-2642-2643-2644-2645-2646-2647-2648-2649-2650-2651-2652-2653-2654-2655-2656-2657-2658-2659-2660-2661-2662-2663-2664-2665-2666-2667-2668-2669-2670-2671-2672-2673-2674-2675-2676-2677-2678-2679-2680-2681-2682-2683-2684-2685-2686-2687-2688-2689-2690-2691-2692-2693-2694-2695-2696-2697-2698-2699-2700-2701-2702-2703-2704-2705-2706-2707-2708-2709-2710-2711-2712-2713-2714-2715-2716-2717-2718-2719-2720-2721-2722-2723-2724-2725-2726-2727-2728-2729-2730-2731-2732-2733-2734-2735-2736-2737-2738-2739-2740-2741-2742-2743-2744-2745-2746-2747-2748-2749-2750-2751-2752-2753-2754-2755-2756-2757-2758-2759-2760-2761-2762-2763-2764-2765-2766-2767-2768-2769-2770-2771-2772-2773-2774-2775-2776-2777-2778-2779-2780-2781-2782-2783-2784-2785-2786-2787-2788-2789-2790-2791-2792-2793-2794-2795-2796-2797-2798-2799-2800-2801-2802-2803-2804-2805-2806-2807-2808-2809-2810-2811-2812-2813-2814-2815-2816-2817-2818-2819
```

0V 1 WFTSGVDEHYBTBTVQVCNMDHSCNNMI BNTTIDBNGAOTVYET KEET DDCUXTTII 6A

[illegible]

1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Figure 1**
 10. **Figure 2**
 11. **Figure 3**
 12. **Figure 4**
 13. **Figure 5**
 14. **Figure 6**
 15. **Figure 7**
 16. **Figure 8**
 17. **Figure 9**
 18. **Figure 10**
 19. **Figure 11**
 20. **Figure 12**
 21. **Figure 13**
 22. **Figure 14**
 23. **Figure 15**
 24. **Figure 16**
 25. **Figure 17**
 26. **Figure 18**
 27. **Figure 19**
 28. **Figure 20**
 29. **Figure 21**
 30. **Figure 22**
 31. **Figure 23**
 32. **Figure 24**
 33. **Figure 25**
 34. **Figure 26**
 35. **Figure 27**
 36. **Figure 28**
 37. **Figure 29**
 38. **Figure 30**
 39. **Figure 31**
 40. **Figure 32**
 41. **Figure 33**
 42. **Figure 34**
 43. **Figure 35**
 44. **Figure 36**
 45. **Figure 37**
 46. **Figure 38**
 47. **Figure 39**
 48. **Figure 40**
 49. **Figure 41**
 50. **Figure 42**
 51. **Figure 43**
 52. **Figure 44**
 53. **Figure 45**
 54. **Figure 46**
 55. **Figure 47**
 56. **Figure 48**
 57. **Figure 49**
 58. **Figure 50**
 59. **Figure 51**
 60. **Figure 52**
 61. **Figure 53**
 62. **Figure 54**
 63. **Figure 55**
 64. **Figure 56**
 65. **Figure 57**
 66. **Figure 58**
 67. **Figure 59**
 68. **Figure 60**
 69. **Figure 61**
 70. **Figure 62**
 71. **Figure 63**
 72. **Figure 64**
 73. **Figure 65**
 74. **Figure 66**
 75. **Figure 67**
 76. **Figure 68**
 77. **Figure 69**
 78. **Figure 70**
 79. **Figure 71**
 80. **Figure 72**
 81. **Figure 73**
 82. **Figure 74**
 83. **Figure 75**
 84. **Figure 76**
 85. **Figure 77**
 86. **Figure 78**
 87. **Figure 79**
 88. **Figure 80**
 89. **Figure 81**
 90. **Figure 82**
 91. **Figure 83**
 92. **Figure 84**
 93. **Figure 85**
 94. **Figure 86**
 95. **Figure 87**
 96. **Figure 88**
 97. **Figure 89**
 98. **Figure 90**
 99. **Figure 91**
 100. **Figure 92**
 101. **Figure 93**
 102. **Figure 94**
 103. **Figure 95**
 104. **Figure 96**
 105. **Figure 97**
 106. **Figure 98**
 107. **Figure 99**
 108. **Figure 100**
 109. **Figure 101**
 110. **Figure 102**
 111. **Figure 103**
 112. **Figure 104**
 113. **Figure 105**
 114. **Figure 106**
 115. **Figure 107**
 116. **Figure 108**
 117. **Figure 109**
 118. **Figure 110**
 119. **Figure 111**
 120. **Figure 112**
 121. **Figure 113**
 122. **Figure 114**
 123. **Figure 115**
 124. **Figure 116**
 125. **Figure 117**
 126. **Figure 118**
 127. **Figure 119**
 128. **Figure 120**
 129. **Figure 121**
 130. **Figure 122**
 131. **Figure 123**
 132. **Figure 124**
 133. **Figure 125**
 134. **Figure 126**
 135. **Figure 127**
 136. **Figure 128**
 137. **Figure 129**
 138. **Figure 130**
 139. **Figure 131**
 140. **Figure 132**
 141. **Figure 133**
 142. **Figure 134**
 143. **Figure 135**
 144. **Figure 136**
 145. **Figure 137**
 146. **Figure 138**
 147. **Figure 139**
 148. **Figure 140**
 149. **Figure 141**
 150. **Figure 142**
 151. **Figure 143**
 152. **Figure 144**
 153. **Figure 145**
 154. **Figure 146**
 155. **Figure 147**
 156. **Figure 148**
 157. **Figure 149**
 158. **Figure 150**
 159. **Figure 151**
 160. **Figure 152**
 161. **Figure 153**
 162. **Figure 154**
 163. **Figure 155**
 164. **Figure 156**
 165. **Figure 157**
 166. **Figure 158**
 167. **Figure 159**
 168. **Figure 160**
 169. **Figure 161**
 170. **Figure 162**
 171. **Figure 163**
 172. **Figure 164**
 173. **Figure 165**
 174. **Figure 166**
 175. **Figure 167**
 176. **Figure 168**
 177. **Figure 169**
 178. **Figure 170**
 179. **Figure 171**
 180. **Figure 172**
 181. **Figure 173**
 182. **Figure 174**
 183. **Figure 175**
 184. **Figure 176**
 185. **Figure 177**
 186. **Figure 178**
 187. **Figure 179**
 188. **Figure 180**
 189. **Figure 181**
 190. **Figure 182**
 191. **Figure 183**
 192. **Figure 184**
 193. **Figure 185**
 194. **Figure 186**
 195. **Figure 187**
 196. **Figure 188**
 197. **Figure 189**
 198. **Figure 190**
 199. **Figure 191**
 200. **Figure 192**
 201. **Figure 193**
 202. **Figure 194**
 203. **Figure 195**
 204. **Figure 196**
 205. **Figure 197**
 206. **Figure 198**
 207. **Figure 199**
 208. **Figure 200**
 209. **Figure 201**
 210. **Figure 202**
 211. **Figure 203**
 212. **Figure 204**
 213. **Figure 205**
 214. **Figure 206**
 215. **Figure 207**
 216. **Figure 208**
 217. **Figure 209**

01 VOICENET INI MESSDDHGVNFKEHF I AIDI IAADESI QUMDEGKILALNIEIREV L20

|||||: |||: / : |||||:

DB 116 VLGICKETFLYLIESDESHGTFKFKPSQYIKIDTIADESFTQMDLGDRILKLNTEVREV 175

QY 121 GPNKKGFYLAFOVGACVALSVRYFKKCPYKLNLMFPDTP-MDSQSLVEVRGSC 179

Db 176 GPIERKGFYLAFDIGACIALVSVRFYKKCPETVRNLAMFPDTIPRVDSSSLVEVRGSC 235

OV 180 VNNSKEEDPBRMYCSTEGEWLVPIGKCSNAGYEE 214

nh
236 YKSSEFDTPKTYCCADCDWIYBICBCICTCTTCGYEE 370

|::| |::| ::|||::| |||
|::| |::| ::|||::| |||

RESULT 5

receptor protein-tyrosine kinase - human

C;species: Homo sapiens (man)
C;Date: 20-Mar-1998 #accuacc 20-Mar-1998 #4-ent 10-Mar-1998

C;Accession: I78844

Oncogene 10, 897-905, 1995

A: Reference number: 158351; MUID: 95206782

A/Accession: I/8844

A;Molecule type: mRNA

A;Cross-references: GB:L366645; NID:q551613; PIDN:AA74246.1; PID:q551614

A:Gene: HEK8
C:Gene:cs:
C:Gene:cs:

C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin typ

Query Match	Similarity	75.5%	Score	905.5	DB 2	Length	986
Best Local	Similarity	73.3%	Pred. No.	1.6e-74			
Matches	Conservative	30	Mismatches	28	Indels	1	Gaps
QY	1	WEISGVDEHYPIRFTYQVCNVMDSQNNMLTNTNWPNSAQRIYELKFTLDCNSIPL	60				
Db	54	MEEVIMDEKNTPIRITTYQVCNVMESQNNMLTDTWITREGAQRVYIEIKFTLDCNSLPG	113				
QY	61	VLGTCKEFNLYYMRSDDHGKFRPHOHTKIDTIAADESFQOMLGDDILKLNTEIRRY	120				
Db	114	VMGTCKEFNLYYSDNDKRFIRENQVKIDTIAADESFQVDDGGRIMKLNTEIRRY	173				
QY	121	GPVNNKGGYLLAFQDYGACVALYSVRYEFKCPFTYKLNLMFEDTPV-MDSQSLVEYRGSC	179				
Db	174	GPLSKRGYLLAFQDYGACIALYSVRVYFKCPDLYRNLAQFDLTIGADTSLSVEYRGSC	233				
QY	180	VNNSKEEDPRMYCSTEGEMLYPIRIGKSCNNAIYERGFMCQ	220				
Db	234	VNNSKEEDVPRMYCGADGEMLYPIRIGKSCNNAIHEERSGCQ	274				

RESULT 6
151549
Receptor tyrosine kinase - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text-change 18-Jun-1999
C:Accession: 151549
R:Winning, R.S.; Sargent, T.D.
Mech. Dev. 46, 219-229, 1994
A:Title: Pagliaccio, a member of the Eph family of receptor tyrosine kinase genes, has 1
A:Reference number: 151549; MUID:95001564
A:Accession: 151549
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-985 <WIN>
A:Cross-references: GB:IL26099; NID:g416402; PIDN:AAA64464.1; PID:g416403
A:Genetics:
A:Gene: Pag
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C:Keywords: ATP; transmembrane protein
E:618-884/Domain: protein kinase homology <KIN>
E:626-634/Region: protein kinase ATP-binding motif

[illegible]

RESULT 7
S78059
protein-tyrosine kinase (EC 2.7.1.12) Eph precursor - mouse
C1:Species: Mus musculus (house mouse)
C1:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 18-Jun-1999
C1:Accession: S78059, S30505, I58366
R:Charnay, P.
submitted to the EMBL Data Library, March 1992

A:Reference number: S78059
A:Accession: S78059
A:Molecule type: mRNA
A:Residues: 1-986 <CHA>
A:Cross-references: EMBL:X65138; NID:954083; PIDN:CAA6268.1; PID:954084
R:Giardi-Hebenstreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chester, A.; Wilkin
Oncogene 7, 2449-2506, 1992
A:Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed
A:Reference number: S30496; MUID:93096484
A:Accession: S30505
A:Molecule type: mRNA
A:Residues: 1-31,55-986 <GIL>
A:Cross-references: EMBL:X65138
C:Genetics:
A:Gene: Sek
C:Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repa
C:Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransf
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-986/Product: protein-tyrosine kinase Eph #status predicted <MAT>
F:548-569/Domain: transmembrane #status predicted <TM>
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif
F:908-974/Domain: SAM homology <SAM>
F:1235,340,408,423/Binding site: carboxylate (asn) (covalent) #status predicted

[illegible]

RESULT 8
I48967
brain-specific kinase - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I48967
R:Zhou, R.R.; Copeland, T.D.; Kromer, L.F.; Schulz, N.T.
J. Neurosci. Res. 37, 129-143, 1994
A:Title: Isolation and characterization of Bsk, a growth factor receptor-like tyrosin
A:Reference number: I48967; MUID:94194581
A:Accession: I48967
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-877 <RES>
A:Cross-references: EMBL:U07357; NID:g466369; PIDN:AAA17038.1; PID:g466370
C:Genetics:
A:Gene: Bsk
C:Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repea
C:Keywords: Arp; transmembrane protein
F:512-778/Domain: protein kinase homology <IN>
F:520-528/Region: protein kinase Arp-binding motif
;801-868/Domain: SAM homology <SAM>

Query Match	72.28;	Score 866.5;	DB 2;	Length 877;
Best Local Similarity	68.38;	Pred. NO. 5e-71;		

[illegible]

A:Molecule type: mRNA
A:Residues: 1-893 <MAI>
A:Cross-references: EMBL:S68028
A>Note: The authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; transmembrane protein
F:563-829/Domain: protein kinase homology <KIN>
F:571-579/Region: protein kinase ATP-binding motif

Query Match 72.0% Score 863.5; DB 2; Length 893;
Best Local Similarity 67.9%; Pred. No. 9,5e-71;
Matches 150; Conservative 36; Mismatches 34; Indels 1; Gaps 1;

QY 1 WEELSGVDEHTPTRTIOVCNVDHSONNMWLRITMVPNRNSAKRIYELKFTLRDCNSIPL 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 85 WEEIGEVDENAPPHITYOVCKVMEOQNMMTLTSMISNEGSRIFIELKFTLRDCNSLPG 144
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 VLGTCKETFNLYMESDDDHGVKFRHEOFTKIDITIAADESTFDLDGRILIKLTETEIREV 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 145 GLGTCKEFTNNMYEESDDENGRIKNDQYIKIDITIAADESTFELDLDGRVKMLTEVRDY 204
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 GPVNKKGGTYLAFOVGACVALVSRYVFYFKCPFTYKNLAMEPDTVP-MDSQSLEYVNGSC 179
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 205 GPLSKKGTYLAFOVGACIALVSVRYVYKKCPSVYRHLAVPDITTGADSSQLLETVSGSC 264
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 180 VNNSKEEDPPRMYSCTEGEWLVPIGKCSNCNAGYEERGFMCQ 220
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 265 VNHSTYDDPPRMHCASBGEMLVPIGCKCKRAGYEEKNGTQ 305
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
S51604
receptor-like tyrosine kinase Ehk-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence,revision 21-Jul-1995 #text-change 29-May-1998
C:Accession: S51604
R:Macosplaire, P.C.; Barrezuela, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase
A:Reference number: S49015; MUID:94067777
A:Accession: S51604
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-981 <MAI>
A:Cross-references: EMBL:S68029
A>Note: The authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; transmembrane protein
F:651-917/Domain: protein kinase homology <KIN>
F:659-667/Region: protein kinase ATP-binding motif

RESULT 12
S49015
receptor tyrosine kinase Etk-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C:Accession: S49015; S51602
R:Maizomleire, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A:Reference number: S49015; MUID:94067777
A:Accession: S49015
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1005 <MA1>
A:Cross-references: EMBL:S68024
A:Note: the authors translated the codon GAC for residue 170 as Glu
A:Accession: S51602
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305, 'G', 359-1005 <MA2>
A:Cross-references: EMBL:S68026
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C:Keywords: ATP; transmembrane protein
F:675-941/Domain: protein kinase homology <KIN>
F:683-691/Region: protein kinase ATP-binding motif

Query Match 72.0%; Score 863.5; DB 2; length 1005;
Best Local Similarity 67.9%; Pred. No. 1.1e-70;
Matches 150; Conservative 36; Mismatches 34; Indels 1; Gaps 1;

QY 1 WEISGVDEHYPIRTYQVCNWDHSONNWLRTNWPFRSAQIYVELKFTLRDCNSIPL 60
DB 85 WEISGVDEHYPIRTYQVCNWDHSONNWLRTNWPFRSAQIYVELKFTLRDCNSIPL 60
QY 61 VLGTCKEFTNLYMESDDHGVKFRHOFTKIDITIADESFTOMDGRILKLTREIRY 120
DB 145 GLGTCKEFTNLYMESDDHGVKFRHOFTKIDITIADESFTOMDGRILKLTREIRY 120
QY 121 GPNKKGFLAODVAGACALVSVRYEFKCPFTYKNLAMPDTPV-MDSQSLVEYRGSC 179
DB 205 GPNKKGFLAODVAGACALVSVRYEFKCPFTYKNLAMPDTPV-MDSQSLVEYRGSC 179
QY 180 VNNSKEEDPPRMVCTEGEVLVPIGKSCNAGYEREGFMQ 220
DB 265 VNNSKEEDPPRMVCTEGEVLVPIGKSCNAGYEREGFMQ 220

RESULT 13
178843
receptor protein-tyrosine kinase - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C:Accession: 178843
R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welch,
Oncogene 10, 897-905, 1995
A:Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein-ty
A:Reference number: 158351; MUID:95206782
A:Accession: 178843
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-991 <RES>
A:Cross-references: GB:L36644; NID:9551611; PIDN:AAA74245.1; PID:9551612
C:Genetics:
A:Gene: HEK7
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
F:627-893/Domain: protein kinase homology <KIN>
F:916-982/Domain: SAM homology <SAM>

Query Match 71.7%; Score 860.5; DB 2; length 991;

Best Local Similarity 67.9%; Pred. No. 2e-70;
Matches 150; Conservative 35; Mismatches 35; Indels 1; Gaps 1;
QY 1 WEISGVDEHYPIRTYQVCNWDHSONNWLRTNWPFRSAQIYVELKFTLRDCNSIPL 60
DB 59 WEISGVDEHYPIRTYQVCNWDHSONNWLRTNWPFRSAQIYVELKFTLRDCNSIPL 60
QY 61 VLGTCKEFTNLYMESDDHGVKFRHOFTKIDITIADESFTOMDGRILKLTREIRY 120
DB 119 GLGTCKEFTNLYMESDDHGVKFRHOFTKIDITIADESFTOMDGRILKLTREIRY 120
QY 121 GPNKKGFLAODVAGACALVSVRYEFKCPFTYKNLAMPDTPV-MDSQSLVEYRGSC 179
DB 179 GPNKKGFLAODVAGACALVSVRYEFKCPFTYKNLAMPDTPV-MDSQSLVEYRGSC 179
QY 180 VNNSKEEDPPRMVCTEGEVLVPIGKSCNAGYEREGFMQ 220
DB 239 VNNSKEEDPPRMVCTEGEVLVPIGKSCNAGYEREGFMQ 220

RESULT 14
JC5673
receptor tyrosine kinase (EC 2.7.-.-) Etk-td1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 07-May-1999
C:Accession: JC5673
R:Takekoshi, A.H.; Muramatsu, T.; Kaneda, N.
Cell Struct. Funct. 22, 477-485, 1997
A:Title: A novel truncated variant form of Etk/MDKI receptor tyrosine kinase is expre
A:Reference number: JC5672; MUID:98035156
A:Accession: JC5673
A:Molecule type: mRNA
A:Residues: 1-605 <TAL>
A:Experimental source: embryo
A:Comment: This enzyme plays a regulatory role during neural development and embryoge
C:Keywords: brain; phosphotransferase
F:1-30/Domain: signal sequence status predicted <SIG>
F:31-605/Product: receptor tyrosine kinase Etk-td1 status predicted <MAT>
F:31-548/Domain: extracellular status predicted <EXT>
F:331-438/Domain: fibronectin type III repeat <FNI>
F:441-534/Domain: fibronectin type III repeat <FNI2>
F:549-574/Domain: transmembrane status predicted <TM>

Query Match 71.5%; Score 857.5; DB 2; length 605;
Best Local Similarity 70.0%; Pred. No. 2.1e-70;
Matches 156; Conservative 36; Mismatches 28; Indels 3; Gaps 2;

QY 1 WEISGVDEHYPIRTYQVCNWDHSONNWLRTNWPFRSAQIYVELKFTLRDCNSIPL 60
DB 55 WEISGVDEHYPIRTYQVCNWDHSONNWLRTNWPFRSAQIYVELKFTLRDCNSIPL 60
QY 61 VLGTCKEFTNLYMESDDHGVKFRHOFTKIDITIADESFTOMDGRILKLTREIRY 120
DB 115 VLGTCKEFTNLYMESDDHGVKFRHOFTKIDITIADESFTOMDGRILKLTREIRY 120
QY 121 GPNKKGFLAODVAGACALVSVRYEFKCPFTYKNLAMPDTPV-MDSQSLVEYRGSC 179
DB 175 GPNKKGFLAODVAGACALVSVRYEFKCPFTYKNLAMPDTPV-MDSQSLVEYRGSC 179
QY 180 VNNSKEEDPPRMVCTEGEVLVPIGKSCNAGYEREGFMQ 220
DB 235 VNNSKEEDPPRMVCTEGEVLVPIGKSCNAGYEREGFMQ 220

RESULT 15
148612
developmental kinase 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 148612; S51741
R:Ciossek, T.; Millauer, B.; Ullrich, A.
Oncogene 9, 97-108, 1995

A:Title: Identification of alternatively spliced mRNA encoding variants of MDK1, a novel
A:Reference number: 148611
A:Accession: 148612
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-610 <RES>
A:Cross-references: EMBL:X79083; NID:g607135; PIDN:CAAS5688.1; PID:g607136

Query Match	71.5%;	Score 857.5;	DB 2;	Length 610;
Best Local Similarity	70.0%;	Pred. No. 2.1e-70;		
Matches 156;	Conservative 36;	Mismatches 28;	Indels 3;	Gaps 2;

```

Qy 1 MEEISGVEHENTPIRTIYOVCMNMMHSONNMLRTMWPVNSOKRTIYVEKFLRDCNSIPL 60
Db 55 MEEISGDEBENTPIRTIYOVCMMEBNONNMLRTMWSKGNORLTVEKFLRDCNSLPG 114
Qy 61 VLGCTKETFNLYMESDDHGKVFKEHOFTIDYIADDESTQMDLGDRLIKLNTETREY 120
Db 115 VLGCTKETFNLYYETDYDGTGRNIRENLYKIDITIADESTQDGLDERKMKLNTETREI 174
Qy 121 GPVKKKGYTLAFQDVGACVALSVKRYVKKCPFTYVKLIAMFPDVP--MDSOLVEYRGSC 179
Db 175 GPLSKRGFYTLAFODGACIALSVKVVYKKCMWTIVENILAVFPDVTGSEFSESLVEYRGTC 234
Qy 180 VNNSKE--EDPPRMVCSCEGELVPIGKCSGNAGIEERGFQCO 220
Db 235 VSSAEELAEENSPRMHCSAEGELVPIGKCIKNAQKQGDGTCE 277

```

Search completed: May 9, 2000, 22:27:14
Job time: 4153 sec

CC production and/or function of pre-B, B and T cells. The TK and its
CC analogues have activity in transducing signals or in stimulating
CC cellular responses such as growth and/or differentiation.
SQ Sequence 983 AA;

Query Match 100.0%; Score 1200; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 7,8e-119;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEESGVDEHTPIRTYOVCNMVDSQNMNLRITMVPNSAKIYVELKFTLRDNCNSIPL 60
DB 52 WEESGVDEHTPIRTYOVCNMVDSQNMNLRITMVPNSAKIYVELKFTLRDNCNSIPL 111
QY 61 VLGTCKEFTNLYMESDDHGVKFRHOFTKIDTIADESFTQMDLGRILKLTETIREV 120
DB 112 VLGTCKEFTNLYMESDDHGVKFRHOFTKIDTIADESFTQMDLGRILKLTETIREV 171
QY 121 GPVKKKGFTYLAFOVGACVALSVRYVFKKCPFTYKNIAMFPDTPVMDQSLEVRGSCV 180
DB 172 GPVKKKGFTYLAFOVGACVALSVRYVFKKCPFTYKNIAMFPDTPVMDQSLEVRGSCV 231
QY 181 NNSKEEDPPRMKCTEGEMLVPIGKSCNAGYEERGFMCQ 220
DB 232 NNSKEEDPPRMKCTEGEMLVPIGKSCNAGYEERGFMCQ 271

RESULT 2

ID R75711 standard; Protein; 983 AA.
AC R75711;
DT 11-NOV-1995 (first entry)
DE Eph-related PTK Cdk4.
KM Cdk4; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
OS prognosis.
PN MO9515375-A.
PD 08-JUN-1995.
PE 07-SEP-1994; U10140.
PR 03-DEC-1993; US-162809.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PI Pasquale EB, Sajdeli FG;
DR WPI: 95-215256/28.
DR N-PSDB; Q90659.
PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
PT cancer.
PS Disclosure; Page 85-89; 129pp; English.
CC Probes derived from the Eph-related PTKs Cdk4 (Q90659) and Cdk5
CC (Q90660) were used to isolate novel cDNA clones (Q90652-58,
CC Q90661-62) from chicken embryo and embryonic brain libraries.
CC Cdk4 is highly expressed in the chicken developing brain and
CC embryonic tissues and also in the adult brain and retina.
SQ Sequence 983 AA;

Query Match 94.7%; Score 1136; DB 1; Length 983;
Best Local Similarity 94.1%; Pred. No. 4,9e-112;
Matches 207; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEESGVDEHTPIRTYOVCNMVDSQNMNLRITMVPNSAKIYVELKFTLRDNCNSIPL 60
DB 51 WEESGVDEHTPIRTYOVCNMVDSQNMNLRITMVPNSAKIYVELKFTLRDNCNSIPL 110
QY 61 VLGTCKEFTNLYMESDDHGVKFRHOFTKIDTIADESFTQMDLGRILKLTETIREV 120
DB 111 VLGTCKEFTNLYMESDDHGVKFRHOFTKIDTIADESFTQMDLGRILKLTETIREV 170
QY 121 GPVKKKGFTYLAFOVGACVALSVRYVFKKCPFTYKNIAMFPDTPVMDQSLEVRGSCV 180
DB 171 GPVKKKGFTYLAFOVGACVALSVRYVFKKCPFTYKNIAMFPDTPVMDQSLEVRGSCV 230
QY 181 NNSKEEDPPRMKCTEGEMLVPIGKSCNAGYEERGFMCQ 220
DB 232 NNSKEEDPPRMKCTEGEMLVPIGKSCNAGYEERGFMCQ 271

DB 231 NNSKEEDPPRMKCTEGEMLVPIGKSCNAGYEERGFMCQ 270

RESULT 3

ID W83148 standard; Protein; 948 AA.
AC W83148;
DT 11-FEB-1999 (first entry)
DE Rat receptor tyrosine kinase Etk-2.
KM Receptor tyrosine kinase; Ror-1; Ror-2; Etk-1; Etk-2; detection;
KM neurotrophin activity; tkB; proto-oncogene; tyrosine kinase receptor;
KM binding protein; BDNF; Nr-3; diagnosis.
OS Rattus sp.
PN US5843749-A.
PD 01-DEC-1998.
PE 06-JUN-1995; 469537.
PR 17-MAR-1995; US-406247.
PR 26-JUL-1991; US-736559.
PR 28-OCT-1993; US-144992.
PR 06-JUN-1995; US-469537.
PA (REGG-) REGENERON PHARM INC.
PI Malsomple PC, Maslakowski P, Yancopoulos GD;
DR WPI: 99-044584/04.
DR N-PSDB; V70208.
PT DNA encoding receptor tyrosine kinase proteins - and corresponding
PT proteins
PS Example; Fig 21; 194pp; English.
CC The present invention describes nucleic acid molecules for ror-1.
CC ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins:
CC Ror-1; Ror-2; Etk-1; and Etk-2. The proteins are orphan receptor
CC tyrosine kinases. The present sequence represents rat Etk-2.
SQ Sequence 948 AA;

Query Match 76.2%; Score 914.5; DB 1; Length 948;
Best Local Similarity 74.0%; Pred. No. 1,5e-88;
Matches 159; Conservative 31; Mismatches 24; Indels 1; Gaps 1;

QY 1 WEESGVDEHTPIRTYOVCNMVDSQNMNLRITMVPNSAKIYVELKFTLRDNCNSIPL 60
DB 56 WDATTEDEHNRPHTIYQVCNMVDSQNMNLRITMVPNSAKIYVELKFTLRDNCNSIPL 115
QY 61 VLGTCKEFTNLYMESDDHGVKFRHOFTKIDTIADESFTQMDLGRILKLTETIREV 120
DB 116 VLGTCKEFTNLYMESDDHGVKFRHOFTKIDTIADESFTQMDLGRILKLTETIREV 175
QY 121 GPVKKKGFTYLAFOVGACVALSVRYVFKKCPFTYKNIAMFPDTPVMDQSLEVRGSCV 179
DB 176 GPVKKKGFTYLAFOVGACVALSVRYVFKKCPFTYKNIAMFPDTPVMDQSLEVRGSCV 235
QY 180 VNSKEEDPPRMKCTEGEMLVPIGKSCNAGYE 214
DB 236 VNSKEEDPPRMKCTEGEMLVPIGKSCNAGYE 270

RESULT 4

ID R85936 standard; Protein; 986 AA.
AC R85936;
DT 14-FEB-1996 (first entry)
DE Protein tyrosine-kinase bptk7.
KM Protein tyrosine-kinase; PTK; bptk7; agonist; cell growth;
KM differentiation.
OS Homo sapiens.
PN location/Qualifiers
PD peptide
PE 1, 19
PR /label= Sig_peptide
PR /label= 20, 547
PR /label= Extracellular_domain
PR /label= 548, 570
PR /label= Transmembrane_domain
PR /label= 571, 986
PR /label= Intracellular_tyrosine_kinase_domain
FT domain

MO95227061-A1.
PD 12-OCT-1995.
PR 04-APR-1995; U04228.
PR 04-APR-1994; US-222616.
PA (GETH) GENENTECH INC.
PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
PI Wood WZ;
PI WPI: 95-36160/47.
DR N-PSDB: T03100.
PR Agonist antibodies which activate specific protein tyrosine
PT kinase(s) - also activate chimeric proteins of kinase extracellular
PR domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of cell growth and differentiation
PS Disclosure: Page 95-99: 125pp: English.
CC DNA probes based on protein tyrosine-kinase (ptk) sequences were used
CC to screen cDNA libraries to identify novel ptk genes. The bptks,
CC bptk1, bptk2, bptk3, bptk4, bptk5 and bptk7 (R85924-28 and R85935,
CC respectively) are expressed in human brain tissue and show homology
CC to known ptk's. A full-length sequence for bptk7 (R85936) was also
CC obtd. bptk7 can be used to design drugs that modulate ptk activity.
SQ Sequence 986 AA;

Query Match 75.5%; Score 905.5; DB 1; Length 986;
Best Local Similarity 73.3%; Pred. No. 1.4e-87;
Matches 162; Conservative 30; Mismatches 26; Indels 1; Gaps 1;

QY 1 WEISGVDEHYTPIRITYOVCCNMDHSONNWLTNTNWPVPRNSAQRIYVELKFTLDCNSIPL 60
Db 54 WEVVSIMDEKNTPIRTYOVCCNMEPSQNNWLTMTDITRGARVYIEIKFTLDCNSLPDG 113
QY 61 VLGTKEKFNLYMESDDDHGKVFREHOFTKIDTTLADESFTQMDGDRILKLTIREYV 120
Db 114 VMGTKEKFNLYMESDDDHGKVFREHOFTKIDTTLADESFTQMDGDRILKLTIREYV 173
QY 121 GPVNKKGGYLAQDVGACALVSVYFEKCFETYNKLAPEFDTPV-MDSOSLYVGRSC 179
Db 174 GPLSKKGGYLAQDVGACALVSVYFEKCFETYNKLAPEFDTPV-MDSOSLYVGRSC 233
QY 180 VNNSEKEDPPRMVCTSTEGEMLVPIKSCSNAGYEERGFMCQ 220
Db 234 VNNSEKEDPPRMVCTSTEGEMLVPIKSCSNAGYEERGFMCQ 274

RESULT 5
R85091
R85091 standard; Protein: 986 AA.

ID AC R85091.
DI 16-APR-1996 (first entry)
DE EPH-1-like receptor protein tyrosine kinase HEK8.
KW EPH-1-like receptor protein tyrosine kinase; PTK; HEK8;
KW human eph-1-like kinase; therapy; diagnosis; vector; antibody.
PN Homo sapiens.
PN MO9528484-A1.
PD 26-OCT-1995.
PR 14-APR-1995; U04681.
PR 15-APR-1994; US-229509.
PA (AMGE-) AMGEN INC.
PI Fox GM, Jing S, Welcher AA;
PI WPI: 95-373799/48.
DR N-PSDB: T02948.
PR New nucleic acid encoding EPH-1-like receptor tyrosine kinase(s) -
PT and related vectors, host cells, proteins, antibodies etc., used
PT diagnostically and therapeutically to modulate receptor activation
or proth.

PS Claim 18; Page 62-65; 133pp: English.
CC 4 Novel human EPH-1-like receptor protein tyrosine kinases, HEK5, HEK7,
CC HEK8 and HEK11 (R85089-92), respectively, were identified following
CC isolation of their encoding cDNAs (T02946-49) from a human foetal brain
CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
CC catalytic domain of chicken EPH-1-like receptors Cck5, Cck7 and Cck8.
CC HEK11 shows no homology to any known EPH-1-like receptor. Recombinant
CC HEK receptors (or their soluble extracellular domains) are produced by

Query Match	75.5%	Score 905.5	DB 1	Length 986
Best Local Similarity	73.3%	Pred. No. 1,4e-87		
Matches 162	Conservative 30	Mismatches 28	Indels 1	Gaps
OY	1	WEEISGVDEHETPIKTYOVNVMDHSONNMTKTNVNPNSAKIKYVEKFTLRDNCNIP	60	
DB	54	WEVSIMDEKNTPIITTYQVNCVMESQNNMLRTDITTEEGQRYVTEIKFTLRDNCNIP	113	
OY	61	VLGTCKETFNLYMESDDHGVKREHOFTKIDITIADESEFTQMDLGRDILKLTREIV	120	
DB	114	VWGCTKEFNLYYYYSSDNDKEREIFRENOFVKIDITIADESEFTQVIGRIMKLTREIV	173	
OY	121	GPVNNKGYTLAFQDYGACALYSAVRYFKKCPFTYKTNLAMPDYP-NDOSQVYVRSSC	179	
DB	174	GPLSKRGYTLAFQDYGACIALYSAVFYKKCPFTYRNLAQPFDTTGADTSLSVEVRSC	233	
OY	180	VNNSKEEDPRMYCSTEGEWLPIPIKCSGNNAGEERGEMQC	220	
DB	234	VNNSKEEDVPRMYCSTEGEWLPIPIKCSGNNAGEERGEMQC	274	
RESULT	6			
ID	W71628			
ID	W71628	standard; Protein; 877 AA.		
AC	W71628			
DT	25-NOV-1998	(first entry)		
DE	Mouse Bsk receptor-like tyrosine kinase.			
KW	Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neoplasm;			
KW	neurodegenerative disease; limbic system neuron regeneration;			
KW	chromosomal abnormality; degenerative growth; development disorder;			
KW	viral infection; bacterial infection; Alzheimer's disease; epilepsy;			
KW	schizophrenia; stroke; cerebral ischaemia.			
OS	Mus sp.			
PN	US814479-A.			
PD	29-SEP-1998.			
PF	11-JUN-1996; 673789.			
PR	04-JAN-1994; US-177812.			
PR	11-JUN-1996; US-673789.			
PA	(KROM/) KROMER L F.			
PA	(SCHU/) SCHULZ N T.			
PA	(WOUD/) WOUDE G F V.			
PA	(ZHOU/) ZHOU R.			
PI	Kromer LF, Schulz NT, Woude GF, Zhou R;			
DR	WPI: 98-541751/46.			
DR	N-PDB: V818192.			
PT	Isolated nucleic acid sequence encoding protein - used in Bsk			
PT	nucleic acid probes, used in detecting alterations in level of Bsk			
PT	messenger-RNA in biological samples isolated from mammal afflicted			
PT	with disease			
PS	Claim 1; Fig 2; 72pp. English.			
CC	The present sequence represents mouse Bsk, which is a receptor-like			
CC	tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in			
CC	Bsk nucleic acid probes, which can be used in detecting alterations in			
CC	the level of Bsk messenger-RNA (mRNA) in biological samples isolated			
CC	from a mammal afflicted with a disease, such as neurodegenerative			
CC	diseases or disorders and neoplasms. The nucleic acid sequence can also			
CC	be delivered into the limbic system of patients with limbic system			
CC	neurodegenerative disease, disorder or injury, to promote or enhance			
CC	limbic system neuron regeneration or growth. Such neurodegenerative			
CC	diseases include, chromosomal abnormalities, degenerative growth and			
CC	development disorders, viral infections, bacterial infections, brain			
CC	injuries, neoplastic conditions, Alzheimer's disease, epilepsy,			
CC	schizophrenia, or stroke and cerebral ischaemia.			
CC	Sequence 877 AA;			

Query Match 72.2%; Score 866.5; DB 1; Length 877;
Best Local Similarity 68.3%; Pred. No. 1,7e-83;
Matches 151; Conservative 35; Mismatches 34; Indels 1; Gaps 1;

QY 1 WEELSGVDENHTPIRTYOVCNVMDSQNNMLRTNWPVNSAQKIYELKFTLRDCNSIPL 60
DB 85 WEELGEVDENHTPIRTYOVCNVMDSQNNMLRTNWPVNSAQKIYELKFTLRDCNSIPL 144
QY 61 VLGTCKETFNLYMESDDHGVKREHOFKIDITIADESFQMDLGDRIKLKNTETREV 120
DB 145 GLGTCKETFNLYMESDDHGVKREHOFKIDITIADESFQMDLGDRIKLKNTETREV 204
QY 121 GPVKKGFYLAFOVGVACVAVSVRYVFKKCPFTYKNIAMPDTPV-MDSQSLVEVNGSC 179
DB 205 GPLSKKGFYLAFOVGVACVAVSVRYVFKKCPFTYKNIAMPDTPVITGADSSQLLEVSGSC 264
QY 180 VNNSKEEDPPRMKCSAGEWLVPIGKCSNAGYERGFMCQ 220
DB 265 VNHSVTDDPPRMKCSAGEWLVPIGKCKCKAGYEKNGTCQ 305

RESULT 7
ID W83147
AC W83147 standard; Protein; 1005 AA.
DT 11-FEB-1999 (first entry)
DE Rat receptor tyrosine kinase Etk-1.
KW Receptor tyrosine kinase; Ror-1; Ror-2; Etk-1; Etk-2; detection;
KM neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
KW binding protein; BDNF; NT-3; diagnosis.
OS Rattus sp.
PN US843749-A.
PD 01-DEC-1998.
PF 06-JUN-1995; 469537.
PR 17-MAR-1995; US-406247.
PR 26-JUL-1991; US-736559.
PR 28-OCT-1993; US-144992.
PR 06-JUN-1995; US-469537.
PA (REGG-) REGENERON PHARM INC.
PI Maisongierre PC, Maslakowski P, Yancopoulos GD;
DR WPI; 99-044584/04.
DR N-PSDB; V70207.
PT DNA encoding receptor tyrosine kinase proteins - and corresponding
PT proteins
PS Example; Fig 22; 194pp; English.
CC The present invention describes nucleic acid molecules for ror-1,
CC ror-2, etk-1 and etk-2. Also described are the corresponding proteins:
CC Ror-1; Ror-2; Etk-1; and Etk-2. The proteins are orphan receptor
CC tyrosine kinases. The present sequence represents rat Etk-1.
SQ Sequence 1005 AA;

Query Match 72.2%; Score 866.5; DB 1; Length 1005;
Best Local Similarity 68.3%; Pred. No. 2.1e-83;
Matches 151; Conservative 35; Mismatches 34; Indels 1; Gaps 1;

QY 1 WEELSGVDENHTPIRTYOVCNVMDSQNNMLRTNWPVNSAQKIYELKFTLRDCNSIPL 60
DB 85 WEELGEVDENHTPIRTYOVCNVMDSQNNMLRTNWPVNSAQKIYELKFTLRDCNSIPL 144
QY 61 VLGTCKETFNLYMESDDHGVKREHOFKIDITIADESFQMDLGDRIKLKNTETREV 120
DB 145 GLGTCKETFNLYMESDDHGVKREHOFKIDITIADESFQMDLGDRIKLKNTETREV 204
QY 121 GPVKKGFYLAFOVGVACVAVSVRYVFKKCPFTYKNIAMPDTPV-MDSQSLVEVNGSC 179
DB 205 GPLSKKGFYLAFOVGVACVAVSVRYVFKKCPFTYKNIAMPDTPVITGADSSQLLEVSGSC 264
QY 180 VNNSKEEDPPRMKCSAGEWLVPIGKCSNAGYERGFMCQ 220
DB 265 VNHSVTDDPPRMKCSAGEWLVPIGKCKCKAGYEKNGTCQ 305

RESULT 8
ID R97853
AC R97853 standard; Protein; 928 AA.
DT 05-JAN-1997 (first entry)
DE Rat ReK7 eph-related tyrosine kinase receptor.
KW ReK7; eph-related tyrosine kinase receptor; AL-1; ligand;
KM neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis.
OS Rattus sp.
FH key location/Qualifiers
FT peptide 1..57
FT protein /label= sig_peptide
FT domain /label= Mat_protein
FT domain /label= Extracellular_domain
PN W09613518-AL.
PD 09-MAY-1996.
PF 26-OCT-1995; U14016.
PR 27-OCT-1994; US-330128.
PR 07-JUN-1995; US-486449.
PA (GETH) GENENTECH INC.
PI Caras JW, Winslow JW;
DR WPI; 96-239448/24.
DR N-PSDB; T18893.
PT AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in
PT treatment and diagnosis of neuronal disorders and
PT angiogenesis-related conditions.
PS Example 1; Page 50-53; 75pp; English.
CC Rat ReK7 (R97853) is an eph-related tyrosine kinase receptor, for
CC which AL-1 (see also W97854) is a ligand. Its amino acid sequence
CC was deduced from a cDNA clone (T18893) isolated from a hippocampal
CC cDNA library. An REK-1g fusion was used to screen cultured cell
CC lines for surface expression of ReK7-binding activity. Primers
CC (see also T44382-83) based on peptide sequences (R97855-59) of
CC isolated ligands were used to amplify human breast carcinoma BT20
CC cell cDNA, and an amplified fragment was used to screen a human
CC foetal brain cDNA library, leading to the isolation of AL-1 cDNA
CC (T18897).
SQ Sequence 928 AA;

Query Match 72.1%; Score 865.5; DB 1; Length 928;
Best Local Similarity 68.3%; Pred. No. 2.3e-83;
Matches 151; Conservative 35; Mismatches 34; Indels 1; Gaps 1;

QY 1 WEELSGVDENHTPIRTYOVCNVMDSQNNMLRTNWPVNSAQKIYELKFTLRDCNSIPL 60
DB 85 WEELGEVDENHTPIRTYOVCNVMDSQNNMLRTNWPVNSAQKIYELKFTLRDCNSIPL 144
QY 61 VLGTCKETFNLYMESDDHGVKREHOFKIDITIADESFQMDLGDRIKLKNTETREV 120
DB 145 GLGTCKETFNLYMESDDHGVKREHOFKIDITIADESFQMDLGDRIKLKNTETREV 204
QY 121 GPVKKGFYLAFOVGVACVAVSVRYVFKKCPFTYKNIAMPDTPV-MDSQSLVEVNGSC 179
DB 205 GPLSKKGFYLAFOVGVACVAVSVRYVFKKCPFTYKNIAMPDTPVITGADSSQLLEVSGSC 264
QY 180 VNNSKEEDPPRMKCSAGEWLVPIGKCSNAGYERGFMCQ 220
DB 265 VNHSVTDDPPRMKCSAGEWLVPIGKCKCKAGYEKNGTCQ 305

RESULT 9
ID R85090
AC R85090 standard; Protein; 991 AA.
DT 16-APR-1996 (first entry)
DE Eph-like receptor protein tyrosine kinase HEK7.
KW Eph-like receptor protein tyrosine kinase; PK; HEK7;
KW human eph-like kinase; therapy; diagnosis; vector; antibody.
OS Homo sapiens.

PN W09528484-A1.
 PD 26-OCT-1995.
 PF 14-APR-1995; U04681.
 PR 15-APR-1994; US-229509.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Welcher AA;
 DR WPI: 95-373799/48.
 DR N-PSDB: T02947.
 PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -
 PT and related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation
 PT or prodn.
 PS Claim 18; Page 54-57; 133pp; English.
 CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (R85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (T02946-49) from a human foetal brain
 CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8.
 CC HEK11 shows no homology to any known EPH-like receptor. Recombinant
 CC HEK receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in prokaryotic or eucaryotic host
 CC cells, and are used to produce antibodies (utilised in diagnostic
 CC assays), or to identify and purify ligands for HEK receptors, or
 CC therapeutically to modulate the activation of cell-associated
 CC receptors. Soluble HEK7 receptor may primarily affect
 CC proliferation and/or differentiation of brain cells.
 CC pancreatic cells.
 SQ Sequence 991 AA.

Query Match 71.7%; Score 860.5; DB 1; Length 991;
 Best Local Similarity 67.9%; Pred. No. 8.7e-83;
 Matches 150; Conservative 35; Mismatches 35; Indels 1; Gaps 1;

QY 1 WEISGVDEHYPIRTYQVCNWDHSONNWLRTNWP/PRNSAQIYELKFTLDCNSIP 60
 DB 59 WEISGVDEHYPIRTYQVCNWDHSONNWLRTNWP/PRNSAQIYELKFTLDCNSIP 118
 QY 61 YGTGCTETNLYMESDDHGVKFRHOFTKIDTIADESFQMDGDRILKNTETIRY 120
 DB 119 GGTGCTETNLYMESDDHGVKFRHOFTKIDTIADESFQMDGDRILKNTETIRY 178
 QY 121 GPVNRKGFYLAQDVACALVSVRYFKKCPFTYKLNLFPTDVP-MDSQSLVEYRGSC 179
 DB 179 GPLSKRGFLAQDVACALVSVRYFKKCPFTYKLNLFPTDVP-MDSQSLVEYRGSC 238
 QY 180 VNNSKEDEPPRMVCTSTEGEWLVPIGKCSNAGYEERGFMCQ 220
 DB 239 VNHSVTDEPPKMHCSAEGEWLVPIGKCMCKAGYEERKNGTCQ 279

RESULT 10
 W03422
 ID W03422 standard; Protein; 610 AA.
 AC W03422;
 DT 11-NOV-1996 (first entry)
 DE Mouse developmental kinase 1 MDK1 T1.
 KW Mouse developmental kinase 1; MDK1 T1; receptor tyrosine kinase;
 KW RTK; signal transduction; probe; diagnosis; gene therapy;
 KW neurodegeneration; neuroproliferation; cancer.
 OS Mus sp.
 FH Key
 FT peptide
 FT 1.28 Location/Qualifiers
 FT /label= Sig_peptide
 FT modified_site
 FT /label= N-glycosylation_site
 FT modified_site
 FT /label= N-glycosylation_site
 FT modified_site
 FT /label= N-glycosylation_site
 FT modified_site
 FT /label= N-glycosylation_site
 FT domain
 FT /label= Transmembrane_domain
 FT misc_difference 600.610

FT W09621013-A1. /note= "product of alternative splicing"
 PN 11-JUL-1996.
 PD 03-JAN-1996; U00419.
 PF 03-JAN-1995; US-368776.
 PR (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA (SUGC-) SUGEN INC.
 PI Closssek T, Millner B, Ullrich A;
 DR WPI: 96-333988/33.
 DR N-PSDB: T32961.
 PT New mouse development kinase 1 gene - used for developng prods. for
 PT diagnosis and treatment of abnormalities in signal transduction
 PT pathways
 PS Example 1; Page 109-111; 128pp; English.
 CC cDNA cloning using adult mouse brains and Northern blotting
 CC identified 2 truncated versions, MDK1 T1 (W03422) and MDK1 T2
 CC (W03423), of the novel mouse developmental kinase 1 (MDK1) (see also
 CC W03421), a new member of the eck/eph family of receptor tyrosine
 CC kinases. Their amino acid sequences were deduced from cDNA clones
 CC (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2
 CC each possess the entire ectodomain, the transmembrane domain and
 CC part of the juxtamembrane region of MDK1, but lack the catalytic
 CC tyrosine kinase domain. They can be used to screen for potential
 CC agents useful for treatment of diseases characterised by abnormal
 CC signal transduction.
 SQ Sequence 610 AA.

Query Match 71.5%; Score 857.5; DB 1; Length 610;
 Best Local Similarity 70.0%; Pred. No. 9.2e-83;
 Matches 156; Conservative 36; Mismatches 28; Indels 3; Gaps 2;

QY 1 WEISGVDEHYPIRTYQVCNWDHSONNWLRTNWP/PRNSAQIYELKFTLDCNSIP 60
 DB 55 WEISGVDEHYPIRTYQVCNWDHSONNWLRTNWP/PRNSAQIYELKFTLDCNSIP 114
 QY 61 YGTGCTETNLYMESDDHGVKFRHOFTKIDTIADESFQMDGDRILKNTETIRY 120
 DB 115 GGTGCTETNLYMESDDHGVKFRHOFTKIDTIADESFQMDGDRILKNTETIRY 174
 QY 121 GPVNRKGFYLAQDVACALVSVRYFKKCPFTYKLNLFPTDVP-MDSQSLVEYRGSC 179
 DB 175 GPLSKRGFLAQDVACALVSVRYFKKCPFTYKLNLFPTDVP-MDSQSLVEYRGSC 234
 QY 180 VNNSKE--EDPPRMVCTSTEGEWLVPIGKCSNAGYEERGFMCQ 220
 DB 235 VSSAEEREAENSPRMHCSAEGEWLVPIGKCIKAGYQOKGDTC 277

RESULT 11
 W03423
 ID W03423 standard; Protein; 626 AA.
 AC W03423;
 DT 11-NOV-1996 (first entry)
 DE Mouse developmental kinase 1 MDK1 T2.
 KW Mouse developmental kinase 1; MDK1 T2; receptor tyrosine kinase;
 KW RTK; signal transduction; probe; diagnosis; gene therapy;
 KW neurodegeneration; neuroproliferation; cancer.
 OS Mus sp.
 FH Key
 FT peptide
 FT 1.28 Location/Qualifiers
 FT /label= Sig_peptide
 FT modified_site
 FT /label= N-glycosylation_site
 FT modified_site
 FT /label= N-glycosylation_site
 FT modified_site
 FT /label= N-glycosylation_site
 FT modified_site
 FT /label= N-glycosylation_site
 FT domain
 FT /label= Transmembrane_domain
 FT misc_difference 600.626
 FT /note= "product of alternative splicing"
 PN W09621013-A1.

PD 11-JUL-1996. U00419.
 PF 03-JAN-1996; US-368776.
 PR (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA (SUGEN-) SUGEN INC.
 PI Ciossek T, Millauner B, Ullrich A;
 DR WPI, 96-333988/33.
 DR N-PSDB; T32962.
 PT New mouse development kinase 1 gene - used for developing prods. for
 PT diagnosis and treatment of abnormalities in signal transduction
 PT pathways
 PS Example 1: Page 113-115; 128pp; English.
 CC cDNA cloning using adult mouse brains and Northern blotting
 CC identified 2 truncated versions, MDK1 T1 (W03422) and MDK1 T2
 CC (W03423), of the novel mouse developmental kinase 1 (MDK1) (see also
 CC W03421), a new member of the eck/eph family of receptor tyrosine
 CC kinases. Their amino acid sequences were deduced from cDNA clones
 CC (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2
 CC each possess the entire ectodomain, the transmembrane domain and
 CC part of the juxtamembrane region of MDK1, but lack the catalytic
 CC tyrosine kinase domain. They can be used to screen for potential
 CC agents useful for treatment of diseases characterised by abnormal
 CC signal transduction.
 SQ Sequence 626 AA;

Query Match 71.5%; Score 857.5; DB 1; Length 626;
 Best Local Similarity 70.0%; Pred. No. 9.5e-83;
 Matches 156; Conservative 36; Mismatches 28; Indels 3; Gaps 2;

QY 1 WEISGVDEHYTPRTYQVCNVMDHSONNMLRTNWPVRNSAQKIYVELKFTLRDCNSIPL 60
 DB 55 WEISGIDENYTPRTYQVCNVEPNONNMRLRNWISKGNAGIIFELKFTLRDCNSIPL 114
 QY 61 VLGTCKETFNLYYESDDHGKVFREHQTFRIDTIADESFTQMDLGRILKLTETIREV 120
 DB 115 VLGTCKETFNLYYESDYDGRNIRENLVYKIDTIADESFTQDLGRKRLKLTETIREV 174
 QY 121 GPVKKGFYLAFODVGCALVSVRYVFKKCPFTVKMLAMPDTPV-MDSQSLVEVRGSC 179
 DB 175 GPISKKGFYLAFODVGCIALVSVRYVKKCWITVENLAVPPDVTGSEFSLSVEVRGTC 234
 QY 180 VNNSKE--EDPPRMVCTEGEMLVPIGKCSNAGYBERGFMCQ 220
 DB 235 VSSAEBAENSPRNHCSAESEMLVPIGKCIKAGYQKGDTC 277

RESULT 12
 ID W03421 standard; Protein; 998 AA.
 AC W03421;
 DT 11-NOV-1996 (first entry)
 DE Mouse developmental kinase 1.
 KW Mouse developmental kinase 1; MDK1; receptor tyrosine kinase; RTK;
 KW signal transduction; probe; diagnosis; therapy;
 KW neurodegeneration; neuroproliferation; cancer.
 OS Mus sp.
 FH Key
 FT peptide
 FT 1.28
 FT /label= sig_peptide
 FT modified_site
 FT 64.66
 FT /label= N-glycosylation_site
 FT modified_site
 FT 343.345
 FT /label= N-glycosylation_site
 FT modified_site
 FT 410.412
 FT /label= N-glycosylation_site
 FT domain
 FT 555.579
 FT /label= transmembrane_domain
 PN W0621013-A1.
 PD 11-JUL-1996.
 PF 03-JAN-1996; U00419.
 PR 03-JAN-1995; US-368776.
 PR (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PA (SUGEN-) SUGEN INC.
 PI Ciossek T, Millauner B, Ullrich A;
 DR WPI, 96-333988/33.
 DR N-PSDB; T32960.
 PT New mouse development kinase 1 gene - used for developing prods. for
 PT diagnosis and treatment of abnormalities in signal transduction
 PT pathways
 PS Example 1: Page 105-108; 128pp; English.
 CC Mouse developmental kinase 1 (MDK1) (W03421) is a new member of the
 CC eck/eph family of receptor tyrosine kinases (RTKs). Its amino
 CC acid sequence was deduced from a cDNA clone (T32960) isolated
 CC from mouse embryo and adult brain libraries. The distinct
 CC patterns of MDK1 expression during mouse development suggest an
 CC important role for MDK1 in the formation of neuronal structures.
 CC MDK1 may be obtd. by expression in host cells. It can be used
 CC in methods for the diagnosis of diseases characterised by
 CC abnormality in a signal transduction pathway, such as
 CC neuroproliferative or neurodegenerative disorders or cancer,
 CC to screen for (ant)agonists, and to raise antibodies.
 SQ Sequence 998 AA;

Query Match 71.5%; Score 857.5; DB 1; Length 998;
 Best Local Similarity 70.0%; Pred. No. 1.8e-82;
 Matches 156; Conservative 36; Mismatches 28; Indels 3; Gaps 2;

QY 1 WEISGVDEHYTPRTYQVCNVMDHSONNMLRTNWPVRNSAQKIYVELKFTLRDCNSIPL 60
 DB 55 WEISGIDENYTPRTYQVCNVEPNONNMRLRNWISKGNAGIIFELKFTLRDCNSIPL 114
 QY 61 VLGTCKETFNLYYESDDHGKVFREHQTFRIDTIADESFTQMDLGRILKLTETIREV 120
 DB 115 VLGTCKETFNLYYESDYDGRNIRENLVYKIDTIADESFTQDLGRKRLKLTETIREV 174
 QY 121 GPVKKGFYLAFODVGCALVSVRYVFKKCPFTVKMLAMPDTPV-MDSQSLVEVRGSC 179
 DB 175 GPISKKGFYLAFODVGCIALVSVRYVKKCWITVENLAVPPDVTGSEFSLSVEVRGTC 234
 QY 180 VNNSKE--EDPPRMVCTEGEMLVPIGKCSNAGYBERGFMCQ 220
 DB 235 VSSAEBAENSPRNHCSAESEMLVPIGKCIKAGYQKGDTC 277

RESULT 13
 ID R85092 standard; Protein; 998 AA.
 AC R85092;
 DT 16-APR-1996 (first entry)
 DE EPH-like receptor protein tyrosine kinase HEK11.
 KW EPH-like receptor protein tyrosine kinase; PRK; HEK11;
 KW human eph-like kinase; therapy; diagnosis; antibody; vector.
 OS Homo sapiens.
 PN W09528484-A1.
 PD 26-OCT-1995.
 PF 14-APR-1995; U04681.
 PR 15-APR-1994; US-229509.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Welcher AA;
 DR WPI, 95-373799/48.
 DR N-PSDB; T02949.
 PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -
 PT and related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation
 PT or prodn.
 PS Claim 18: Page 71-75; 133pp; English.
 CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (R85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (T02946-49) from a human foetal brain
 CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8.
 CC HEK11 shows no homology to any known EPH-like receptor. Recombinant
 CC HEK receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in procarcynotic or eucaryotic host

cells, and are used to produce antibodies (utilised in diagnostic assays), or to identify and purify ligands for HER receptors, or therapeutically to modulate the activation of cell-associated receptors.

Sequence 998 AA:

Query Match 71.4%; Score 856.5; DB 1; Length 998;
Best Local Similarity 69.5%; Pred. No. 2.3e-82;
Matches 155; Conservative 37; Mismatches 28; Indels 3; Gaps 2;

```
QY 1 WEISGVDEHYPIRTYQVCNMDHSONNMLRTNWPVNSAQKIYELKFTLDCNSIPL 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 55 WEISGIDENYPIRTYQVCNMDHSONNMLRTNWPVNSAQKIYELKFTLDCNSIPL 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VLGCTKEFTNLYMESDDHGVKFRHQFTKIDITIADESFQMDLGRILKLTNTEIRY 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 115 VLGCTKEFTNLYMESDDHGVKFRHQFTKIDITIADESFQMDLGRILKLTNTEIRY 174
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GPVNRKGFYLAFOYDGVACALVSVRYFKKCPFTYKNLAMPDTPV-MDSOSLYEVK 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 175 GPLSKRGFLAODYDGCALVSVRYFKKCPFTYKNLAMPDTPV-MDSOSLYEVK 234
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 VNSKRE--EDPPRMVSTEGEVLVPIGKCSNAGYEERGFMCQ 220
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 225 VSSAEAEANAPRMHCSAGEMLVPIGKCIKAGYQKGDTC 277
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 14

R75712 R75712 standard; Protein; 995 AA.

AC R75712:
DT 11-NOV-1995 (first entry)
DE Eph-related PTK Cdk5.
KW Cdk5; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
KW prognosis.
OS Gallus sp.
PN W09515375-A.
PD 08-JUN-1995.
PE 07-SEP-1994; U10140.
PR 03-DEC-1993; US-162809.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PI Pasquale EB, Sajjadi FG;
DR N-PSDB: 090657.
PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
PT cancer.
PS Disclosure: Page 92-96; 129pp; English.
CC Probes derived from the Eph-related PTKs Cdk4 (090659) and Cdk5
CC (090660) were used to isolate novel cDNA clones (090652-58,
CC 090661-62) from chicken embryo and embryonic brain libraries.
SQ Sequence 995 AA;

Query Match 59.4%; Score 713; DB 1; Length 995;
Best Local Similarity 56.1%; Pred. No. 4e-67;
Matches 128; Conservative 48; Mismatches 44; Indels 8; Gaps 4;

```
QY 1 WEISGVDEHYPIRTYQVCNMDHSONNMLRTNWPVNSAQKIYELKFTLDCNSIPL 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 51 WEISGIDENYPIRTYQVCNMDHSONNMLRTNWPVNSAQKIYELKFTLDCNSIPL 110
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VLGCTKEFTNLYMESDDHGVKFRHQFTKIDITIADESFQMDLGRILKLTNTEIRY 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 111 VLGCTKEFTNLYMESDDHGVKFRHQFTKIDITIADESFQMDLGRILKLTNTEIRY 170
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 117 IREVGPNVKKGFYLAFOYDGVACALVSVRYFKKCPFTYKNLAMPDTPV-MDSOSLYEV 175
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 171 VRSFPGVSKNGFYLAFOYDGVACALVSVRYFKKCPFTYKNLAMPDTPV-MDSOSLYEV 230
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 RSCVNSKEDDP--RMVSTEGEVLVPIGKCSNAGYE--ERGFMCQ 220
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 231 RGTCTISNAEVDVPIKLYCNGDGEMLVPIGRCMCRPGESYENGTVCR 278
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 15

R75709 R75709 standard; Protein; 1011 AA.

AC R75709:
DT 11-NOV-1995 (first entry)
DE Eph-related PTK Cdk5+.
KW Cdk5+; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
KW prognosis.
OS Gallus sp.
PN W09515375-A.
PD 08-JUN-1995.
PE 07-SEP-1994; U10140.
PR 03-DEC-1993; US-162809.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PI Pasquale EB, Sajjadi FG;
DR N-PSDB: 090657.
PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
PT cancer.
PS Claim 11; Page 71-75; 129pp; English.
CC A cDNA clone encoding a novel variant of Eph-related PTK Cdk5,
CC Cdk5+ (090657), was isolated from a chick embryo library in
CC lambda gtl1. Cdk5+ protein (R75709) contains a 16-amino acid
CC insertion in the juxtamembrane domain, and be a result of
CC alternative splicing. Cdk5+ is exclusively expressed in the CNS.
SQ Sequence 1011 AA;

Query Match 59.4%; Score 713; DB 1; Length 1011;
Best Local Similarity 56.1%; Pred. No. 4.1e-67;
Matches 128; Conservative 48; Mismatches 44; Indels 8; Gaps 4;

```
QY 1 WEISGVDEHYPIRTYQVCNMDHSONNMLRTNWPVNSAQKIYELKFTLDCNSIPL 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 51 WEISGIDENYPIRTYQVCNMDHSONNMLRTNWPVNSAQKIYELKFTLDCNSIPL 110
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VLGCTKEFTNLYMESDDHGVKFRHQFTKIDITIADESFQMDLGRILKLTNTEIRY 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 111 VLGCTKEFTNLYMESDDHGVKFRHQFTKIDITIADESFQMDLGRILKLTNTEIRY 170
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 117 IREVGPNVKKGFYLAFOYDGVACALVSVRYFKKCPFTYKNLAMPDTPV-MDSOSLYEV 175
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 171 VRSFPGVSKNGFYLAFOYDGVACALVSVRYFKKCPFTYKNLAMPDTPV-MDSOSLYEV 230
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 RSCVNSKEDDP--RMVSTEGEVLVPIGKCSNAGYE--ERGFMCQ 220
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 231 RGTCTISNAEVDVPIKLYCNGDGEMLVPIGRCMCRPGESYENGTVCR 278
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Search completed: May 9, 2000, 21:52:01
Job time: 3753 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 22:31:07 ; Search time 71.69 seconds
(without alignments)
21.277 Million cell updates/sec

Title: US-09-104-340-2
Percent score: 119
Sequence: 1 VNLDSKRTIGELGWISYPSHG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 6934122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

SPTREMBL_12.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	66.4	985	13	Q91694 xenopus lae
2	79	66.4	986	13	Q91845 xenopus lae
3	71	59.7	981	13	Q13146 brachydanio
4	61	51.3	993	13	Q42422 gallus gall
5	58	48.7	985	13	Q91571 xenopus lae
6	57	47.9	974	13	Q91735 xenopus lae
7	56	47.1	1055	4	Q43477 homo sapien
8	55	46.2	943	4	Q43569 homo sapien
9	55	46.2	984	4	Q95142 homo sapien
10	53	44.5	952	13	Q07494 gallus gall
11	52	43.7	1006	4	Q15197 homo sapien
12	52	43.7	1014	11	Q08644 mus musculu
13	51	42.9	366	2	Q50031 mycobacteri
14	49	40.3	368	2	Q53825 mycobacteri
15	48	40.3	1763	5	Q17901 caenorhabdi
16	48	40.3	1769	5	Q9XTJ1 caenorhabdi
17	46	38.7	134	9	Q38422 bacterioph
18	46	38.7	217	5	Q61063 physarum po
19	46	38.7	809	10	Q9ZP66 craterostig
20	45	37.8	90	2	Q33642 salmonella

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	985 AA.
091694	091694	091694		
AC	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	TYROSINE-PROTEIN KINASE RECEPTOR PAG PRECURSOR (EC 2.7.1.112) (PAGLIACCIO).			
GN	PAG.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia;			
OC	Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;			
CC	Xenopus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-NEURAL CREST;			
RX	MEDLINE; 95001564.			
RA	WINNING R.S., SARGENT T.D.;			
RT	"Pagliaccio, a member of the Eph family of receptor tyrosine kinase genes, has localized expression in a subset of neural crest and neural tissues in Xenopus laevis embryos.";			
RL	Mech. Dev. 46:219-229(1994).			
CC	- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY (BY SIMILARITY). MAY PLAY A ROLE IN THE DIFFERENTIATION OF CRANIAL NEURAL CREST AND OTHER TISSUES.			
CC	- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: LOCALIZED EXPRESSION IN A SUBSET OF NEURAL CREST AND NEURAL TISSUES IN EMBRYOS.			
CC	- DEVELOPMENTAL STAGE: PRESENT TRANSIENTLY IN VISCERAL ARCH 3. ALSO EXPRESSED IN THE FOREBRAIN, RHOMOMERES R3 AND R5 OF THE HINDBRAIN AND IN THE PRONEPHROS.			
CC	- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPH FAMILY.			
DR	EMBL; L26099; AAA64464.1; -.			
DR	HSSP; P00523; ZPTK.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.			
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.			

21	45	37.8	464	5	Q21794	Q21794 caenorhabdi
22	45	37.8	530	12	Q83884	Q83884 norway vir
23	45	37.8	1151	5	Q96993	Q96993 heterodera
24	44	37.0	89	2	P71504	P71504 methylobact
25	44	37.0	234	2	Q92CV2	Q92CV2 rickettsia
26	44	37.0	540	12	Q9YS14	Q9YS14 norway vir
27	44	37.0	794	12	Q66530	Q66530 european br
28	44	37.0	2334	12	Q96725	Q96725 european br
29	43	36.1	338	2	Q59082	Q59082 azospirillum
30	43	36.1	360	5	Q18228	Q18228 caenorhabdi
31	43	36.1	435	10	Q23393	Q23393 arabidopsis
32	43	36.1	489	3	Q14237	Q14237 schizosacch
33	43	36.1	530	12	Q83876	Q83876 norway vir
34	43	36.1	652	5	Q60993	Q60993 crithidia f
35	43	36.1	1364	4	Q9YSP7	Q9YSP7 homo sapien
36	43	36.1	1368	4	Q9Y657	Q9Y657 homo sapien
37	42.3	35.7	85	1	Q28496	Q28496 archaoglob
38	42.5	35.7	537	2	Q05459	Q05459 mycobacteri
39	42.5	35.7	1252	5	Q77403	Q77403 sclera ocel
40	42	35.3	112	12	Q9YR39	Q9YR39 aleutian ml
41	42	35.3	112	12	Q9YR38	Q9YR38 aleutian ml
42	42	35.3	217	8	Q99544	Q99544 parmesopod
43	42	35.3	358	2	Q34753	Q34753 bacillus su
44	42	35.3	627	5	Q15832	Q15832 leishmania
45	41.5	34.9	284	5	Q17213	Q17213 caenorhabdi

DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V.2; 1.
 DR PFAM; PF00041; fn3; 2.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR_1.
 DR PFAM; PF00536; SAM; 1.
 DR PFAM; PF01404; EPH_Lbd; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRINTS; PR00014; FNTYPEIIT.
 KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KM Immunoglobulin domain.
 FT SIGNAL 1 20
 FT CHAIN 1 20
 FT DOMAIN 21 985
 FT TRANSMEM 21 547
 FT DOMAIN 548 569
 FT TRANSMEM 570 985
 FT DOMAIN 570 985
 FT DOMAIN 66 115
 FT DOMAIN 191 325
 FT DOMAIN 326 435
 FT DOMAIN 436 533
 FT DOMAIN 620 881
 FT NP_BIND 626 634
 FT DISULFID 73 108
 FT BINDING 652 652
 FT ACT_SITE 745 745
 FT MOD_RES 778 778
 FT CARBOHYD 340 340
 FT CARBOHYD 407 407
 SQ SEQUENCE 985 AA; 109729 MW; 026BA6A5 CRC32;

Query Match 66.4%; Score 79; DB 13; Length 985;
 Best Local Similarity 63.6%; Pred. No. 0.00037;
 Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 VNLDSTKIQELGWIISYPSHG 22
 ID 091845 PRELIMINARY; PRT; 986 AA.
 DB 31 VILLDSRSYQELGWIASPLEG 52

RESULT 2
 ID 091845 PRELIMINARY; PRT; 986 AA.
 AC 091845:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE TYROSINE-PROTEIN KINASE RECEPTOR SEK-1 PRECURSOR (EC 2.7.1.112).
 GN SEK-1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
 OC Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96125143.
 RA XU Q., ALLDUS G., HOLDER N., WILKINSON D.G.;
 RT "Expression of truncated sek-1 receptor tyrosine kinase disrupts the
 RT segmental restriction of gene expression in the Xenopus and zebrafish
 RT hindbrain."
 RT Development 121:4005-4016(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY (BY
 CC SIMILARITY). REQUIRED FOR INTERACTIONS THAT REGULATE THE SEGMENTAL
 CC IDENTITY OR MOVEMENT OF CELLS.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION OCCURS IN R3, R5 AND TRANSIENTLY
 CC AT LOWER LEVELS IN R2.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPH FAMILY.
 DR EMBL; X91191; CAA62601.1; -.

DR HSSP; P00523; 2PTK.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V.1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V.2; 1.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00069; PKINASE; 1.
 DR PFAM; PF00536; SAM; 1.
 DR PFAM; PF01404; EPH_Lbd; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRINTS; PR00014; FNTYPEIIT.
 KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KM Immunoglobulin domain.
 FT SIGNAL 1 15
 FT CHAIN 16 986
 FT DOMAIN 16 547
 FT TRANSMEM 548 569
 FT TRANSMEM 570 986
 FT DOMAIN 570 986
 FT DOMAIN 66 115
 FT DOMAIN 191 325
 FT DOMAIN 326 435
 FT DOMAIN 436 533
 FT DOMAIN 620 881
 FT NP_BIND 626 634
 FT DISULFID 73 108
 FT BINDING 652 652
 FT ACT_SITE 745 745
 FT MOD_RES 778 778
 FT CARBOHYD 340 340
 FT CARBOHYD 407 407
 SQ SEQUENCE 986 AA; 109840 MW; 028DBBDA CRC32;

Query Match 66.4%; Score 79; DB 13; Length 986;
 Best Local Similarity 63.6%; Pred. No. 0.00037;
 Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 VNLDSTKIQELGWIISYPSHG 22
 ID 013146 PRELIMINARY; PRT; 981 AA.
 DB 31 VILLDSRSYQELGWIASPLEG 52

RESULT 3
 ID 013146 PRELIMINARY; PRT; 981 AA.
 AC 013146:
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE EPH-LIKE KINASE 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE
 DE RECEPTOR ZEK1).
 GN ZEK1.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinidae; Rasbora; Danio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97329578.
 RA BOVENKAMP D.E., GREER P.;
 RT "Novel Eph-family receptor tyrosine kinase is widely expressed in the
 RT developing zebrafish nervous system."
 RT Dev. Dyn. 209:166-181(1997).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. MAY PLAY A
 CC ROLE IN EARLY PATTERN FORMATION WITHIN THE DEVELOPING NERVOUS
 CC SYSTEM.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE DEVELOPING ZEBRAFISH
 CC NERVOUS SYSTEM.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR EMBL: U89295; AAC60220.1; -.
DR HSRP: P00523; 2PTRK.
DR ZFIN: ZDB-GENE-990415-58; zek1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_2; FALSE_NEG.
DR PFAM: PF00069; kinase; 1.
DR PFAM: PF00336; SAM; 1.
DR PFAM: PF01404; EPH_Lbd; 1.
DR PFAM: PF00041; fn3; 2.
DR PRINTS: PR00109; TYRKINASE.
DR PRINTS: PR00014; ENTRYPELII.
KW TRANSFERASE; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain.
FT SIGNAL 1 20
FT CHAIN 21 981
FT DOMAIN 21 545
FT TRANSMEM 546 566
FT DOMAIN 567 981
FT DOMAIN 64 113
FT DOMAIN 192 325
FT DOMAIN 326 438
FT DOMAIN 439 532
FT DOMAIN 626 887
FT NP_BIND 632 640
FT DISULFID 71 106
FT BINDING 758 658
FT ACT_SITE 751 751
FT MOD_RES 784 784
FT CARBOHYD 340 340
FT CARBOHYD 410 410
FT CARBOHYD 435 435
FT CARBOHYD 485 485
FT VARIANT 141 141
SQ SEQUENCE 981 AA; 109654 MW; 10D38182 CRC32;

Query Match 59.7%; Score 71; DB 13; Length 981;
Best Local Similarity 59.1%; Pred. No. 0.0067;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 VNLDSKTIQGLGWISYPSHG 22
DB 30 VLLDSMSAPGDLGWEPYSEG 51

RESULT 4
ID 042422 PRELIMINARY; PRT; 993 AA.
AC 042422;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DI 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DI 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE EPH-LIKE RECEPTOR TYROSINE KINASE PRECURSOR (EC 2.7.1.112) (TYROSINE-
PROTEIN KINASE RECEPTOR CEPHA7).
GN CEPHA7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYO.
RX MEDLINE; 98092111.
RA ARABJO M., NIETO M.A.;
RT "The expression of chick EphA7 during segmentation of the central and
peripheral nervous system";
RL Mech. Dev. 68:173-177(1997).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN FAMILY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN

CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM. EXPRESSION IS
RESTRICTED TO PROSOMERES 1 AND 2 IN THE Diencephalon AND ALL THE
RHOMBOMERES IN THE HINDBRAIN DURING SEGMENTATION STAGES. LATER ON,
A SUPERIMPOSED PATTERN APPEARS THAT CORRELATES WITH THE FORMATION
OF SEVERAL AXONAL TRACTS. IN THE SOMATIC MESODERM, THE EXPRESSION
CORRELATES WITH SEGMENTATION AND THE GUIDANCE OF BOTH NEURAL CREST
AND MOTOR AXONS THROUGH THE SCLEROTOMES.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR EMBL: Y14271; CAA74643.1; -.
DR HSRP: P00523; 2PTRK.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; kinase; 1.
DR PFAM: PF00336; SAM; 1.
DR PFAM: PF01404; EPH_Lbd; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRINTS: PR00014; ENTRYPELII.
KW TRANSFERASE; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain.
FT SIGNAL 1 30
FT CHAIN 31 993
FT DOMAIN 31 551
FT TRANSMEM 552 572
FT DOMAIN 573 993
FT DOMAIN 67 116
FT DOMAIN 132 328
FT DOMAIN 329 438
FT DOMAIN 439 536
FT DOMAIN 628 889
FT NP_BIND 634 642
FT DISULFID 74 109
FT BINDING 660 660
FT ACT_SITE 753 753
FT MOD_RES 786 786
FT CARBOHYD 343 343
FT CARBOHYD 410 410
SQ SEQUENCE 993 AA; 111366 MW; 6B6BFD17 CRC32;

Query Match 51.3%; Score 61; DB 13; Length 993;
Best Local Similarity 63.6%; Pred. No. 0.26;
Matches 14; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 VNLDSKTIQGLGWISYPSHG 22
DB 33 VLLDSKAQCTLEWISSPPNG 54

RESULT 5
ID 091571 PRELIMINARY; PRT; 985 AA.
AC 091571;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR XEK PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
KINASE RECEPTOR XEK).
GN XEK.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95215070.

RA JONES T.L., KARAVANOVA I., MAENO M., ONG R.C., KUNG H.-F., DAAR I.O.;
 RT Expression of an amphibian homolog of the Eph family of receptor
 RT tyrosine kinases is developmentally regulated.";
 RL Oncogene 10:1111-1117(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. MAY PLAY A
 CC ROLE IN THE DEVELOPMENT OR FUNCTION OF THE CENTRAL NERVOUS SYSTEM.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DEVELOPMENTAL STAGE: MATERNALLY EXPRESSED, IT DECREASES AT MID
 CC BLASTULA TRANSITION AND REAPPEARS AT LATE NEURULATION. EXPRESSED
 CC AT HIGHER LEVELS IN THE ANTERIOR AND DORSAL REGIONS OF EMBRYONIC
 CC STAGES 16, 24 AND 37. IN ADULT IT APPEARS TO BE UNROUTINELY
 CC EXPRESSED WITH HIGHER EXPRESSION IN BRAIN AND OVARY. EXPRESSION IN
 CC THE BRAIN, BRACHIAL ARCHES, TRIGEMINAL FACIAL GANGLION, AND THE
 CC RETINA OF SWIMMING TADPOLE STAGE OF DEVELOPMENT.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC EMBL: U01414; AAA74888.1; -.
 DR HSSP: P00523; 2PTK.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; FALSE_NEG.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00069; PKINASE; 1.
 DR PFAM: PF00536; SAM; 1.
 DR PFAM: PF01404; EPH_Lbd; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR TRANSFERASE: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain.
 FT SIGNAL 1 19
 FT CHAIN 20 985
 FT DOMAIN 6 12
 FT TRANSMEM 543 563
 FT DOMAIN 564 985
 FT DOMAIN 56 105
 FT DOMAIN 185 321
 FT DOMAIN 432 529
 FT DOMAIN 620 883
 FT NP_BIND 626 634
 FT DISULFID 63 98
 FT BINDING 652 745
 FT ACT_SITE 779 779
 FT MOD_RES 336 336
 FT CARBOHYD 428 428
 FT CARBOHYD 482 482
 SO SEQUENCE 985 AA; 110104 MW; 2416ABF9 CRC32;

Query Match 48.7%; Score 58; DB 13; Length 985;
 Best Local Similarity 50.0%; Pred. No. 0.76;
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 3 LDSKTIQGLGWISYPSHG 22
 Db 24 LMDTKTATAGLWGNANSSG 43

RESULT 6
 ID 091735 PRELIMINARY; PRT; 974 AA.
 AC 091735;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE EPHRIN TYPE-B RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN

DE KINASE RECEPTOR (TCK).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia;
 OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
 CC Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96068901.
 RA SCALES J.B., WINNING R.S., RENAUD C.S., SHEA L.J., SARGENT T.D.;
 RT "Novel members of the eph receptor tyrosine kinase subfamily expressed
 RT during xenopus development.";
 RL Oncogene 11:1745-1752(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN PRE-SOMITIC
 CC MESODERM, CAUDAL SOMITES, MIDBRAIN, AND CEMENT GLAND. MOST
 CC ABUNDANT IN ADULT BRAIN, EYE, HEART, LUNG AND OVARY. LOWER LEVELS
 CC IN INTESTINE, KIDNEY, OVIDUCT AND PHARYNX.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC EMBL: L43620; AAA93526.1; -.
 DR HSSP: P00523; 2PTK.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00069; PKINASE; 1.
 DR PFAM: PF00536; SAM; 1.
 DR PFAM: PF01404; EPH_Lbd; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR TRANSFERASE: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain.
 FT SIGNAL 1 16
 FT CHAIN 17 974
 FT DOMAIN 17 334
 FT TRANSMEM 535 555
 FT DOMAIN 556 974
 FT DOMAIN 53 102
 FT DOMAIN 178 315
 FT DOMAIN 316 423
 FT DOMAIN 424 520
 FT NP_BIND 609 872
 FT DISULFID 60 95
 FT BINDING 641 641
 FT ACT_SITE 734 734
 FT MOD_RES 330 330
 FT CARBOHYD 330 330
 FT CARBOHYD 420 420
 SO SEQUENCE 974 AA; 108263 MW; BD419F6D CRC32;

Query Match 47.9%; Score 57; DB 13; Length 974;
 Best Local Similarity 45.0%; Pred. No. 1.1;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 3 LDSKTIQGLGWISYPSHG 22
 Db 21 LMDTKTTSGLWVAYPDSG 40

RESULT 7
 ID 043477 PRELIMINARY; PRT; 1055 AA.
 AC 043477;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE EPHRIN TYPE-B RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN

DR PFAM; PF00069; pklnase; 1.
 DR PFAM; PF01404; Eph_lbd; 1.
 DR PFAM; PF00041; fn3; 2.
 FT NON_TER
 SQ SEQUENCE 952 AA; 105994 MW; D939D7D0 CRC32;

Query Match 44.5%; Score 53; DB 13; Length 952;
 Best Local Similarity 45.0%; Pred. No. 4.5;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 LDDSKITGELGWISYPSHG 22
 1:1:1 1111:1
 Db 3 LMDTRTAEELGWTANPPSG 22

RESULT 11

ID 015197 PRELIMINARY; PRT; 1006 AA.

AC 015197;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
 DE EPH-FAMILY RECEPTOR PROTEIN PRECURSOR (EC 2.7.1.112) (HEP).
 GN EPHB6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97350806.
 RA MATSUOKA H., IWATA N., ITO M., SHIMOMAYA M., NAGATA A., CHIHARA K.,
 RA TAKAI S., MATSUI T.;
 RT "Expression of a kinase-defective Eph-like receptor in the normal
 RT human brain."
 RL Biochem. Biophys. Res. Commun. 235:487-492(1997).
 RN [2]
 RP SEQUENCE OF 1-804 FROM N.A.
 RA TAUDEIN S., ROSENTHAL A.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: KINASE-DEFECTIVE RECEPTOR FOR MEMBERS OF THE EPHRIN-B
 CC FAMILY.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: STRONG EXPRESSION IN THE BRAIN AND PANCREAS,
 CC AND WEAK EXPRESSION IN OTHER TISSUES, SUCH AS THE HEART, PLACENTA,
 CC LUNG, LIVER, SKELETAL MUSCLE AND KIDNEY.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC EMBL; D83492; BAA21560.1; -.
 DR EMBL; AF107256; BAA03058.1; -.
 DR HSSP; P00523; 2PTK.
 DR MIM; 602757; -.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; FALSE_NEG.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FALSE_NEG.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00069; pklnase; 1.
 DR PFAM; PF00536; SAM; 1.
 DR PFAM; PF01404; Eph_lbd; 1.
 DR PRINTS; PR00014; FNTYPEPIT.
 DR Transferrase; ATP-binding; Phosphorylation; Receptor; Transmembrane;
 KW Glycoprotein; Signal; Immunoglobulin domain.
 FT CHAIN 1 16
 FT SIGNAL 16
 FT DOMAIN 17 1006
 FT TRANSMEM 17 579
 FT TRANSMEM 580 600
 FT DOMAIN 601 1006
 FT DOMAIN 53 106
 FT DOMAIN 151 161
 FT DOMAIN 204 351
 FT DOMAIN 352 468
 FT DOMAIN 404 407
 FT POLY-GLY.
 FT POLY-GLY.

FT DOMAIN 469 566 FIBRONECTIN TYPE-III.
 FT DOMAIN 655 904 PROTEIN KINASE-LIKE.
 FT DOMAIN 866 869 POLY-PRO.
 FT NP_BIND 661 669 ATP (BY SIMILARITY).
 FT DISULFID 60 99 BY SIMILARITY.
 FT CARBOHYD 465 465 POTENTIAL.
 SQ SEQUENCE 1006 AA; 109272 MW; B7CDB1E CRC32;

Query Match 43.7%; Score 52; DB 4; Length 1006;
 Best Local Similarity 45.0%; Pred. No. 6.8;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 LDDSKITGELGWISYPSHG 22
 111:1111:1
 Db 21 LDDTGTSEIGWITPPSG 40

RESULT 12

ID 008644 PRELIMINARY; PRT; 1014 AA.

AC 008644;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
 DE EPH/ELK RECEPTOR-LIKE PROTEIN PRECURSOR (MEP).
 GN CEKL OR MEP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BALB/C X 129 F2; TISSUE-THYMUS;
 RX MEDLINE; 96358627.
 RA GURINAK C.B., BERG L.J.;
 RT "A new member of the Eph family of receptors that lacks protein
 RT tyrosine kinase activity."
 RL Oncogene 13:777-786(1996).
 CC -1- FUNCTION: KINASE-DEFECTIVE RECEPTOR FOR MEMBERS OF THE EPHRIN-B
 CC FAMILY.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE TWO SHORTER
 CC ISOFORMS ARE SECRETED.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: HIGH LEVEL IN THYMUS, AND BRAIN. VERY LOW
 CC LEVELS OF EXPRESSION IN KIDNEY, LUNG, LIVER, BONE MARROW, SKELETAL
 CC MUSCLE, SPLEEN FROM 2 WEEK OLD AND ADULT MICE, HEART, TESTES AND
 CC EMBRYONIC STEM CELLS.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC EMBL; L77867; AB51430.1; -.
 DR HSSP; P00523; 2PTK.
 DR MGD; MGI:108444; Cekl.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; FALSE_NEG.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FALSE_NEG.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00069; pklnase; 1.
 DR PFAM; PF00536; SAM; 1.
 DR PFAM; PF01404; Eph_lbd; 1.
 DR PRINTS; PR00014; FNTYPEPIT.
 DR Transferrase; ATP-binding; Phosphorylation; Receptor; Transmembrane;
 KW Glycoprotein; Signal; Immunoglobulin domain; Alternative splicing.
 FT CHAIN 1 32
 FT SIGNAL 32
 FT DOMAIN 33 1014
 FT TRANSMEM 33 591
 FT TRANSMEM 592 612
 FT DOMAIN 613 1014
 FT DOMAIN 69 122
 FT DOMAIN 168 173
 FT DOMAIN 214 361
 FT DOMAIN 362 476
 FT FIBRONECTIN TYPE-III.

FT DOMAIN 477 574 FIBRONECTIN TYPE-III.
 FT DOMAIN 663 912 PROTEIN KINASE-LIKE.
 FT DOMAIN 874 877 POLY-PRO.
 FT VARSPLIC 328 328 P -> PCPAPLFTFHSRPPVC (IN CDNA 2).
 FT VARSPLIC 329 1014 MISSING (IN CDNA 2).
 FT VARSPLIC 583 583 P -> S (IN CDNA 3).
 FT VARSPLIC 584 1014 MISSING (IN CDNA 3).
 FT N_BIND 669 677 ATP (BY SIMILARITY).
 FT DISULFID 76 115 BY SIMILARITY.
 FT CARBOHYD 473 473 POTENTIAL.
 SQ SEQUENCE 1014 AA; 110076 MW; F3723C39 CRC32;

Query Match 43.7%; Score 52; DB 11; Length 1014;
 Best Local Similarity 45.0%; Pred. No. 6.9;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 3 LDDSTIGELGWSYPSHG 22
 DB 37 LDDTGTSEIGWLTYPGPG 56

RESULT 13
 ID Q50031 PRELIMINARY; PRT; 366 AA.
 AC Q50031;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)
 DE U2266F.
 OS Mycobacterium leprae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SMITH D.R.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA ROBISON K.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U15182; AAA62976.1; -;
 SQ SEQUENCE 366 AA; 39212 MW; 6C314913 CRC32;

Query Match 42.9%; Score 51; DB 2; Length 366;
 Best Local Similarity 50.0%; Pred. No. 3.1;
 Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 5 DSKTIGELGWSYPSHG 22
 DB 226 DQRTIPHEVGMIGPGG 243

RESULT 14
 ID Q53825 PRELIMINARY; PRT; 368 AA.
 AC Q53825;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE HYPOTHETICAL 39.4 KD PROTEIN.
 GN MYV04.03C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-H37RV;
 RC HANLIN N.; CHURCHER C.M.;
 RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.

RC STRAIN-H37RV;
 RA COLE S.T., PARKILL J., BARRELL B.G., RAJANDREAM M.A.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE; 96181548.
 RA PHILIPP W.J., POULET S., EIGMEIER K., PASCOPELLA L.,
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.;
 RT "An integrated map of the genome of the tubercle bacillus,
 RT Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium
 RT leprae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
 DR EMBL; AL022004; CAAL7617.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 368 AA; 39447 MW; 61502D73 CRC32;

Query Match 41.2%; Score 49; DB 2; Length 368;
 Best Local Similarity 50.0%; Pred. No. 6.5;
 Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 5 DSKTIGELGWSYPSHG 22
 DB 230 DERTIPHEVGMIGPGG 247

RESULT 15
 ID Q17901 PRELIMINARY; PRT; 1763 AA.
 AC Q17901; Q20887;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
 DE C10C5.6A PROTEIN.
 GN C10C5.6A.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditioidea; Rhabditidae; Pelodierinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MATTHEWS P.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94150718.
 RA WILSON R., AINSOUDH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAYELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAVREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWKNEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDRAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MATTHEWS P.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 269662; CAA93506.1; -;
 DR EMBL; 268214; CAA93506.1; JOINED.
 DR EMBL; 268214; CAA92448.1; -;
 DR EMBL; 269662; CAA92448.1; JOINED.
 SQ SEQUENCE 1763 AA; 201072 MW; EBD434C5 CRC32;

Query Match 40.3%; Score 48; DB 5; Length 1763;
 Best Local Similarity 53.3%; Pred. No. 55;

Matches	8;	Conservative	3;	Mismatches	4;	Indels	0;	Gaps	0;
Oy	2	NILDSKTIQGEIGWI	16						
		: :							
Db	359	NLAERRTVLGELNWI	373						

Search completed: May 9, 2000, 22:31:10
Job time: 2375 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 22:32:06 ; Search time 49.21 Seconds
(without alignments)
13.615 Million cell updates/sec

Title: US-09-104-340-2

Perfect score: 119
Sequence: 1 VMLDSKRIQGEIGWISYPSHG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	100.0	983	EPA3_CHICK	P29318 gallus gall
2	119	100.0	983	EPA3_HUMAN	P29320 homo sapien
3	119	100.0	983	EPA3_MOUSE	P29319 mus musculu
4	119	100.0	984	EPA3_RAT	O08680 rattus norv
5	93	78.2	1013	EPAS_CHICK	P47755 gallus gall
6	89	74.8	877	EPAS_MOUSE	O06052 mus musculu
7	89	74.8	1004	EPAS_MOUSE	O09127 mus musculu
8	89	74.8	1037	EPAS_HUMAN	P24756 homo sapien
9	87	73.1	1005	EPAS_RAT	P24757 rattus norv
10	79	66.4	986	EPAS_CHICK	O07456 gallus gall
11	79	66.4	986	EPAS_HUMAN	P24764 homo sapien
12	79	66.4	986	EPAS_MOUSE	O03137 mus musculu
13	73	61.3	948	EPAS_RAT	P24758 rattus norv
14	72	60.3	1035	EPAS_MOUSE	O62413 mus musculu
15	61	51.3	998	EPAS_HUMAN	Q15375 homo sapien
16	59	49.6	998	EPAS_MOUSE	O61772 mus musculu
17	59	49.6	998	EPAS_MOUSE	P24759 rattus norv
18	58	48.7	977	EPAS_MOUSE	O03145 mus musculu
19	57	47.9	966	EPAS_MOUSE	P29318 gallus gall
20	56	47.1	976	EPAS_HUMAN	P29320 homo sapien
21	56	47.1	986	EPAS_HUMAN	P29319 mus musculu
22	56	47.1	987	EPAS_MOUSE	O08680 rattus norv
23	56	47.1	988	EPAS_CHICK	P47755 gallus gall
24	56	47.1	993	EPAS_MOUSE	O06052 mus musculu
25	55	46.2	984	EPAS_HUMAN	P24756 homo sapien
26	55	46.2	984	EPAS_HUMAN	P24757 rattus norv
27	55	46.2	984	EPAS_HUMAN	P24758 rattus norv
28	55	46.2	984	EPAS_HUMAN	P24759 rattus norv
29	53	44.5	976	EPAS_HUMAN	P29318 gallus gall
30	52	43.7	1006	EPAS_HUMAN	P29320 homo sapien
31	48	40.3	1002	EPAS_MOUSE	O08680 rattus norv
32	47	39.5	309	EPAS_CHICK	P47755 gallus gall
33	47	39.5	309	EPAS_CHICK	P47755 gallus gall
34	46	38.7	746	EPAS_MOUSE	O06052 mus musculu

35	45	37.8	619	1	SELB_HAEM	P43927 haemophilus
36	45	37.8	1577	1	MYSH_ACACA	P47808 acanthamoeb
37	43	36.1	124	1	PA2_ACPHA	P80966 ophiophagus
38	43	36.1	309	1	WAP_COCIM	P42783 coccidioides
39	43	36.1	367	1	YMPA_STRCO	P43167 streptomyces
40	43	36.1	551	1	FIXN_AZCOA	P98056 azorhizobiu
41	43	36.1	551	1	EPB4_MOUSE	P54761 mus musculu
42	42.5	35.7	331	1	YIAH_ECOLI	P37669 escherichia
43	42.5	35.7	392	1	DCAM_LEIDO	Q25264 leishmania
44	42.5	35.7	2483	1	COA2_HUMAN	O00763 homo sapien
45	42	35.3	125	1	FRDD_MYCTU	Q10763 mycobacteri

ALIGNMENTS

RESULT 1
ID EPA3_CHICK STANDARD; PRT; 983 AA.
AC P29318;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (CEK4).
GN EPHRA3 OR ETK1 OR CEK4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92031278.
RA Sajjad F.G., Pasquale E.B., Subramani S.;
RT "Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor.";
RL New Biol. 3:765-778(1991).
CC
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC -1- PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE BRAIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL; M68514; AAA48666.1; -.
CC PIR; B45583; B45583.
CC HSSP; P00523; 2PTK.
CC PRINTS; P00014; ENTPEIIT.
CC PRINTS; P00109; TYRKINASE.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
CC PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
CC PROSITE; PS01166; EGF_2; UNKNOWN_1.
CC PIRAM; PF00041; fn3. 2.
CC PIRAM; PF00069; pkinase; 1.
CC PIRAM; PF00536; SAM; 1.
CC PIRAM; PF01404; EPH_1bd; 1.
CC Trasnferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
CC Receptor; Transmembrane; Glycoprotein; Signal.
KW

FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 983 EPHRIN TYPE-A RECEPTOR 3.
FT DOMAIN 20 540 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 541 564 POTENTIAL.
FT DOMAIN 565 983 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 320 CYS-RICH.
FT DOMAIN 321 431 FIBRONECTIN TYPE-III.
FT DOMAIN 432 528 FIBRONECTIN TYPE-III.
FT DOMAIN 621 882 PROTEIN KINASE.
FT NP_BIND 627 653 ATP (BY SIMILARITY).
FT BINDING 653 653 ATP (BY SIMILARITY).
FT ACT_SITE 746 746 BY SIMILARITY.
FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 231 231 POTENTIAL.
FT CARBOHYD 336 336 POTENTIAL.
FT CARBOHYD 390 390 POTENTIAL.
FT CARBOHYD 403 403 POTENTIAL.
FT CARBOHYD 492 492 POTENTIAL.
SQ SEQUENCE 983 AA; 109910 MW; E8895F0BD77651E CRC64;

Query Match 100.0%; Score 119; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VNLDKSTIOGELGWISPSHG 22
Db 29 VNLDKSTIOGELGWISPSHG 50

RESULT 2
EPA3_HUMAN STANDARD; PRT; 983 AA.
ID EPA3_MOUSE

AC P29320;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (HEK).
GN EPAH3 OR ETK1 OR ETK OR HEK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92179233.
RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed by human lymphoid tumor cell lines."
RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
RN [2]
RN SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
RX MEDLINE; 92147681.
RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A., Welch K., Loudovaris M., Rockman S., Busmanis I.;
RT "Isolation and characterization of a novel receptor-type protein tyrosine kinase (hek) from a human pre-B cell line."
RL J. Biol. Chem. 267:3262-3267(1992).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID FUNCTION.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: RESTRICTED TO LYMPHOID TUMOR CELL LINES.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; M83941; AAA58633.1; -;
DR EMBL; A28003; CAA01906.1; -;
DR PIR; A38224; A38224.
DR HSSP; P00523; 2PTK.
DR MIM; 179611; -;
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PFM; PF00041; fn3; 2.
DR PFM; PF00069; PKINASE; 1.
DR PFM; PF00536; SAM; 1.
DR PFM; PF01404; EPH_1bd; 1.
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 983 EPHRIN TYPE-A RECEPTOR 3.
FT DOMAIN 21 541 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 542 565 POTENTIAL.
FT DOMAIN 566 983 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 21 320 CYS-RICH.
FT DOMAIN 321 431 FIBRONECTIN TYPE-III.
FT DOMAIN 432 528 FIBRONECTIN TYPE-III.
FT NP_BIND 627 635 ATP (BY SIMILARITY).
FT BINDING 653 653 ATP (BY SIMILARITY).
FT ACT_SITE 746 746 BY SIMILARITY.
FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 232 232 POTENTIAL.
FT CARBOHYD 337 337 POTENTIAL.
FT CARBOHYD 391 391 POTENTIAL.
FT CARBOHYD 404 404 POTENTIAL.
FT CARBOHYD 493 493 POTENTIAL.
FT CONFLICT 507 507 F -> L (IN CAA01906).
FT CONFLICT 724 724 V -> L (IN CAA01906).
SQ SEQUENCE 983 AA; 110086 MW; B8D90DFA80FF5121 CRC64;

Query Match 100.0%; Score 119; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VNLDKSTIOGELGWISPSHG 22
Db 30 VNLDKSTIOGELGWISPSHG 51

RESULT 3
EPA3_MOUSE STANDARD; PRT; 983 AA.
ID EPA3_MOUSE

AC P29319;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (MER4).
GN EPAH3 OR ETK1 OR MER4 OR TYR04.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ICR X SWISS WEBSTER; TISSUE-EMBRYO;
RX MEDLINE; 92031278.
RA Sajjadi F.G., Pasquale E.B., Subramani S.;

RT Identification of a new eph-related receptor tyrosine kinase gene
 RT from mouse and chicken that is developmentally regulated and encodes
 RT at least two forms of the receptor."
 RL New Biol. 3:769-778(1991).

CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: A SECRETED VARIANT WITHOUT THE TRANSMEMBRANE
 CC REGION AND THE KINASE DOMAIN IS PRODUCED BY ALTERNATIVE SPLICING
 CC OF THE SAME GENE.
 CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE
 CC BRAIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN, BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: M68513; AAA39521.1; -;
 DR EMBL: M68515; AAA39522.1; ALT_SEQ.
 DR PIR: A45583; A45583.
 DR HSP: P16109; IRSB.
 DR MGD: MGI:99612; EPHA3.
 DR PRINTS: PRO0014; ENTPEIIT.
 DR PRINTS: PRO0109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PFM: PFO0041; fn3; 2.
 DR PFM: PFO0069; PKINASE; 1.
 DR PFM: PFO0536; SAM; 1.
 DR PFM: PFO1404; EPH_1bd; 1.
 DR Transferrase: Tyrosine-protein kinase: ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.

FT SIGNAL 1 20
 FT CHAIN 21 983
 FT DOMAIN 21 540
 FT TRANSMEM 541 564
 FT DOMAIN 565 983
 FT DOMAIN 21 320
 FT DOMAIN 321 431
 FT DOMAIN 432 528
 FT DOMAIN 529 621
 FT NP_BIND 627 635
 FT BINDING 653 653
 FT ACT_SITE 746 746
 FT MOD_RES 779 779
 FT CARBOHYD 231 231
 FT CARBOHYD 336 336
 FT CARBOHYD 390 390
 FT CARBOHYD 403 403
 FT CARBOHYD 492 492
 FT VARSPIC 530 983
 FT SEQUENCE 983 AA; 109955 MW; BE44A655D8107A2 CRC64;

Query Match 100.0%; Score 119; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 VNLDSKTIQGLGWSYPSHG 22
 ||||||||||||||||||||

DB 30 VNLDSKTIQGLGWSYPSHG 51

RESULT 4
 ID EPH3_RAT STANDARD; PRT; 984 AA.
 AC 00680;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR REK4).
 GN EPHA3 OR REK4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE; 98120505.
 RA Li Y.Y., McTieran C.F., Feldman A.M.;
 RT "IL-1 beta alters the expression of the receptor tyrosine kinase gene
 RL t-Pha3 in neonatal rat cardiomyocytes.";
 RL Am. J. Physiol. 274:H331-H341(1998).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN, BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: U69278; AAC06273.1; -;
 DR HSP: P16109; IRSB.
 DR PRINTS: PRO0014; ENTPEIIT.
 DR PRINTS: PRO0109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PFM: PFO0041; fn3; 2.
 DR PFM: PFO0069; PKINASE; 1.
 DR PFM: PFO0536; SAM; 1.
 DR PFM: PFO1404; EPH_1bd; 1.
 DR Transferrase: Tyrosine-protein kinase: ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 984
 FT DOMAIN 21 541
 FT TRANSMEM 542 565
 FT DOMAIN 566 984
 FT DOMAIN 21 321
 FT DOMAIN 322 432
 FT DOMAIN 433 529
 FT NP_BIND 622 622
 FT BINDING 654 654
 FT ACT_SITE 747 747
 FT MOD_RES 780 780
 FT CARBOHYD 232 232
 FT CARBOHYD 337 337
 FT CARBOHYD 391 391

FT SEQUENCE 984 AA; 109955 MW; BE44A655D8107A2 CRC64;

Query Match 100.0%; Score 119; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 VNLDSKTIQGLGWSYPSHG 22
 ||||||||||||||||||||

FT CAROBYD 404 404 POTENTIAL.
 FT CAROBYD 493 POTENTIAL.
 SQ SEQUENCE 984 AA: 110227 MW: F170C49312F7A0AB CRC64;

Query Match 100.0%; Score 119; DB 1; Length 984;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNLDSTKTIQELGWSYPSHG 22
 ||||||||||||||||
 DB 30 VNLDSTKTIQELGWSYPSHG 51

RESULT 5
 ID EPAS_CHICK STANDARD; PRT: 1013 AA.
 AC P54755;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK7).
 GN EPHAS OR CEK7
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.

RA Slevier D.A., Verderame M.F.;
 RT "Identification of a complete Cek7 receptor protein tyrosine kinase coding sequence and cDNAs of alternatively spliced transcripts."; RL Gene 148:219-226(1994).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U03910; AAB60613.1; -
 DR EMBL: U03910; AAB60614.1; -
 DR EMBL: U03910; AAB60612.1; -
 DR HSSP: P00523; 2PTR.
 DR PRINTS: PR00014; FNTYPEIII.
 DR PRINTS: PR00109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PFM: PFM0041; fn3; 2.
 DR PFM: PFM0069; kinase; 1.
 DR PFM: PFM0536; SAM; 1.
 DR PFM: PFM01404; EPH_Lbd; 1.
 DR Transferrase: Tyrosine-protein kinase: ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
 FT SIGNAL 1 31 POTENTIAL.

FT CHAIN 32 1013 EPHRIN TYPE-A RECEPTOR 5.
 FT DOMAIN 32 549 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 550 570 POTENTIAL.
 FT DOMAIN 571 1013 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 651 912 PROTEIN KINASE.
 FT NP_BIND 657 665 ATP (BY SIMILARITY).
 FT BINDING 683 683 ATP (BY SIMILARITY).
 FT ACT_SITE 776 776 BY SIMILARITY.
 FT CAROBYD 240 240 POTENTIAL.
 FT CAROBYD 275 275 POTENTIAL.
 FT CAROBYD 345 345 POTENTIAL.
 FT CAROBYD 399 399 POTENTIAL.
 FT CAROBYD 412 412 POTENTIAL.
 FT CAROBYD 437 437 POTENTIAL.
 FT VARSPLIC 280 443 MISSING (IN ISOFORM 2).
 FT VARSPLIC 573 595 SCDHGCGMASSLRVAVPSLIW -> R (IN ISOFORM 1 AND ISOFORM 2).
 SQ SEQUENCE 1013 AA: 112245 MW: AC36FDBAEF38382 CRC64;

Query Match 78.2%; Score 93; DB 1; Length 1013;
 Best Local Similarity 68.2%; Pred. No. 1.1e-06;
 Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDSTKTIQELGWSYPSHG 22
 |||||||:|:|:|:|:|:|
 DB 37 VNLDSTKTIQELGWSYPSHG 58

RESULT 6
 ID EPAS_MOUSE STANDARD; PRT: 877 AA.
 AC Q60629;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOG KINASE-1) (BRAIN-SPECIFIC KINASE) (CEK-7).
 GN EPHAS OR EHK1 OR CEK7 OR BSK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.

RA Zhou R., Copeland T.D., Kromer L.F., Schulz N.T.;
 RT "Isolation and characterization of Bsk, a growth factor receptor-like tyrosine kinase associated with the limbic system."; RL J. Neurosci. Res. 37:129-143(1994).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U07357; AAA17038.1; -
 DR HSSP: P00523; 2PTR.
 DR MGD: MGI:99654; EPHAS.
 DR PRINTS: PR00014; FNTYPEIII.


```

CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
CC SYSTEM.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sib.ch).
CC -----
DR EMBL: X85425; CAA64700.1; -
DR EMBL: L36644; AAI74245.1; -
DR HSSP: P00523; 2PTR.
DR MIM: 600004; -
DR PRINTS: PRO0104; FNTYPEIIT.
DR PRINTS: PS00109; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PRAM: PF00041; fn3; 2.
DR PRAM: PF00069; PKINASE; 1.
DR PRAM: PF00536; SAM; 1.
DR PRAM: PF01404; EPH_Lbd; 1.
DR PRAM: PF01404; EPH_Lbd; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 1037 EPHRIN TYPE-A RECEPTOR 5.
FT DOMAIN 25 573 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 574 594 POTENTIAL.
FT DOMAIN 595 1037 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 675 936 PROTEIN KINASE.
FT NP_BIND 681 689 ATP (BY SIMILARITY).
FT BINDING 707 707 ATP (BY SIMILARITY).
FT ACT_SITE 800 800 BY SIMILARITY.
FT CARBOHYD 264 264 POTENTIAL.
FT CARBOHYD 299 299 POTENTIAL.
FT CARBOHYD 369 369 POTENTIAL.
FT CARBOHYD 423 423 POTENTIAL.
FT CARBOHYD 436 436 POTENTIAL.
FT CARBOHYD 461 461 POTENTIAL.
FT VARSPPLIC 597 619 SCCECGCGGRASSICANVAHPTLIW -> R (IN ISOFORM
2).
SQ SEQUENCE 1037 AA; 114784 MW; FC2C46C959AFB699 CAC664;

```

```

Query Match 74.8%; Score 89; DB 1; Length 1037;
Best Local Similarity 63.6%; Pred. No. 4.9e-06;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 VNLDSTKIOGELGWSIPSHG 22
| | | | | : | : | | | : | : |
DB 61 VNLDSTWMDLGMIAFPKNG 82

```

```

RESULT 9
ID EPH5_RAT STANDARD; PRT; 1005 AA.
AC P54757;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EHK-1) (EPH HOMOLOG KINASE-1).
GN EPH5 OR EKH1 OR EHK-1.

```

```

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE: 94067777.
RA Maisonneuve P.C., Barrezaeta N.X., Yancopoulos G.D.;
RT "Ehk-1 and EHK-2: two novel members of the Eph receptor-like tyrosine
RT kinase family with distinctive structures and neuronal expression.";
RL Oncogene 8:3277-3288(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE: 95206467.
RA Taylor V., Pfaff S., Miescher G.C., Honegger P., Bretschopf H.,
RA Lässmann H., Steck A.J.;
RT "Expression and developmental regulation of EHK-1, a neuronal
RT Elk-like receptor tyrosine kinase in brain.";
RL Neuroscience 63:163-178(1994).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
CC SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sib.ch).
CC -----
DR EMBL: X78689; CAA55357.1; -
DR HSSP: P00523; 2PTR.
DR PRINTS: PRO0104; FNTYPEIIT.
DR PRINTS: PS00109; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PRAM: PF00041; fn3; 2.
DR PRAM: PF00069; PKINASE; 1.
DR PRAM: PF01404; EPH_Lbd; 1.
DR PRAM: PF01404; EPH_Lbd; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 1037 EPHRIN TYPE-A RECEPTOR 5.
FT DOMAIN 25 573 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 597 596 POTENTIAL.
FT DOMAIN 597 1005 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 677 938 PROTEIN KINASE.
FT BINDING 683 691 ATP (BY SIMILARITY).
FT BINDING 709 709 ATP (BY SIMILARITY).
FT ACT_SITE 802 802 BY SIMILARITY.
FT CARBOHYD 266 266 POTENTIAL.
FT CARBOHYD 301 301 POTENTIAL.
FT CARBOHYD 371 371 POTENTIAL.
FT CARBOHYD 425 425 POTENTIAL.
FT CARBOHYD 438 438 POTENTIAL.
FT CARBOHYD 463 463 POTENTIAL.
FT VARSPPLIC 10 20 SPICED FORMS).

```

```

FT VARSPLIC 306 358 VCRPFKASPHSQTSCPPHSYTHEASTSCVCKDYFR
FT RESDPTACTR -> G (IN SPLICED FORMS).
FT VARSPLIC 358 470 RPSAPRNAINSVNVEYLEWIPADGGGADVXYLLCK
FT KONSAGVCECGGCHVRIPOIGIKNTSYMADIALATNY
FT TPEIVANVSDELSPGTGTROYSVANTTMOAA -> T (IN
FT SPLICED FORMS).
FT VARSPLIC 597 621 SSCCECGCGRASSICAVANPSLIW -> R (IN
FT SPLICED FORMS).
FT CONFLICT 170 170 D -> E (IN REF. 2).
FT CONFLICT 566 566 G -> A (IN REF. 2).
FT CONFLICT 578 578 G -> A (IN REF. 2).
FT CONFLICT 669 669 G -> A (IN REF. 2).
FT CONFLICT 708 708 T -> I (IN REF. 2).
FT CONFLICT 979 979 T -> I (IN REF. 2).
SQ SEQUENCE 1005 AA; 111007 MW; 1AED42C9963C574 CRC64;

Query Match 73.1%; Score 87; DB 1; Length 1005;
Best Local Similarity 63.6%; Pred. No. 9.6e-06;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNLDSKTIGELGWSYPSHG 22
Db 63 VNLDSRTVLGDLGWIAFPRNG 84

RESULT 10
EPA4_CHICK STANDARD: PRT: 986 AA.
AC 007496; Q90772;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR CEK8).
GN EPHA4 OR CEK8.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPINAL CORD;
RA MEDLINE; 96404128.
RA Ohta K., Nakamura M., Hirokawa K., Tanaka S., Iwama A., Suda T.,
RA Ando M., Tanaka H.;
RT "The receptor tyrosine kinase, CEK8, is transiently expressed on
RT subtypes of motoneurons in the spinal cord during development.";
RL Mech. Dev. 54:59-69(1996).
RN [2]
RP SEQUENCE OF 138-986 FROM N.A.
RC TISSUE-EMBRYO;
RA MEDLINE; 93286394.
RA Sajjadi F.G., Pasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed.";
RL Oncogene 8:1807-1813(1993).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1 -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 AND A-3.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sib.ch).
CC -----

```

```

DR EMBL; D38174; BAA07373.1; -
DR EMBL; Z19059; CAI79509.1; -
DR HSSP; P00523; 2PTRK.
DR PRINTS; PR00014; FNTYPEIT.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR. 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM. 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V. 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V. 2. 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00069; PKINASE. 1.
DR PFAM; PF00536; SAM; 1.
DR PFAM; PF01404; EPH_1bd; 1.
KM Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KM Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 986 EPHRIN TYPE-A RECEPTOR 4.
FT DOMAIN 20 547 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 548 569 POTENTIAL.
FT DOMAIN 570 586 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 325 435 FIBRONECTIN TYPE-III (BY SIMILARITY).
FT DOMAIN 436 532 FIBRONECTIN TYPE-III (BY SIMILARITY).
FT DOMAIN 621 882 PROTEIN KINASE.
FT NP_BIND 627 635 ATP (BY SIMILARITY).
FT BINDING 653 653 ATP (BY SIMILARITY).
FT ACT_SITE 746 746 BY SIMILARITY.
FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CARBOHYD 235 235 POTENTIAL.
FT CARBOHYD 340 340 POTENTIAL.
FT CARBOHYD 408 408 POTENTIAL.
FT CONFLICT 138 138 R -> G (IN REF. 2).
FT CONFLICT 487 487 S -> T (IN REF. 2).
SQ SEQUENCE 986 AA; 109482 MW; BD86C2A5BD840A0F CRC64;

Query Match 66.4%; Score 79; DB 1; Length 986;
Best Local Similarity 63.6%; Pred. No. 0.00017;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VNLDSKTIGELGWSYPSHG 22
Db 31 VNLDSRSVQSLGWIASPLSG 52

RESULT 11
EPA4_HUMAN STANDARD: PRT: 986 AA.
AC P54764;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR SEK) (RECEPTOR PROTEIN-TYROSINE KINASE HEK8).
GN EPHA4 OR SEK OR HEK8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MEDLINE; 95206782.
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA Basu R., Welcher A.A.;
RT "cDNA cloning and tissue distribution of five human EPH-like receptor
RT protein-tyrosine kinases.";
RL Oncogene 10:897-905(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 AND A-3.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -----

```

```
CC -1 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1 SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
-----
DR EMBL: L36645; AAA4246.1; -
DR HSP: P00523; 2PTK.
DR MIM: 602188; -.
DR PRINTS: PRO0014; FNTYPEP11.
DR PRINTS: PRO0109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V.1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V.2; 1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; pk_nase; 1.
DR PFAM: PF00536; SAM; 1.
DR PFAM: PF01404; EPH_Lbd; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 986
FT DOMAIN 20 547
FT TRANSMEM 548 569
FT DOMAIN 570 585
FT DOMAIN 570 585
FT DOMAIN 335 435
FT DOMAIN 436 532
FT DOMAIN 621 882
FT NP_BIND 637 635
FT BINDING 653 653
FT ACT_SITE 746 746
FT MOD_RES 779 779
FT CARBOHYD 235 235
FT CARBOHYD 340 340
FT CARBOHYD 408 408
FT CARBOHYD 545 545
FT SEQUENCE 986 AA; 109859 MW; 0C39C1152EDD46F CRC64;

Query Match 66.4%; Score 79; DB 1; Length 986;
Best Local Similarity 63.6%; Pred. No. 0.00017;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 VMLDSKTIQGLGWSYPSHG 22
DB 31 VTLDSRSVQGLGWASPLEG 52

RESULT 12
EPA4_MOUSE STANDARD; PRT; 986 AA.
AC EPA4_MOUSE 3137;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR SEK) (MPK-3).
GN EPA4 OR SEK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL; TISSUE-EMBRYONIC BRAIN;
RX MEDLINE; 93096484.
```

```
RA Glardl-Hebenstreit P., Nieto M.A., Frahn M., Mattei M.-G.,
RA Chetlier A., Wilkinson D.G., Charney P.;
RT "An Eph-related receptor protein tyrosine kinase gene segmentally
RT expressed in the developing mouse hindbrain.";
RL Oncogene 7:2499-2506(1992).
RN [2]
RP ERRATUM.
RX MEDLINE; 93205393.
RA Glardl-Hebenstreit P., Nieto M.A., Frahn M., Mattei M.-G.,
RA Chetlier A., Wilkinson D.G., Charney P.;
RL Oncogene 8:1103-1103(1993).
CC -1 FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 AND A-3.
CC MAY PLAY A ROLE IN A SIGNAL TRANSDUCTION PROCESS INVOLVED IN
CC HINDRAIN PATTERN FORMATION.
CC -1 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1 ALTERNATIVE PRODUCTS: A SHORTER FORM WITH A DELETION OF 49
CC AMINO ACIDS ALTERING THE CATALYTIC SITE MAY BE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -1 TISSUE SPECIFICITY: HIGHEST LEVELS IN THE BRAIN, LOWER LEVELS
CC IN THE HEART, LUNG AND KIDNEY. IT IS SEGMENTALLY EXPRESSED
CC IN THE EMBRYONIC BRAIN.
CC -1 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1 SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
-----
DR EMBL: X65138; CAA46268.1; -
DR EMBL: X57241; CAA40517.1; -
DR EMBL: S57168; AAB25836.1; -
DR HSP: P00523; 2PTK.
DR MGD: MG1:98277; EPA4.
DR PRINTS: PRO0014; FNTYPEP11.
DR PRINTS: PRO0109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V.1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V.2; 1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; pk_nase; 1.
DR PFAM: PF00536; SAM; 1.
DR PFAM: PF01404; EPH_Lbd; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 986
FT DOMAIN 20 547
FT TRANSMEM 548 569
FT DOMAIN 570 585
FT DOMAIN 570 585
FT DOMAIN 335 435
FT DOMAIN 436 532
FT DOMAIN 621 882
FT NP_BIND 637 635
FT BINDING 653 653
FT ACT_SITE 746 746
FT MOD_RES 779 779
FT CARBOHYD 235 235
FT CARBOHYD 340 340
FT CARBOHYD 408 408
FT CARBOHYD 423 423
FT VARSPIC 783 832
FT SEQUENCE 986 AA; 109801 MW; D16AD8B8568C80E CRC64;
```


Query Match 66.4%; Score 79; DB 1; Length 986;
Best Local Similarity 63.6%; Pred. No. 0.00017;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 VNLDSKTIGELGWISYPSHG 22
DB 31 VLLDSRSVOGELGWIASPLG 52

RESULT 13

EP66_RAT STANDARD; PRT; 948 AA.
AC P54758;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-2) (EPH HOMOLOG KINASE-2).
GN EPHA6 OR EHK2 OR EHK-2.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE: 94067777.
RA Malsompierre P.C., Barrezueta N.X., Yancopoulos G.D.;
RT "Ehk-1 and Ehk-2, two novel members of the eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression.";
RL Oncogene 8:3377-3288(1993).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR HSSP: P00523; 2PTK.
DR PRINTS: PRO00104; ENTPEP11.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; PKINASE; 1.
DR PFAM: PF01404; EPH_1bd; 1.
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 948
FT DOMAIN 23 549
FT TRANSMEM 550 570
FT DOMAIN 571 948
FT NP_BIND 630 943
FT BINDING 636 644
FT ACT_SITE 662 662
FT CARBOHYD 342 342
FT CARBOHYD 396 396
FT CARBOHYD 409 409
SEQUENCE 948 AA; 106235 MW; A47DC78EDB2DEF30 CRC64;

Query Match 61.3%; Score 73; DB 1; Length 948;
Best Local Similarity 59.1%; Pred. No. 0.0014;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
OY 1 VNLDSKTIGELGWISYPSHG 22
DB 31 VLLDSRSVOGELGWIASPLG 52

DB 34 VLLDSRSVOGELGWISYPSHG 55

RESULT 14

EP66_MOUSE STANDARD; PRT; 1035 AA.
AC Q62413;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-2) (EPH HOMOLOG KINASE-2).
GN EPHA6 OR EHK2 OR EHK-2.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE: 97047913.
RA Lee A.M., Navarathnam D., Ichimura S., Greene M.I., Davis J.G.;
RT "Cloning of m-ehk2 from the murine inner ear, an eph family receptor tyrosine kinase expressed in the developing and adult cochlea.";
RL DNA Cell Biol. 15:817-825(1996).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U58332; AAB53836.1; -.
DR HSSP: P00523; 2PTK.
DR MGD: MGI:108034; EPHA6.
DR PRINTS: PRO00104; ENTPEP11.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; PKINASE; 1.
DR PFAM: PF00536; SAM; 1.
DR PFAM: PF01404; EPH_1bd; 1.
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 1035
FT DOMAIN 23 549
FT TRANSMEM 550 570
FT DOMAIN 571 1035
FT NP_BIND 630 943
FT BINDING 662 662
FT ACT_SITE 797 797
FT CARBOHYD 342 342
FT CARBOHYD 396 396
FT CARBOHYD 409 409
SEQUENCE 1035 AA; 116137 MW; 560B264194A5EF74 CRC64;

Query Match 60.5%; Score 72; DB 1; Length 1035;
Best Local Similarity 59.1%; Pred. No. 0.0021;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 VNLDSKTIQELGWISYPSHG 22
| | | | | : | | | | | : | |
DB 34 VVLDITTTMGLGKTYPLNG 55

RESULT 15
EPA7_HUMAN STANDARD; PRT; 998 AA.
AC 015375;
DI 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DI 15-JUL-1998 (Rel. 36, Last annotation update)
DI EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EHK-3) (EPH HOMOLOG KINASE-3) (RECEPTOR PROTEIN-
DE TYROSINE KINASE HEK11).
GN EPHA7 OR EHK3 OR HEK11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 95206782.
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA Basu R., Welcher A.A.;
RT "cDNA cloning and tissue distribution of five human EPH-like receptor
protein-tyrosine kinases."
RL Oncogene 10:897-905(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L36642; AAA74243.1; -
DR HSP; P00523; PTK.
DR MIM; 602190; -
DR PRINTS; PRO0014; FNTYPEIII.
DR PRINTS; PRO0109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00069; kinase; 1.
DR PFAM; PF00536; SAM; 1.
DR PFAM; PF01404; EPH_Lbd; 1.
KW transferase; tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 998 EPHRIN TYPE-A RECEPTOR 7.
FT DOMAIN 25 556 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 557 577 POTENTIAL.
FT DOMAIN 578 998 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 329 438 FIBRONECTIN TYPE-III.
FT DOMAIN 439 537 FIBRONECTIN TYPE-III.

FT DOMAIN 633 894 PROTEIN KINASE.
FT NP_BIND 639 647 ATP (BY SIMILARITY).
FT BINDING 665 665 ATP (BY SIMILARITY).
FT ACT_SITE 758 758 BY SIMILARITY.
FT MOD_RES 791 791 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 343 343 POTENTIAL.
FT CARBOHYD 410 410 POTENTIAL.
SQ SEQUENCE 998 AA; 112096 MW; 479B9CA0D2B06EB CRC64;

Query Match 51.3%; Score 61; DB 1; Length 998;
Best Local Similarity 63.6%; Pred. No. 0.11;
Matches 14; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 VNLDSKTIQELGWISYPSHG 22
| | | | | : | | | | | : | |
DB 33 VVLDLSKMQTLEWISSPPNG 54

Search completed: May 9, 2000, 22:32:08
Job time: 2399 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 22:27:14 ; Search time 64.29 Seconds
(without alignments)
20.063 Million cell updates/sec

Title: US-09-104-340-2

Perfect score: 119

Sequence: 1 VNLDSTKIQGELGWISYPSHG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR_63:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	983	2 B45583	receptor tyrosine
2	119	100.0	983	2 A38224	protein-tyrosine k
3	119	100.0	983	2 A45583	receptor tyrosine
4	93	78.2	1013	2 I50615	receptor-type prot
5	89	74.8	877	2 I48967	brain-specific kin
6	89	74.8	991	2 I78843	receptor protein-t
7	87	73.1	893	2 S51603	receptor-like tyro
8	87	73.1	898	2 S47489	receptor tyrosine
9	87	73.1	981	2 S51604	receptor-like tyro
10	87	73.1	1005	2 S49015	receptor tyrosine
11	79	66.4	985	2 I51549	receptor tyrosine
12	79	66.4	986	2 S78059	receptor tyrosine
13	79	66.4	986	2 I78844	protein-tyrosine k
14	73	61.3	948	2 S51605	receptor protein-t
15	61	51.3	998	2 I58351	receptor-like tyro
16	59	49.6	605	2 JC5675	receptor tyrosine
17	59	49.6	610	2 I48612	receptor tyrosine
18	59	49.6	626	2 I48614	developmental kina
19	59	49.6	998	2 JC5672	developmental kina
20	58	48.7	975	2 I48974	receptor tyrosine
21	58	48.7	977	2 S49004	receptor protein t
22	58	48.7	985	2 I51672	tyrosine kinase Mp
23	57	47.9	968	2 I51672	receptor tyrosine
24	56	47.1	970	2 I78842	alanine--tRNA liga
25	56	47.1	984	1 A34076	receptor protein-t
26	56	47.1	995	2 A56599	protein-tyrosine k
27	55	46.2	984	2 A37553	embryo kinase 5 -
28	55	46.2	993	2 A37553	protein-tyrosine k
29	55	46.2	998	2 S37627	mouse developmenta
30	53	44.5	952	2 I50612	protein-tyrosine k

31	53	44.5	976	2 A36355	protein-tyrosine k
32	52	43.7	1006	2 JC5526	kinase-defective E
33	49	41.2	368	2 C70809	hypothetical prote
34	48	40.3	1763	2 T19183	hypothetical prote
35	48	40.3	1769	2 T19184	hypothetical prote
36	47	39.5	309	2 C65088	hypothetical prote
37	47	39.5	967	1 SYMTAV	alanine--tRNA liga
38	46	38.7	134	2 S28678	hypothetical prote
39	46	38.7	457	2 C71614	eIF-4A-like DEAD f
40	46	38.7	746	2 S50226	CSD3 protein - yea
41	45	37.8	464	2 T24011	hypothetical prote
42	45	37.8	530	2 B37471	capsid protein - N
43	45	37.8	619	2 I64087	translation elonga
44	45	37.8	1576	1 A23662	myosin I, high mol
45	44	37.0	234	2 A71666	hypothetical prote

ALIGNMENTS

```

RESULT 1
B45583
receptor tyrosine kinase Cerk - chicken
C:Species: Gallus gallus (chicken)
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: B45583
R:Saljedi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
A:Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
A:Reference number: A45583; MUID:92031278
A:Accession: B45583
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-983 <SAU>
A:Cross-references: GB:M68514; NID:G454809; PIDN:AAA48666.1; PID:G211447
A>Note: sequence extracted from NCBI backbone (NCBI:62405; NCBI:62411)
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP, autophosphorylation, phosphoprotein; transmembrane protein
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif

Query Match 100.0%; Score 119; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLDSTKIQGELGWISYPSHG 22
|||||
DB 29 VNLDSTKIQGELGWISYPSHG 50

RESULT 2
A38224
protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C:Accession: A38224; B38224
R:Wilks, I.P.; Wilkinson, D.; Salvaris, E.; Boyd, A.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
A:Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expre
A:Reference number: A38224; MUID:92179233
A:Accession: A38224
A:Molecule type: mRNA
A:Residues: 1-983 <WIC>
A:Cross-references: GB:M63941; NID:G183931; PIDN:AAA58633.1; PID:G183932
A:Experimental source: pre-B-cell leukemia cell line tk63
A>Note: sequence extracted from NCBI backbone (NCBI:86627)
A:Accession: B38224
A:Molecule type: protein
A:Residues: 21-39;810-860 <W12>
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP, autophosphorylation; glycoprotein; phosphoprotein; phosphotransferas
F:1-20/Domain: signal sequence #status predicted <SIG>

```

F:21-983/Product: protein-tyrosine kinase hek #status experimental <MAT>
F:542-565/Domain: transmembrane #status predicted <TM>
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif
F:232,337,391,404,493/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 100.0%; Score 119; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNLDSTKTQGLGWIYSYPSHG 22
DB 30 VNLDSTKTQGLGWIYSYPSHG 51

RESULT 3
A:Accession: A45583
C:Species: Mus musculus (house mouse)
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: A45583
R:Sajjadi, F.G.; Pasquale, E.B.; Subraman, S.
New Biol. 3, 769-778, 1991
A:Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse an
A:Reference number: A45583; MUID:92031278
A:Accession: A45583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-983 <SAJ>
A:Cross-references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A>Note: Sequence extracted from NCBI backbone (NCBIN:62398; NCBIIP:62401)
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif

Query Match 100.0%; Score 119; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNLDSTKTQGLGWIYSYPSHG 22
DB 30 VNLDSTKTQGLGWIYSYPSHG 51

RESULT 4
150615
receptor-tyr protein-tyrosine kinase Cck7, long splice form - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C:Accession: I50615; I50616; I50614
R:Stever, D.A.; Verderame, M.F.
Gene 148, 219-226, 1994
A:Title: Identification of a complete Cck7 receptor protein tyrosine kinase coding seque
A:Reference number: I50614; MUID:95047429
A:Accession: I50615
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1013 <STE>
A:Cross-references: EMBL:U03910; NID:g555617; PIDN:AAB60612.1; PID:g555618
A:Accession: I50616
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-572, 'R', 596-1013 <SI2>
A:Cross-references: EMBL:U03910; NID:g555617; PIDN:AAB60613.1; PID:g555619
A:Accession: I50614
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-279, 444-572, 'R', 596-1013 <SI3>
A:Cross-references: EMBL:U03910; NID:g555617; PIDN:AAB60614.1; PID:g555620
C:Genetics:

A:Gene: Cck7
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: alternative splicing; ATP; transmembrane protein
F:649-915/Domain: protein kinase homology <KIN>
F:657-665/Region: protein kinase ATP-binding motif
F:938-1004/Domain: SAM homology <SAM>

Query Match 78.2%; Score 93; DB 2; Length 1013;
Best Local Similarity 68.2%; Pred. No. 1.7e-06;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDSTKTQGLGWIYSYPSHG 22
DB 37 VNLDSTRTVMGDLGWIAYPKNG 58

RESULT 5
148967
brain-specific kinase - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I48967
R:Zhou, R.R.; Copeland, T.D.; Kromer, L.F.; Schulz, N.T.
J. Neurosci. Res. 37, 129-143, 1994
A:Title: Isolation and characterization of Bsk, a growth factor receptor-like tyrosin
A:Reference number: I48967; MUID:94194581
A:Accession: I48967
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-877 <RES>
A:Cross-references: EMBL:U07357; NID:g466369; PIDN:AAA17038.1; PID:g466370
C:Genetics:
A:Gene: Bsk
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; transmembrane protein
F:512-778/Domain: protein kinase homology <KIN>
F:520-528/Region: protein kinase ATP-binding motif
F:801-868/Domain: SAM homology <SAM>

Query Match 74.8%; Score 89; DB 2; Length 877;
Best Local Similarity 63.6%; Pred. No. 6.2e-06;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDSTKTQGLGWIYSYPSHG 22
DB 63 VNLDSTRTVMGDLGWIAFPKNG 84

RESULT 6
178843
receptor protein-tyrosine kinase - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C:Accession: I78843
R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Landberg, R.A.; Janssen, A.M.; Basu, R.; Welch
Oncogene 10, 897-905, 1995
A:Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein
A:Reference number: I58351; MUID:95206782
A:Accession: I78843
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-991 <RES>
A:Cross-references: GB:L36644; NID:g551611; PIDN:AAA74245.1; PID:g551612
C:Genetics:
A:Gene: HEK7
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
F:627-893/Domain: protein kinase homology <KIN>
F:916-982/Domain: SAM homology <SAM>

Query Match 74.8%; Score 89; DB 2; Length 991;

Best Local Similarity 63.6%; Pred. No. 7.1e-06;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDSTIQTGELGWTSPSHG 22
DB 37 VNLDSTRTVLGDLGWTAFPKNG 58

RESULT 7

S51603
receptor-like tyrosine kinase Etk-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C:Accession: S51603
R:Maizompliere, P.C.; Barreuzeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A:Reference number: S49015; MUID:94067777
A:Accession: S51603
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-893 <MAI>

A:Cross-references: EMBL:S68028
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat H
C:Keywords: ATP; transmembrane protein
F:563-829/Domain: protein kinase homology <KIN>
F:571-579/Region: protein kinase ATP-binding motif

Query Match 73.1%; Score 87; DB 2; Length 893;
Best Local Similarity 63.6%; Pred. No. 1.3e-05;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDSTIQTGELGWTSPSHG 22
DB 63 VNLDSTRTVLGDLGWTAFPKNG 84

RESULT 8

S47489
receptor tyrosine kinase - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C:Accession: S47489
R:Taylor, V.; Pfarr, S.; Miescher, G.C.; Honegger, P.; Breitschopf, H.; Lassmann, H.; St
submitted to the EMBL Data Library, April 1994
A:Description: Expression and developmental regulation of Etk-1, a neuronal ELK-like rec
A:Reference number: S47489
A:Accession: S47489
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-898 <TAI>
A:Cross-references: EMBL:X78689; NID:9531543; PIDN:CA55357.1; PID:9531544
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat H
C:Keywords: ATP; transmembrane protein
F:568-834/Domain: protein kinase homology <KIN>
F:576-584/Region: protein kinase ATP-binding motif

Query Match 73.1%; Score 87; DB 2; Length 898;
Best Local Similarity 63.6%; Pred. No. 1.3e-05;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDSTIQTGELGWTSPSHG 22
DB 68 VNLDSTRTVLGDLGWTAFPKNG 89

RESULT 9

S51604
receptor-like tyrosine kinase Etk-1 - rat
C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C:Accession: S51604
R:Maizompliere, P.C.; Barreuzeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase
A:Reference number: S49015; MUID:94067777
A:Accession: S51604
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-981 <MAI>

A:Cross-references: EMBL:S68029
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; transmembrane protein
F:651-917/Domain: protein kinase homology <KIN>
F:659-667/Region: protein kinase ATP-binding motif

Query Match 73.1%; Score 87; DB 2; Length 981;
Best Local Similarity 63.6%; Pred. No. 1.4e-05;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDSTIQTGELGWTSPSHG 22
DB 63 VNLDSTRTVLGDLGWTAFPKNG 84

RESULT 10

S49015
receptor tyrosine kinase Etk-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C:Accession: S49015; S51602
R:Maizompliere, P.C.; Barreuzeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase
A:Reference number: S49015; MUID:94067777
A:Accession: S49015
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1005 <MAI>
A:Cross-references: EMBL:S68024
A:Note: the authors translated the codon GAC for residue 170 as Glu
A:Accession: S51602
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305, 'G', 359-1005 <MA2>
A:Cross-references: EMBL:S68026
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; transmembrane protein
F:675-941/Domain: protein kinase homology <KIN>
F:683-691/Region: protein kinase ATP-binding motif

Query Match 73.1%; Score 87; DB 2; Length 1005;
Best Local Similarity 63.6%; Pred. No. 1.5e-05;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDSTIQTGELGWTSPSHG 22
DB 63 VNLDSTRTVLGDLGWTAFPKNG 84

RESULT 11

I51549
receptor tyrosine kinase - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C:Accession: I51549
R:Winning, R.S.; Sargent, T.D.
Mech. Dev. 46, 219-229, 1994
A:Title: Pagliaccio, a member of the Eph family of receptor tyrosine kinase genes, ha

A:Reference number: I51549; MUID:95001564
A:Accession: I51549
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Reference number: I58351; MUID:95206782
A:Accession: I78844
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-985 <WIN>
A:Cross-references: GB:L26099; NID:9416402; PIDN:AAA64464.1; PID:9416403
C:Genetics:
A:Gene: Peg
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C:Keywords: ATP; transmembrane protein
F:618-884/Domain: protein kinase homology <KIN>
F:626-634/Region: protein kinase ATP-binding motif

Query Match 66.4%; Score 79; DB 2; Length 985;
Best Local Similarity 63.6%; Pred. No. 0.00026;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VNLDSTIIGELGWISYPSHG 22
| | | | | : | | | | | : | |
DB 31 VTLDSRSVQELGWIASPLEG 52

RESULT 12
S78059
protein-tyrosine kinase (EC 2.7.1.112) Eph precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 18-Jun-1999
C:Accession: S78059; #accession: I58366
R:Charney, P.
submitted to the EMBL Data Library, March 1992
A:Reference number: S78059
A:Accession: S78059
A:Molecule type: mRNA
A:Residues: 1-986 <CHAS>
A:Cross-references: EMBL:X65138; NID:954083; PIDN:CAA6268.1; PID:954084
R:Gillard-Habenstreit, P.; Nicot, M.A.; Frain, M.; Mattei, M.G.; Chestier, A.; Wilkinson
Oncogene 7, 2499-2506, 1992
A:Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed in t
A:Reference number: S30496; MUID:93096484
A:Accession: S30505
A:Molecule type: mRNA
A:Residues: 1-31,55-986 <GIL>
A:Cross-references: EMBL:X65138
C:Genetics:
A:Gene: Sek
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C:Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-986/Product: protein-tyrosine kinase Eph #status predicted <MAT>
F:548-569/Domain: transmembrane #status predicted <TM>
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif
F:908-974/Domain: SAM homology <SAM>
F:235,340,408,423/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.4%; Score 79; DB 2; Length 986;
Best Local Similarity 63.6%; Pred. No. 0.00026;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VNLDSTIIGELGWISYPSHG 22
| | | | | : | | | | | : | |
DB 31 VTLDSRSVQELGWIASPLEG 52

RESULT 13
I78844
receptor protein-tyrosine kinase - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C:Accession: I78844
R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welch,

Oncogene 10, 897-905, 1995
A:Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein
A:Reference number: I58351; MUID:95206782
A:Accession: I78844
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-986 <RES>
A:Cross-references: GB:L36645; NID:9551613; PIDN:AAA74246.1; PID:9551614
C:Genetics:
A:Gene: HEK8
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
F:619-885/Domain: protein kinase homology <KIN>

Query Match 66.4%; Score 79; DB 2; Length 986;
Best Local Similarity 63.6%; Pred. No. 0.00026;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VNLDSTIIGELGWISYPSHG 22
| | | | | : | | | | | : | |
DB 31 VTLDSRSVQELGWIASPLEG 52

RESULT 14
S51605
receptor-like tyrosine kinase Eph-2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C:Accession: S51605
R:Malsonpierre, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Eph-1 and Eph-2: two novel members of the Eph receptor-like tyrosine kinase
A:Reference number: S49015; MUID:94067777
A:Accession: S51605
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-948 <MAT>
A:Cross-references: EMBL:S68030
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; transmembrane protein
F:628-936/Domain: protein kinase homology <KIN>
F:636-644/Region: protein kinase ATP-binding motif

Query Match 61.3%; Score 73; DB 2; Length 948;
Best Local Similarity 59.1%; Pred. No. 0.0022;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 VNLDSTIIGELGWISYPSHG 22
| | | | | : | | | | | : | |
DB 34 VVLDSTVQELGWKTPLNG 55

RESULT 15
I58351
receptor protein-tyrosine kinase - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I58351
R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welch
Oncogene 10, 897-905, 1995
A:Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein
A:Reference number: I58351; MUID:95206782
A:Accession: I58351
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-998 <RES>
A:Cross-references: GB:L36642; NID:9551607; PIDN:AAA74243.1; PID:9551608
C:Genetics:
A:Gene: HEK11
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; transmembrane protein
F:631-897/Domain: protein kinase homology <KIN>

F:639-647/Region: protein kinase ATP-binding motif
F:920-986/Domain: SAM homology <SAM>

Query Match 51.3%; Score 61; DB 2; Length 998;
Best Local Similarity 63.6%; Pred. No. 0.18;

Matches 14; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 VNLDSKTIQGEIGWISYPSHG 22
| | | | | | | | | | | | | | | | | | | | | |
Db 33 VLLDSKRAQTELEWISSPENG 54

Search completed: May 9, 2000, 22:27:16
Job time: 4155 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 22:25:58 ; Search time 44.2 seconds
(without alignments)
7.199 Million cell updates/sec

Title: US-09-104-340-2

Perfect score: 119

Sequence: 1 VNLDKRTIOGELGMSYPSHG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 143561 seqs, 14463640 residues

Total number of hits satisfying chosen parameters: 143561

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCRTUS.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	100.0	982	2	US-08-673-789-4
2	119	100.0	983	1	US-08-162-809-16
3	119	100.0	983	1	US-08-167-919A-10
4	119	100.0	983	2	US-08-449-645A-21
5	119	100.0	983	2	US-08-702-367A-21
6	119	100.0	983	3	US-08-715-106-10
7	119	100.0	983	4	PCT-US95-04681-21
8	89	74.8	877	2	US-08-673-789-2
9	89	74.8	967	2	US-08-449-645A-30
10	89	74.8	967	2	US-08-702-367A-30
11	89	74.8	991	2	US-08-449-645A-13
12	89	74.8	991	2	US-08-702-367A-13
13	89	74.8	991	4	PCT-US95-04681-13
14	87	73.1	928	1	US-08-442-248-2
15	87	73.1	928	1	US-08-440-815-2
16	87	73.1	1005	2	US-08-469-537A-103
17	79	66.4	986	2	US-08-673-789-3
18	79	66.4	986	2	US-08-449-645A-15
19	79	66.4	986	2	US-08-702-367A-15
20	79	66.4	986	4	PCT-US95-04681-15
21	79	66.4	1104	1	US-08-222-616-36
22	79	66.4	1104	4	PCT-US95-04228-36
23	75.5	63.4	687	2	US-08-449-645A-29
24	75.5	63.4	687	2	US-08-702-367A-29
25	73	61.3	948	2	US-08-469-537A-101
26	61	51.3	998	2	US-08-449-645A-17
27	61	51.3	998	2	US-08-702-367A-17
28	61	51.3	998	4	PCT-US95-04681-17
29	59	49.6	610	4	PCT-US96-00419-3

30	59	49.6	626	4	PCT-US96-00419-5	Sequence 5, Appl
31	59	49.6	984	2	PCT-US96-00419-2	Sequence 2, Appl
32	58	48.7	984	2	US-08-673-789-6	Sequence 6, Appl
33	57	47.9	968	1	US-08-426-235-2	Sequence 2, Appl
34	56	47.1	970	2	US-08-449-645A-11	Sequence 11, Appl
35	56	47.1	970	2	US-08-702-367A-11	Sequence 11, Appl
36	56	47.1	970	4	PCT-US95-04681-11	Sequence 11, Appl
37	56	47.1	984	2	US-08-673-789-9	Sequence 9, Appl
38	56	47.1	984	2	US-08-449-645A-19	Sequence 19, Appl
39	56	47.1	984	2	US-08-702-367A-19	Sequence 19, Appl
40	56	47.1	984	4	PCT-US95-04681-19	Sequence 19, Appl
41	56	47.1	995	1	US-08-162-809-18	Sequence 18, Appl
42	56	47.1	995	2	US-08-673-789-5	Sequence 5, Appl
43	56	47.1	1011	1	US-08-162-809-12	Sequence 12, Appl
44	55	46.2	998	2	US-08-449-645A-20	Sequence 20, Appl
45	55	46.2	998	2	US-08-702-367A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-673-789-4
; Sequence 4, Application US/08673789
; Patent No. 5814479
; GENERAL INFORMATION:
; APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
; APPLICANT: GEORGE, F.
; TITLE OF INVENTION: BSK RECEPTOR LIKE
; TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
; TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF INVENTIONS: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,789
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/177,812
; FILING DATE: 04-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 982
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; US-08-673-789-4
Query Match 100.0%; Score 119; DB 2; Length 982;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 VNLLDSKTIQGELGWISYP SHG 22  
        |||||  
Db     29 VNLLDSKTIQGELGWISYP SHG 50
```

RESULT 2
MS-08-163-

Sequence 16, Application US/08162809
Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162, 809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-809-16

Query Match	100.0%;	Score 119;	DB 1;	Length 983;
-------------	---------	------------	-------	-------------

```

QY      1 VNLLDSKTIQGLGWISYPSHG 22
          |||||
Db      29 VNLLDSKTIQGLGWISYPSHG 50

```

RESULT 3

US-06-107-919A-10
Sequence 10, Application US/08167919A
Patent No. 5674691
GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza

CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM
MEDICAL RECORDS

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

FILING DATE: 18-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
FILING DATE: 12-DEC-1991
PRIOR APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 10-FEB-1993

ATTORNEY/AGENT INFORMATION:
NAME: DIGLIO, Frank S.
REGISTRATION NUMBER: 31 346

TELEPHONE: (516) 742-4343

TELEX: 230 901 SANS UR
INFORMATION FOR SEO ID NO:

LENGTH: 983 amino acids
TYPE: amino acid

MOLECULE TYPE: protein
8-167-919A-10

Query Match	100.0%;	Score 119;	DB 1;	Length 983;
-------------	---------	------------	-------	-------------

```
QY      1 VNLLDSKTIQGEIGWISYPSHG 22
          |||||
Db      30 VNLLDSKTIQGEIGWISYPSHG 51
```

RESULT 4
US-08-449-645A-21

; Patent No. 5981245
; GENERAL INFORMATION:
;

TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; Kinases
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 43

ADDRESS: Amgen Patent Operations/RBW
STREET: 1840 Dehaven Drive

CITY: ANSONIA CT
STATE: California
COUNTRY: USA

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;

```

```

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

; FILING DATE:
 ; CLASSIFICATION: 435
 ;

```

: ATTORNEY/AGENT INFORMATION:
: NAME: Winter, Robert B.
: REFERENCE/DOCKET NUMBER: A-287
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 983 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-449-645A-21

Query Match      100.0%; Score 119; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLDSTKTIGELGWISYPSHG 22
   ||||||||||||||||||
Db 30 VNLDSTKTIGELGWISYPSHG 51

RESULT 5
US-08-702-367A-21
: Sequence 21, Application US/08702367A
: Patent No. 5981246
: GENERAL INFORMATION:
: APPLICANT: Fox, Gary M.
: TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
:   KINASES
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Amgen Patent Operations/RBW
: STREET: 1840 Dehavilland Drive
: CITY: Thousand Oaks
: STATE: California
: COUNTRY: USA
: ZIP: 91320
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/702,367A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Winter, Robert B.
: REFERENCE/DOCKET NUMBER: A-287
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 983 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-702-367A-21

Query Match      100.0%; Score 119; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLDSTKTIGELGWISYPSHG 22
   ||||||||||||||||||
Db 30 VNLDSTKTIGELGWISYPSHG 51

RESULT 6
US-08-715-106-10
: Sequence 10, Application US/08715106
: Patent No. 6020306
```

```

: GENERAL INFORMATION:
: APPLICANT: Boyd, Andrew W.
: APPLICANT: Simpson, Richard J.
: APPLICANT: Wicks, Ian
: APPLICANT: Ward, Larry D.
: APPLICANT: Wilkinson, David
: TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Scully, Scott, Murphy & Presser
: STREET: 400 Garden City Plaza
: CITY: Garden City
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 11530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/715,106
: FILING DATE: 18-SEP-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/167,919
: FILING DATE: 18-APR-1994
: APPLICATION NUMBER: PK6841 (AU)
: FILING DATE: 21-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PK6992 (AU)
: FILING DATE: 12-DEC-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/AU92/00294
: FILING DATE: 19-JUN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Digiglio, Frank S.
: REGISTRATION NUMBER: 31,346
: REFERENCE/DOCKET NUMBER: 9159
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (516) 742-4343
: TELEFAX: (516) 742-4366
: TELEX: 230 901 SANS UR
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 983 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-715-106-10

Query Match      100.0%; Score 119; DB 3; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLDSTKTIGELGWISYPSHG 22
   ||||||||||||||||||
Db 30 VNLDSTKTIGELGWISYPSHG 51

RESULT 7
PCT-US95-04681-21
: Sequence 21, Application PC/TUS9504681
: GENERAL INFORMATION:
: APPLICANT: Fox, Gary M.
: TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
:   KINASES
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Amgen Patent Operations/RBW
: STREET: 1840 Dehavilland Drive
```

CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-21

Query Match 100.0%; Score 119; DB 4; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNLDSKTIQGLGWIYSYPSHG 22
Db 30 VNLDSKTIQGLGWIYSYPSHG 51

RESULT 8
US-08-673-789-2
Sequence 2, Application US/08673789
Patent No. 5814479
GENERAL INFORMATION:
APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOIDE,
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 877
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
US-08-673-789-2

Query Match 74.8%; Score 89; DB 2; Length 877;
Best Local Similarity 63.6%; Pred. No. 6.8e-06;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VNLDSKTIQGLGWIYSYPSHG 22
Db 63 VNLDSRTVMGDLGWIAPFKNG 84

RESULT 9
US-08-449-645A-30
Sequence 30, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 967 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-30

Query Match 74.8%; Score 89; DB 2; Length 967;
Best Local Similarity 63.6%; Pred. No. 7.6e-06;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VNLDSKTIQGLGWIYSYPSHG 22
Db 13 VNLDSRTVMGDLGWIAPFKNG 34

RESULT 10
US-08-702-367A-30
Sequence 30, Application US/08702367A
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.

TOPLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-13

Query Match
Best Local Similarity 74.8%; Score 89; DB 2; Length 967;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNLDSTKIQELGWIYPSHG 22
DB 13 VNLDSTKTVMGDLGWIAPFKNG 34

RESULT 11
US-08-449-645A-13
Sequence 13, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 967 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367A-30

Query Match
Best Local Similarity 74.8%; Score 89; DB 2; Length 967;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNLDSTKIQELGWIYPSHG 22
DB 13 VNLDSTKTVMGDLGWIAPFKNG 34

RESULT 11
US-08-449-645A-13
Sequence 13, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 991 amino acids
TYPE: amino acid

TOPLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-13

Query Match
Best Local Similarity 74.8%; Score 89; DB 2; Length 991;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNLDSTKIQELGWIYPSHG 22
DB 37 VNLDSTKTVMGDLGWIAPFKNG 58

RESULT 12
US-08-702-367A-13
Sequence 13, Application US/08702367A
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 991 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367A-13

Query Match
Best Local Similarity 74.8%; Score 89; DB 2; Length 991;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNLDSTKIQELGWIYPSHG 22
DB 37 VNLDSTKTVMGDLGWIAPFKNG 58

RESULT 13
PCT-US95-04681-13
Sequence 13, Application PC/TUS9504681
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California

COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 991 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-13

Query Match 74.8% Score 89; DB 4; Length 991;
Best Local Similarity 63.6%; Pred. No. 7.8e-06;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VNLDSKTIQELGWIYSYPSHG 22
Db 37 VNLDSRTVLDGLGWIAPFKNG 58

RESULT 14
US-08-442-248-2
Sequence 2, Application US/08442248
Patent No. 5759863
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,248
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-442-248-2

Query Match 73.1% Score 87; DB 1; Length 928;
Best Local Similarity 63.6%; Pred. No. 1.5e-05;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VNLDSKTIQELGWIYSYPSHG 22
Db 63 VNLDSRTVLDGLGWIAPFKNG 84

RESULT 15
US-08-440-815-2
Sequence 2, Application US/08440815
Patent No. 5798448
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,815
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-440-815-2

Query Match 73.1% Score 87; DB 1; Length 928;
Best Local Similarity 63.6%; Pred. No. 1.5e-05;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VNLDSKTIQELGWIYSYPSHG 22
Db 63 VNLDSRTVLDGLGWIAPFKNG 84

Search completed: May 9, 2000, 22:25:59
Job time: 4148 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 21:52:01 ; Search time 50.71 Seconds

(without alignments)
10.276 Million cell updates/sec

Title: US-09-104-340-2

Perfect score: 119

Sequence: 1 VNLLDSKTIGELGWISYPSHG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A.Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	983	1 R31466	HEK polypeptide. R
2	119	100.0	983	1 R75711	Eph-related PTK Ce
3	89	74.8	877	1 W71628	Mouse Bsk receptor
4	89	74.8	991	1 R85090	EPH-like receptor
5	87	73.1	928	1 R97853	Rat REK7 eph-relat
6	87	73.1	1005	1 W83147	Rat receptor tyros
7	79	66.4	986	1 R85936	Protein tyrosine-X
8	79	66.4	986	1 R85091	EPH-like receptor
9	73	61.3	948	1 W83148	Rat receptor tyros
10	62	52.1	977	1 W19258	Embryonic stem cel
11	61	51.3	998	1 R85092	EPH-like receptor
12	59	46.6	610	1 W03422	Mouse developmenta
13	59	46.6	626	1 W03423	Mouse developmenta
14	59	46.6	968	1 W03421	Mouse developmenta
15	57	47.9	968	1 W19668	Human alanyl-tRNA
16	57	47.9	1004	1 Y07088	Renal cancer assoc
17	56	47.1	970	1 R85089	EPH-like receptor
18	56	47.1	994	1 R87018	Receptor tyrosine
19	56	47.1	994	1 W26366	Mouse Nuk tyrosine
20	56	47.1	995	1 R75712	Eph-related PTK Ce
21	56	47.1	1011	1 R75709	Eph-related PTK Ce
22	55	46.2	984	1 R44513	elk. Expression of
23	55	46.2	990	1 R51899	Human embryonal Ki
24	53	44.5	951	1 R75704	Human embryonal Ki
25	52	44.7	1006	1 W72256	Eph-related CEK6.
26	52	43.7	1006	1 W70525	Human thymus recep
27	52	43.7	1021	1 W70526	Human thymus recep
28	48	40.3	973	1 R75707	Eph-related PTK Ce
29	46	38.7	619	1 W75771	Human GTP binding
30	45	37.8	530	1 R50972	Normal virus stra
31	45	37.8	630	1 W32213	Mutase of penici
32	45	37.8	630	1 W89392	Penicillium purpur
33	45	37.8	630	1 W97037	Penicillium purpur
34	43	36.1	530	1 R57091	Small round virus

35	43	36.1	573	1 W62295	Glutathionylspermi
36	42	35.3	330	1 R85959	Broccoli ACC synth
37	42	35.3	333	1 R46298	Homologue of flavo
38	42	35.3	335	1 R46300	Homologue of flavo
39	42	35.3	374	1 R98598	Broccoli ACC synth
40	41.5	34.9	426	1 R10997	Xenopus Bone Morph
41	41	34.5	122	1 W28109	Amino acid sequenc
42	41	34.5	276	1 W07620	Human NES1 polypep
43	41	34.5	483	1 R07445	Secretory signal p
44	41	34.5	958	1 W19669	Yeast alanyl-tRNA
45	40.5	34.0	511	1 W71519	Helicobacter polyp

ALIGNMENTS

RESULT 1	
ID R31466	
AC R31466: standard; Protein; 983 AA.	
DT 24-MAY-1993 (first entry)	
DE HEK polypeptide.	
KW Primer; expression vector; extracellular domain; human; HEK;	
KW eph/erbB-like; kinase; pre-B; cell; T; tumour; lymphoid; LK63;	
KW lila-1; JM; epithelial; Hela; receptor-type; thymidine kinase;	
KW TK; ligand; Bicellular response; growth; differentiation.	
OS Homo sapiens.	
FH Key	Location/Qualifiers
FT peptide	1..20
FT protein	/note= "Signal peptide"
FT protein	21..39
FT protein	/note= "Purified HEK protein #1"
FT protein	840..860
FT modified_site	232..234
FT modified_site	/note= "Purified HEK protein #2"
FT modified_site	337..339
FT modified_site	/note= "N-link glycosylation"
FT modified_site	/note= "N-link glycosylation"
FT modified_site	391..393
FT modified_site	/note= "N-link glycosylation"
FT modified_site	404..406
FT modified_site	/note= "N-link glycosylation"
FT modified_site	493..495
FT domain	/note= "N-link glycosylation"
FT domain	542..565
FT binding_site	/note= "Transmembrane domain"
FT binding_site	628
FT binding_site	/note= "ATP binding site"
FT binding_site	630
FT binding_site	/note= "ATP binding site"
FT binding_site	633
FT binding_site	/note= "ATP binding site"
FT modified_site	779
FT modified_site	/note= "Putative autophosphorylation site"
PN W03300425-A.	
PD 07-JAN-1993.	
PF 19-JUN-1992; AU0294.	
PR 21-JUN-1991; AU-006841.	
PR 12-DEC-1991; AU-009992.	
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.	
PI Boyd AD, Simpson R, Ward LD, Wicks I, Wilkinson D;	
PI WPT 93-036373/04.	
DR P-PSDB; R31466.	
PT Receptor-type tyrosine kinase reactive with monoclonal antibody	
PT IIR-14 - is EPH-ERK-like kinase, useful for phosphorylating	
PT proteins in modulating pre-B, B and T cell function, in cancer	
PT therapy etc.	
PS Claim 6: Fig 1; 58pp; English.	
CC This sequence represents human eph/erbB-like kinase (HEK). HEK is	
CC expressed in both pre-B cells and T cell lines and in a number of	
CC tumours of human origin, eg. lymphoid tumours LK63, lila-1 and JM,	
CC and the epithelial tumour Hela. This receptor-type thymidine kinase	
CC (TK) and/or its ligands are useful as agents in modulation of the	

CC production and/or function of pre-B, B and T cells. The TK and its
CC analogues have activity in transducing signals or in stimulating
CC cellular responses such as growth and/or differentiation.
SQ Sequence 983 AA;

Query Match 100.0%; Score 119; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNLDKTIQGLGWTSPSHG 22
DB 30 VNLDKTIQGLGWTSPSHG 51

RESULT 2

ID R75711 standard; Protein: 983 AA.
AC R75711;
DE EPH-related protein Csk.
DE Csk4; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
KM prognosis.
OS Gallus sp.
PN W09515375-A.
PD 08-JUN-1995.
PF 07-SEP-1994; U10140.
PR 03-DEC-1993; US-162809.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PI Pasquale EB, Sajjadi FG;
DR WPI: 95-215256/28.
DR N-PSDB: Q90659.
PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
PT cancer.
PS Disclosure: Page 85-89; 129pp; English.
CC Probes derived from the EPH-related PTKs Csk4 (Q90659) and Csk5
CC (Q90660) were used to isolate novel cDNA clones (Q90652-58,
CC Q90661-62) from chicken embryo and embryonic brain libraries.
CC Csk4 is highly expressed in the chicken developing brain and
CC embryonic tissues and also in the adult brain and retina.
SQ Sequence 983 AA;

Query Match 100.0%; Score 119; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNLDKTIQGLGWTSPSHG 22
DB 29 VNLDKTIQGLGWTSPSHG 50

RESULT 3

ID W71628 standard; Protein: 877 AA.
AC W71628;
DE 25-NOV-1998 (first entry)
DE Mouse Bsk receptor-like tyrosine kinase.
KM Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neoplasm;
KM neurodegenerative disease; limbic system neuron regeneration;
KM chromosomal abnormality; degenerative growth; development disorder;
KM viral infection; bacterial infection; Alzheimer's disease; epilepsy;
KM schizophrenia; stroke; cerebral ischaemia.
OS Mus sp.
PN US5814479-A.
PD 29-SEP-1998.
PF 11-JUN-1996; 673789.
PR 04-JAN-1994; US-117812.
PR 11-JUN-1996; US-673789.
PA (KROM/) KROMER L F.
PA (SCHU/) SCHULZ N T.
PA (MOUN/) MOUNDE G F V.
PA (ZHOU/) ZHOU R.

PI Kromer LF, Schulz NT, Mounde GFV, Zhou R;
DR WPI: 98-541751/46.
DR N-PSDB: V58192.

PT Isolated nucleic acid sequence encoding protein - used in Bsk
PT nucleic acid probes, used in detecting alterations in level of Bsk
PT messenger-RNA in biological samples isolated from mammal afflicted
PT with disease
PS Claim 1; Fig 2; 72pp; English.
CC The present sequence represents mouse Bsk, which is a receptor-like
CC tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in
CC Bsk nucleic acid probes, which can be used in detecting alterations in
CC the level of Bsk messenger-RNA (mRNA) in biological samples isolated
CC from a mammal afflicted with a disease, such as neurodegenerative
CC diseases or disorders and neoplasms. The nucleic acid sequence can also
CC be delivered into the limbic system of patients with limbic system
CC neurodegenerative disease, disorder or injury, to promote or enhance
CC limbic system neuron regeneration or growth. Such neurodegenerative
CC diseases include, chromosomal abnormalities, degenerative growth and
CC development disorders, viral infections, bacterial infections, brain
CC injuries, neoplastic conditions, Alzheimer's disease, epilepsy,
CC schizophrenia, or stroke and cerebral ischaemia.
SQ Sequence 877 AA;

Query Match 74.8%; Score 89; DB 1; Length 877;
Best Local Similarity 63.6%; Pred. No. 5.2e-06;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDKTIQGLGWTSPSHG 22
DB 63 VNLDKTIQGLGWTSPSHG 84

RESULT 4

ID R85090 standard; Protein: 991 AA.
AC R85090;
DE 16-APR-1996 (first entry)
DE EPH-like receptor protein tyrosine kinase HEK7.
KM EPH-like receptor protein tyrosine kinase; PTK; HEK7;
KM human eph-like kinase; therapy; diagnosis; vector; antibody.
OS Homo sapiens.
PN W09528484-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04681.
PR 15-APR-1994; US-229509.
PA (AMGE-) AMGEN INC.
PI Fox GM, Jing S, Welcher AA;
DR WPI: 95-373799/48.
DR N-PSDB: T02947.
PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -
PT and related vectors, host cells, proteins, antibodies etc., used
PT diagnostically and therapeutically to modulate receptor activation
PT or prodn.
PS Claim 18; Page 54-57; 133pp; English.
CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
CC HEK8 and HEK11 (R85089-92), respectively, were identified following
CC isolation of their encoding cDNAs (T02946-49) from a human foetal brain
CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
CC catalytic domain of chicken EPH-like receptors Csk5, Csk7 and Csk8.
CC HEK11 shows no homology to any known EPH-like receptor. Recombinant
CC HEK receptors (or their soluble extracellular domains) are produced by
CC expression of encoding sequences in prokaryotic or eucaryotic host
CC cells, and are used to produce antibodies (utilised in diagnostic
CC assays), or to identify and purify ligands for HEK receptors, or
CC therapeutically to modulate the activation of cell-associated
CC receptors. Soluble HEK7 receptor may primarily affect
CC proliferation and/or differentiation of brain cells.
SQ Sequence 991 AA;

Query Match 74.8%; Score 89; DB 1; Length 991;

Best Local Similarity 63.6%; Pred. No. 6e-06; Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDSTKIOGELGWISYPSHG 22
DB 37 VNLDSTRTVLGDLGWIAFPKNG 58

RESULT 5

ID R97853 standard; Protein: 928 AA.
AC R97853:
DT 05-JAN-1997 (first entry)
DE Rat REK7 eph-related tyrosine kinase receptor.
KW REK7; eph-related tyrosine kinase receptor; AL-1; ligand;
KW neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis.
OS Rattus sp.

FT Key location/Qualifiers
FT Peptide 1..57
FT /label- Sig_peptide 58..928
FT protein /label- Mat_protein 58..462
FT domain /label- Extracellular_domain

W09613518-A1.
PD 09-MAY-1986.
PF 26-OCT-1995; U14016.
PR 27-OCT-1994; US-330128.
PR 07-JUN-1995; US-486449.
PA (GETH) GENENTECH INC.
PI Caras IM Winslow JM;
PI WPI: 96-239448/24.
DR N-PSDB: T18893.
PT AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in treatment and diagnosis of neuronal disorders and angiogenesis-related conditions.

PS Example 1: Page 50-53; 75pp; English.
CC Rat REK7 (R97853) is an eph-related tyrosine kinase receptor, for which AL-1 (see also W97854) is a ligand. Its amino acid sequence was deduced from a cDNA clone (T18893) isolated from a hippocampal cDNA library. An REK-19g fusion was used to screen cultured cell lines for surface expression of REK7-binding activity. Primers (see also T44382-83) based on peptide sequences (R97856-59) of isolated ligands were used to amplify human breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human foetal brain cDNA library, leading to the isolation of AL-1 cDNA (T18897).

CC CC
SQ Sequence 928 AA;

Query Match 73.1%; Score 87; DB 1; Length 928;
Best Local Similarity 63.6%; Pred. No. 1.1e-05; Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDSTKIOGELGWISYPSHG 22
DB 63 VNLDSTRTVLGDLGWIAFPKNG 84

RESULT 6

ID W83147 standard; Protein: 1005 AA.
AC W83147:
DT 11-FEB-1999 (first entry)
DE Rat receptor tyrosine kinase Etk-1.
KW Receptor tyrosine kinase; Ror-1; Ror-2; Etk-1; Etk-2; detection;
KW neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
KW binding protein; BDNF; NT-3; diagnosis.
OS Rattus sp.
PN US5843749-A.
PD 01-DEC-1998.
PF 06-JUN-1995; 469537.
PR 17-MAR-1995; US-406247.

PR 26-JUL-1991; US-736559.
PR 28-OCT-1993; US-144992.
PR 06-JUN-1995; US-469537.
PA (REGE-) REGENERON PHARM INC.
PI Malsompierre PC Mastakowski P, Yancopoulos GD;
DR WPI: 96-044584/04.
DR N-PSDB: V70207.
PT DNA encoding receptor tyrosine kinase proteins - and corresponding proteins

PS Example: Fig 22: 194pp; English.
CC The present invention describes nucleic acid molecules for ror-1, ror-2, etk-1 and etk-2. Also described are the corresponding proteins: CC Ror-1; Ror-2; Etk-1; and Etk-2. The proteins are orphan receptor CC tyrosine kinases. The present sequence represents rat Etk-1.
SQ Sequence 1005 AA;

Query Match 73.1%; Score 87; DB 1; Length 1005;
Best Local Similarity 63.6%; Pred. No. 1.3e-05; Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNLDSTKIOGELGWISYPSHG 22
DB 63 VNLDSTRTVLGDLGWIAFPKNG 84

RESULT 7

ID R85936 standard; Protein: 986 AA.
AC R85936:
DT 14-FEB-1996 (first entry)
DE Protein tyrosine-kinase bptk7.
KW Protein tyrosine-kinase; ptk; bptk7; agonist; cell growth;
OS Homo sapiens.

FT Key location/Qualifiers
FT Peptide 1..19
FT /label- Sig_peptide 20..547
FT domain /label- Extracellular_domain 548..570
FT domain /label- Transmembrane_domain 571..986
FT domain /label- Intracellular_tyrosine_kinase_domain

W09527061-A1.
PD 12-OCT-1995.
PF 04-APR-1995; U04228.
PR 04-APR-1994; US-222616.
PA (GETH) GENENTECH INC.
PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
PI Wood WT;
DR WPI: 95-366160/47.
DR N-PSDB: T03100.
PT Agonist antibodies which activate specific protein tyrosine PT kinase(s) - also activate chimeric proteins of kinase extracellular domain and ig constant domain, useful for studying, and therapeutic PT modulation of, cell growth and differentiation

PS Disclosure: Page 95-99; 125pp; English.
CC DNA probes based on protein tyrosine-kinase (ptk) sequences were used CC to screen cDNA libraries to identify novel ptk genes. The bptks, CC bptk1, bptk2, bptk3, bptk4, bptk5 and bptk7 (R85924-28 and R85935, CC respectively) are expressed in human brain tissue and show homology CC to known ptk's. A full-length sequence for bptk7 (R85936) was also CC obtd. bptk7 can be used to design drugs that modulate ptk activity.
SQ Sequence 986 AA;

Query Match 66.4%; Score 79; DB 1; Length 986;
Best Local Similarity 63.6%; Pred. No. 0.00023; Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 VNLDSTKIOGELGWISYPSHG 22
DB 63 VNLDSTRTVLGDLGWIAFPKNG 84

Db 31 VTLDSRSVQELGWIASPLEG 52

RESULT 8

RS5091

ID R85091 standard; Protein; 986 AA.

AC R85091.

DT 16-APR-1996 (first entry)

DE EPH-like receptor protein tyrosine kinase HEK8.

KW EPH-like receptor protein tyrosine kinase; PTK; HEK8;

KW human eph-like kinase; therapy; diagnosis; vector; antibody.

OS Homo sapiens.

PN W09528484-A1.

PD 26-OCT-1995.

PF 14-APR-1995; U04681.

PR 15-APR-1994; US-229509.

PA (AMGE-) AMGEN INC.

PI Fox GM, Jing S, Welcher AA;

DR WPI. 95-373799/48.

DR N-PSDB; T02948.

PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -

PT and related vectors, host cells, proteins, antibodies etc., used

PT diagnostically and therapeutically to modulate receptor activation

PT or proth.

PS Claim 18; Page 62-65; 133pp; English.

CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,

CC HEK8 and HEK11 (R85089-92), respectively, were identified following

CC isolation of their encoding cDNAs (T02946-49) from a human foetal brain

CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the

CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8.

CC HEK11 shows no homology to any known EPH-like receptor. Recombinant

CC HEK receptors (or their soluble extracellular domains) are produced by

CC expression of encoding sequences in prokaryotic or eucaryotic host

CC cells, and are used to produce antibodies (utilised in diagnostic

CC assays), or to identify and purify ligands for HEK receptors, or

CC therapeutically to modulate the activation of cell-associated

CC receptors.

SQ Sequence 986 AA:

Query Match 66.4%; Score 79; DB 1; Length 986;

Best Local Similarity 63.6%; Pred. No. 0.00023;

Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VNLDSKRTIQELGWIYSYSHG 22

Db 31 VTLDSRSVQELGWIASPLEG 52

RESULT 9

W83148

ID W83148 standard; Protein; 948 AA.

AC W83148;

DT 11-FEB-1999 (first entry)

DE Rat receptor tyrosine kinase Etk-2.

KW Receptor tyrosine kinase; Etk-1; Etk-2; Etk-1; Etk-2; detection;

KW neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;

KW binding protein; BDNF; NT-3; diagnosis.

OS Rattus sp.

PN U55843749-A.

PD 01-DEC-1998.

PF 06-JUN-1995; 469537.

PR 17-MAR-1995; US-406247.

PR 26-JUL-1991; US-736559.

PR 28-OCT-1993; US-144992.

PR 06-JUN-1995; US-469537.

PA (REGG-) REGENERON PHARM INC.

PI Maisondierre PC, Maslakowski P, Yancopoulos GD;

DR WPI. 99-044584/04.

DR N-PSDB; V70208.

PT DNA encoding receptor tyrosine kinase proteins - and corresponding

PT proteins

PS Example; Fig 21; 194pp; English.

CC The present invention describes nucleic acid molecules for Etk-1,

CC Etk-2, Etk-1 and Etk-2. Also described are the corresponding proteins:

CC Etk-1; Etk-2; Etk-1; and Etk-2. The proteins are orphan receptor

CC tyrosine kinases. The present sequence represents rat Etk-2.

SQ Sequence 948 AA:

Query Match 61.3%; Score 73; DB 1; Length 948;

Best Local Similarity 59.1%; Pred. No. 0.0019;

Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 VNLDSKRTIQELGWIYSYSHG 22

Db 34 VLLDPTVQELGWIYKPYPLNG 55

RESULT 10

W19258

ID W19258 standard; Protein; 977 AA.

AC W19258;

DT 15-SEP-1997 (first entry)

DE Embryonic stem cell kinase (Esk).

KW Embryonic stem cell kinase; receptor tyrosine kinase; mucositis;

KW epithelium; signal transduction; gene therapy; diagnosis.

OS Mus musculus.

PN Location/Qualifiers

PH Key

FH Peptide

FT 1..26

FT /label= Sig-peptide

FT 27..977

FT /label= Mat-protein

FT 27..348

FT /label= Extracellular_domain

FT 549..569

FT /label= Transmembrane_domain

FT 570..977

FT /label= Intracellular_domain

FT misc_difference 70

FT /note= "conserved Cys residue"

FT misc_difference 107

FT /note= "conserved Cys residue"

FT misc_difference 119

FT /note= "conserved Cys residue"

FT misc_difference 192

FT /note= "conserved Cys residue"

FT misc_difference 205

FT /note= "conserved Cys residue"

FT misc_difference 232

FT /note= "conserved Cys residue"

FT misc_difference 250

FT /note= "conserved Cys residue"

FT misc_difference 263

FT /note= "conserved Cys residue"

FT misc_difference 265

FT /note= "conserved Cys residue"

FT misc_difference 278

FT /note= "conserved Cys residue"

FT misc_difference 281

FT /note= "conserved Cys residue"

FT misc_difference 295

FT /note= "conserved Cys residue"

FT misc_difference 298

FT /note= "conserved Cys residue"

FT misc_difference 312

FT /note= "conserved Cys residue"

FT misc_difference 314

FT /note= "conserved Cys residue"

FT misc_difference 330

FT /note= "conserved Cys residue"

FT misc_difference 384

FT /note= "conserved Cys residue"

FT misc_difference 387

FT /note= "conserved Cys residue"

FT misc_difference 331..441

FT /note= "conserved Cys residue"

FT peptide

```

FT FT /label= Fibronection_type_III_repeat
FT FT /note= "characteristic of Eph subfamily"
FT FT peptide 448..536
FT FT /label= Fibronection_type_III_repeat
FT FT binding_site 632..637
FT FT /label= ATP-binding_motif
FT FT binding_site 657
FT FT /note= "GXXXXG ATP binding motif"
FT FT /label= ATP-binding_motif
FT FT /note= "invariant lysine residue associated with
FT FT ATP binding motif"
FT FT peptide 750..755
FT FT /note= "DLARN motif indicating substrate
FT FT specificity for tyrosine"
FT FT peptide 790..797
FT FT /note= "PIRTRAPE motif indicating substrate
FT FT specificity for tyrosine"
FT FT modified_site 60
FT FT /label= Glycosylation
FT FT modified_site 339
FT FT /note= "potential N-linked glycosylation site"
FT FT modified_site 415
FT FT /note= "potential N-linked glycosylation site"
FT FT modified_site 479
FT FT /note= "potential N-linked glycosylation site"
FT FT modified_site /label= Glycosylation
FT FT /note= "potential N-linked glycosylation site"
PN W09723629-A1.
PD 03-JUL-1997.
PF 20-DEC-1996; AU0826.
PR 22-DEC-1995; AU-007277.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Boyd AW, Lickliter J;
DR WPI: 97-351065/32.
DR N-PSDB: T72320.
PT DNA encoding embryonic stem cell kinase, receptor tyrosine kinase -
PT for production of modulators and antibodies, useful to treat
PT mucositis and other disorders involving epithelium
PS Claim 1; Page 48-54; 98pp; English.
CC Novel mouse embryonic stem cell kinase (Esk) is a receptor tyrosine
CC kinase that belongs to the Eph subfamily. Its amino acid sequence
CC was deduced from a DNA molecule (T72320) isolated from a murine
CC liver cDNA library. Recombinant Esk polypeptides, esp. soluble
CC Esk (extracellular domain), can be produced in host cells and used
CC for ligand isolation, as antagonists of Esk-ligand interaction and
CC as immunogens for prodn. of antibodies useful as diagnostic
CC reagents or therapeutic antagonists. Modulation of Esk expression
CC can be used to treat mucositis (partic. when caused by cancer
CC treatment), and as Esk is expressed in all epithelial tissues its
CC modulation may be used to treat e.g. skin injuries, hair loss,
CC cornel or peptic ulcers, ulcerative colitis, oesophageal reflex,
CC Sjorgren's syndrome and related autoimmune disease, mucosal
CC infections and pancreatitis.
SQ Sequence 977 AA;

```

Query Match 52.18; Score 62; DB 1; Length 977;
 Best Local Similarity 57.9%; Pred. No. 0.11;
 Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

OY 1 VNLDSKTIQELGWISSYP 19
DB 29 VTLMDSTRAQELGWLDP 47

```

RESULT 11
 R85092
 ID R85092 standard; Protein; 998 AA.
 AC R85092; 16-APR-1996 (first entry)
 DT

```

DE Eph-like receptor protein tyrosine kinase HEK11.
KW Eph-like receptor protein tyrosine kinase; PTK; HEK11;
KW human eph-like kinase; therapy; diagnosis; antibody; vector.
OS Homo sapiens.
PN W09528484-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04681.
PR 15-APR-1994; US-229509.
PA (AMGE-) AMGEN INC.
PI Fox GW, Jing S, Welcher AA;
DR WPI: 95-373799/48.
DR N-PSDB: T02949.
PT New nucleic acid encoding Eph-like receptor tyrosine kinase(s) -
PT and related vectors, host cells, proteins, antibodies etc., used
PT diagnostically and therapeutically to modulate receptor activation
PT or prodn.
PS Claim 18; Page 71-75; 133pp; English.
CC 4 Novel human Eph-like receptor protein tyrosine kinases, HEK5, HEK7,
CC HEK8 and HEK11 (R85089-92), respectively, were identified following
CC isolation of their encoding cDNAs (T02946-49) from a human foetal brain
CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
CC catalytic domain of chicken Eph-like receptors Cck3, Cck7 and Cck8.
CC HEK11 shows no homology to any known Eph-like receptor. Recombinant
CC HEK receptors (or their soluble extracellular domains) are produced by
CC expression of encoding sequences in procarcynotic or eucaryotic host
CC cells, and are used to produce antibodies (utilised in diagnostic
CC assays), or to identify and purify ligands for HEK receptors, or
CC therapeutically to modulate the activation of cell-associated
CC receptors.
SQ Sequence 998 AA;

```

Query Match 51.38; Score 61; DB 1; Length 998;
 Best Local Similarity 63.68; Pred. No. 0.16;
 Matches 14; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

```

OY 1 VNLDSKTIQELGWISSYSHG 22
DB 33 VLLDSKRAQGLELMWISSPFG 54

```

```

RESULT 12
W03422
ID W03422 standard; Protein; 610 AA.
AC W03422;
DE 11-NOV-1996 (first entry)
DT Mouse developmental kinase 1 MDR1 T1.
KW Mouse developmental kinase 1; MDR1 T1; receptor tyrosine kinase;
KW RTK; signal transduction; probe; diagnosis; gene therapy;
OS Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..28
FT /label= Sig_peptide
FT modified_site 64..66
FT /label= N-glycosylation_site
FT modified_site 343..345
FT /label= N-glycosylation_site
FT modified_site 410..412
FT /label= N-glycosylation_site
FT domain 555..579
FT /label= Transmembrane_domain
FT misc_difference 600..610
FT /note= "product of alternative splicing"
FT W09621013-A1.
PN 11-JUL-1996.
PD 03-JAN-1996; U00419.
PF 03-JAN-1995; US-368776.
PR 03-JAN-1995; US-368776.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (SUGB-) SUGEN INC.
PI Closssek T, Millauner B, Ullrich A;
DR WPI: 96-333988/33.
DR N-PSDB: T32961.

```

PT	New mouse development kinase 1 gene - used for developing prods. for diagnosis and treatment of abnormalities in signal transduction pathways
PS	Example 1; Page 109-111; 128pp; English.
CC	cDNA cloning using adult mouse brains and Northern blotting
CC	identified 2 truncated versions, MDK1 T1 (W03422) and MDK1 T2 (W03423), of the novel mouse developmental kinase 1 (MDK1) (see also W03421), a new member of the eck/eph family of receptor tyrosine kinases. Their amino acid sequences were deduced from cDNA clones (T32961 and T32962) obt'd. from adult mouse brains. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential agents useful for treatment of diseases characterised by abnormal signal transduction.
SQ	Sequence 610 AA;
Oy	1 VNLDSTRTIGELGWSVPSHG 22
Dd	33 VLLDLSKAQTLEWISSPPSG 54
Query Match	49.6%; Score 59; DB 1; Length 610; Best Local Similarity 63.6%; Pred. No. 0.19;
Matches	14; Conservative 0; Mismatches 8; Indels 0; Gaps
RESULT 13	
ID	W03423
AC	W03423; standard; Protein; 626 AA.
DT	11-NOV-1996 (first entry)
DE	Mouse developmental kinase 1 MDK1 T2.
KW	Mouse developmental kinase 1; MDK1 T2; receptor tyrosine kinase; RTK; signal transduction; probe; diagnosis; gene therapy; neurodegeneration; neuroproliferation; cancer.
OS	Mus sp.
FH	Key
FT	peptide
FT	Location/Qualifiers
FT	1..28
FT	/label= Sig_peptide
FT	modified_site
FT	64..66
FT	/label= N-glycosylation_site
FT	modified_site
FT	343..345
FT	/label= N-glycosylation_site
FT	modified_site
FT	410..412
FT	/label= N-glycosylation_site
FT	domain
FT	555..579
FT	/label= Transmembrane_domain
FT	misc_difference
FT	600..626
FT	/note= "product of alternative splicing"
PN	W09621013-A1.
PD	11-JUL-1996.
PR	03-JAN-1996; U000419.
PA	03-JAN-1995; US-368776. (PLNC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN. (SUGE-) SOGEN INC.
P1	Closek T, Millauer B, Ullrich A;
DR	WPI; 96-333988/33.
DR	N-PDSB; T32962.
PT	New mouse development kinase 1 gene - used for developng prods. for diagnosis and treatment of abnormalities in signal transduction pathways
PS	Example 1; Page 113-115; 128pp; English.
CC	cDNA cloning using adult mouse brains and Northern blotting
CC	identified 2 truncated versions, MDK1 T1 (W03422) and MDK1 T2 (W03423), of the novel mouse developmental kinase 1 (MDK1) (see also W03421), a new member of the eck/eph family of receptor tyrosine kinases. Their amino acid sequences were deduced from cDNA clones (T32961 and T32962) obt'd. from adult mouse brains. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential agents useful for treatment of diseases characterised by abnormal

CC	signal transduction.
SQ	Sequence 626 AA;
Query Match	49.6%; Score 59; DB 1; Length 626;
Best Local Similarity	63.6%; Pred. No. 0.19;
Matches 14; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
QY	1 VNLDSKTIQGLGWIYSYPSHG 22
DB	33 VLLDSKAQGTLEWISSPPSG 54
RESULT 14	
W03421	
ID	W03421 standard; Protein; 998 AA.
AC	W03421:
DT	11-NOV-1996 (first entry)
DE	Mouse developmental kinase 1.
KM	Mouse developmental kinase 1; Mdk1; receptor tyrosine kinase; RTK;
KW	signal transduction; probe; diagnosis; therapy;
KV	neurodegeneration; neuroproliferation; cancer.
OS	Mus sp.
PE	peptide
FT	1..28
FT	/label= Sig_peptide
FT	64..66
FT	/label= N-glycosylation_site
FT	343..345
FT	/label= N-glycosylation_site
FT	410..412
FT	/label= N-glycosylation_site
FT	555..579
FT	/label= Transmembrane_domain
PN	W09621013-A1.
PD	11-JUL-1996.
PF	03-JAN-1996; U00419.
PR	03-JAN-1995; US-368776.
PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PI	(SUGGE-) SUGEN INC.
PI	Cloosek T, Millauner B, Ullrich A;
DR	WPI: 96-333988/33.
DR	N-PEDB: t32960.
PT	New mouse development kinase 1 gene - used for developing prods. for
PT	diagnosis and treatment of abnormalities in signal transduction
PT	pathways
PS	Example 1. Page 105-108; 128pp; English.
CC	Mouse developmental kinase 1 (MDK1) (W03421) is a new member of the
CC	ec/eph family of receptor tyrosine kinases (RTKs). Its amino
CC	acid sequence was deduced from a cDNA clone (73260) isolated
CC	from mouse embryo and adult brain libraries. The distinct
CC	patterns of MDK1 expression during mouse development suggest an
CC	important role for MDK1 in the formation of neuronal structures.
CC	MDK1 may be obtd. by expression in host cells. It can be used
CC	in methods for the diagnosis of diseases characterised by
CC	abnormality in a signal transduction pathway, such as
CC	neuroproliferative or neurodegenerative disorders or cancer.
CC	to screen for (ant)agonists, and to raise antibodies.
SQ	Sequence 998 AA;
Query Match	49.6%; Score 59; DB 1; Length 998;
Best Local Similarity	63.6%; Pred. No. 0.33;
Matches 14; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
QY	1 VNLDSKTIQGLGWIYSYPSHG 22
DB	33 VLLDSKAQGTLEWISSPPSG 54
RESULT 15	
ID	W19968 standard; Protein; 968 AA.
W19968	

AC W19968; 19-AUG-1997 (first entry)
 DT Human alanyl-tRNA synthetase.
 DE Alanyl-tRNA synthetase; ligase; analysis; diagnosis; autoimmune;
 KW disease; antisyntetase syndrome; interstitial lung disease;
 KW arthritis; Raynaud's phenomenon; fever; detection.
 OS Homo sapiens.
 PN US5629188-A.
 PD 13-MAY-1997.
 PF 21-APR-1995; 426236.
 PR 21-APR-1995; US-426236.
 PA (CANC-) CANCER INST JAPANESE FOUND CANCER.
 PA (COBI-) COBIIST PHARM INC.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PI Rikmaster TL, Schimmel PR, Shiba K;
 DR WPI; 97-280271/25.
 DR N-PSDB; 771086.
 PT Human and yeast alanyl-tRNA synthetase genes - useful for production
 PT of recombinant enzymes for diagnostic and analytical applications
 PS Claim 3; Column 43-48; 42pp; English.
 CC W19968 shows the amino acid sequence of human alanyl-tRNA synthetase
 CC (Ala-tRS). Human Ala-tRS and antibodies specific for it, may be useful
 CC in assays for diagnosing and monitoring an autoimmune disease known as
 CC antisyntetase syndrome. A condition in which patients having
 CC polyomyositis and/or dermatomyositis produce antibodies against the
 CC essential synthetase enzyme. Anti-synthetase syndrome is characterised
 CC by a number of clinical presentations, including interstitial lung
 CC disease, arthritis, Raynaud's phenomenon and fever. Human Ala-tRS can
 CC be used to assess the toxic effects of antimicrobial Ala-tRS inhibitors
 CC on human Ala-tRS. Tester strains comprising host cells containing
 CC recombinant Ala-tRS gene which complements or substitutes the
 CC function of the native gene can be used to test for any toxic effects
 CC of such antimicrobial agents that specifically interacts with the human
 CC Ala-tRS gene or protein. Ala-tRS proteins can be used to separate
 CC alanine from other amino acids, to separate L-alanine from D-alanine,
 CC to isolate tRNA that specifically recognises Ala-tRS, and for
 CC quantitative determination of alanine or ATP.
 SQ Sequence 968 AA;

Query Match 47.9%; Score 57; DB 1; Length 968;
 Best Local Similarity 47.6%; Pred. No. 0.66;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 OY 2 NLLDKTIGELGWISYPSHG 22
 : ||||| | : | : : |
 DB 399 SLGDSKITIPGPRWLLIDRYG 419

Search completed: May 9, 2000, 21:52:03
 Job time: 3755 sec

This Page Blank (uspto)


```
RESULT 2
ID 076154 PRELIMINARY: PRT: 1022 AA.
AC 076154:
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE NA+/K+-ATPase ALPHA-SUBUNIT.
GN DJNAK.
OS Dugesia japonica (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Tricladida;
OC Paludicola; Dugesidae; Dugesia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GI: TISSUE-WHOLE ANIMAL;
RA OGATA S., WATANABE K.;
RT "Planarian Na+/K+-ATPase alpha-subunit.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB012391; BAA32798.1;
DR PFAM: PF00122; E1-E2_ATPase; 1.
DR PFAM: PF00689; Na_K_ATPase; 1.
DR HSSP: PF00690; Na_K_ATPase; 1.
DR PRINTS: PR00119; CATATPASE.
DR PRINTS: PR00121; NAKATPASE.
SQ SEQUENCE 1022 AA; 113462 MW; 885294F5 CRC32;
```

```
Query Match 34.0%; Score 50; DB 5; Length 1022;
Best Local Similarity 41.2%; Pred. No. 22;
Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 12 SCSVLDSFGELIPQSN 28
Db 153 SSKIMSFCKMVPQKAN 169
```

```
RESULT 3
ID 081224 PRELIMINARY: PRT: 888 AA.
AC 081224:
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE EXTRA-LARGE G-PROTEIN.
GN XLG.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA LEE Y.-R.J., ASSMANN S.M.;
RT "Arabidopsis thaliana extra-large G-protein: a new class of GTP
binding protein.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF060941; AAC19352.1;
DR HSSP: P10824; 1BH2.
DR PFAM: PF00503; G-alpha; 1.
SQ SEQUENCE 888 AA; 98796 MW; 46255612 CRC32;
```

```
Query Match 33.7%; Score 49.5; DB 10; Length 888;
Best Local Similarity 43.6%; Pred. No. 23;
Matches 17; Conservative 3; Mismatches 8; Indels 11; Gaps 3;
Qy 2 DCOLSI---LLILSCVLDSE-----GELIQ-PSNE 29
Db 116 DCELSSGELLRLSCVKESLDLNESSNPLVPDWESNE 154
```

```
RESULT 4
ID 081225 PRELIMINARY: PRT: 888 AA.
AC 081225:
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE EXTRA-LARGE G-PROTEIN.
GN XLG.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. LANDSBERG;
RA LEE Y.-R.J., ASSMANN S.M.;
RT "Arabidopsis thaliana extra-large G-protein: a new class of GTP
binding protein.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF060942; AAC19353.1;
DR HSSP: P10824; 1BH2.
DR PFAM: PF00503; G-alpha; 1.
SQ SEQUENCE 888 AA; 98860 MW; 3F6B542C CRC32;
```

```
Query Match 33.7%; Score 49.5; DB 10; Length 888;
Best Local Similarity 43.6%; Pred. No. 23;
Matches 17; Conservative 3; Mismatches 8; Indels 11; Gaps 3;
```

```
Qy 2 DCOLSI---LLILSCVLDSE-----GELIQ-PSNE 29
Db 116 DCELSSGELLRLSCVKESLDLNESSNPLVPDWESNE 154
```

```
RESULT 5
ID 080462 PRELIMINARY: PRT: 901 AA.
AC 080462:
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE PUTATIVE GUANINE NUCLEOTIDE-BINDING PROTEIN.
GN F2686.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA ROUNSLEY S.D., KAUL S., LIN X., KETCHUM K.A., CROSBY M.L.,
RA BRANDON R.C., SYKES S.M., MASON T.M., KERLAUAGE A.R., ADAMS M.D.,
RA SOMERVILLE C.R., VENTER J.C.;
RT "Arabidopsis thaliana chromosome II BAC F2686 genomic sequence.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC003040; AAC23761.1;
DR HSSP: P10824; 1AS2.
DR PFAM: PF00503; G-alpha; 1.
SQ SEQUENCE 901 AA; 100285 MW; 93E6ED24 CRC32;
```

```
Query Match 33.7%; Score 49.5; DB 10; Length 901;
Best Local Similarity 43.6%; Pred. No. 23;
Matches 17; Conservative 3; Mismatches 8; Indels 11; Gaps 3;
Qy 2 DCOLSI---LLILSCVLDSE-----GELIQ-PSNE 29
Db 116 DCELSSGELLRLSCVKESLDLNESSNPLVPDWESNE 154
```



```

RESULT 6
ID Q23683 PRELIMINARY; PRT: 147 AA.
AC Q23683;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMblrel. 09, Last annotation update)
DE ZK370.7 PROTEIN.
GN ZK370.7
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA BERKS M.;
RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
DR EMBL; 249073; CAAB8891.1;
SQ SEQUENCE 147 AA; 15913 MW; 37A83B86 CRC32;

Query Match 33.3%; Score 49; DB 5; Length 147;
Best Local Similarity 37.5%; Pred. No. 4.9;
Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 3 COLSTILLSCVDSFGELIPQ 26
DB 2 CRLATLALFVAMVSVYGQDPP 25

RESULT 7
ID Q9WTX3 PRELIMINARY; PRT: 349 AA.
AC Q9WTX3;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE CYTOSINE DNA METHYLTRANSFERASE (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE OF 1-69 FROM N.A.
RA BERKS M.;
RA MEDLINE; 98389705.
RA DENG J., SZIF M.;
RT "Multiple isoforms of DNA methyltransferase are encoded by the
RT vertebrate cytosine DNA methyltransferase gene."
RL J. Biol. Chem. 273:22869-22872(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA DENG J., SZIF M.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF083043; AAD28102.1; JOINED.
DR EMBL; AF083038; AAD28102.1; JOINED.
DR EMBL; AF083039; AAD28102.1; JOINED.
DR EMBL; AF083040; AAD28102.1; JOINED.
DR EMBL; AF083041; AAD28102.1; JOINED.

```

```

DR EMBL; AF083042; AAD28102.1; JOINED.
KW Transferase; Methyltransferase.
FT NON-TER 1
FT NON-TER 349
SQ SEQUENCE 349 AA; 39021 MW; CCB24515 CRC32;

Query Match 32.0%; Score 47; DB 11; Length 349;
Best Local Similarity 33.3%; Pred. No. 22;
Matches 8; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 2 DCQSLILLSCVDSFGELIPQ 25
DB 27 DCNVLLKLVAGETVNSLGRLPQ 50

RESULT 8
ID 002232 PRELIMINARY; PRT: 399 AA.
AC 002232;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JAN-1999 (TREMblrel. 09, Last annotation update)
DE C54C8.4 PROTEIN.
GN C54C8.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA DOBSON R.;
RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
DR EMBL; 283102; CAB05466.1;
SQ SEQUENCE 399 AA; 46244 MW; E9F9AD5C CRC32;

Query Match 32.0%; Score 47; DB 5; Length 399;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 COLSTILLSCVDS 18
DB 6 CKLTIKLLSCFVYS 21

RESULT 9
ID 027520 PRELIMINARY; PRT: 429 AA.
AC 027520;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE TRYPTOPHAN SYNTHASE, BETA SUBUNIT HOMOLOG.
GN MTH1476.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.

```

[1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-DELTA H;
 RC MEDLINE: 98037514.
 RA SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
 RA ALDEDEDE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
 RA HARRISON D., HOANG L., KEAGLE P., LUM W., POTTER B., QIU D.,
 RA SPADAFORA R., VICARE L., WANG Y., WIERZBOWSKI J., GIBSON R.,
 RA JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
 RA MCDUGALL S., SHIMER G., GOYAL A., PETROVSKI S., CHURCH G.M.,
 RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
 RT "Complete genome sequence of *Methanobacterium thermoautotrophicum*
 RT delat: functional analysis and comparative genomics.";
 RL EMBL: AE000908: AAB85951.1: -;
 DR HSSP: P00933: 2MSY.
 DR PFAM: PF00247: trp_synb: 1.
 SQ SEQUENCE 429 AA: 47487 MW: DC78318F CRC32;

Query Match 32.0%; Score 47; DB 1; Length 429;
 Best Local Similarity 28.6%; Pred. No. 27;
 Matches 14; Conservative 5; Mismatches 6; Indels 24; Gaps 2;

QY 4 QUSILLSCSYVD-----SF-----GELIIPPSN 28
 DB 137 QMGTALSLACSLMDLCKYVWVSVFNORPFRTIMQLYGGEVVPSPSN 185

RESULT 10

Q9ZVS8 PRELIMINARY; PRT; 514 AA.

AC Q9ZVS8;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE F15K9.13 PROTEIN.
 GN F15K9.13.
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA VYSOTSKAIA V.S., SCHWARTZ J.R., TORIUMI M., YU G., LI J., LIU S.,
 RA KREMNENSKAIA I., LUTOS J., ARAUJO R., BUEHLER E., CONWAY A.B.,
 RA DEWER K., FENG J., KIM C., LI Y., SHIN P., SUN H., DAVIS R.W.,
 RA ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.;
 RT "Arabidopsis thaliana chromosome 1 BAC F15K9 sequence.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA THEOLOGIS A.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA THEOLOGIS A.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA THEOLOGIS;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC005278: AAC72127.1: -;
 DR MENDEL: 38431: Arabid:3293:38431.
 SQ SEQUENCE 514 AA: 56415 MW: B6C24CB4 CRC32;

Query Match 32.0%; Score 47; DB 10; Length 514;

Best Local Similarity 47.4%; Pred. No. 32;
 Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 7 ILLILSCSYVDSFELIIPQ 25
 DB 120 VAVLLSTVFVLAFFELIIPQ 138

RESULT 11

Q9Y0Y9 PRELIMINARY; PRT; 1146 AA.

AC Q9Y0Y9;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE BCNDNA.ID24702.
 GN BCNDNA.ID24702.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA RUBIN G.M., MAN K.H., HARVEY D., LEWIS S.E., BROKSTEIN P., TSANG G.,
 RA AGABAYANI A., ARCHANA T.T., BAXTER E., BLAZER R.G., BOTENHOFF C.,
 RA CHAMPE M., CHAVEZ C., CHEW M., DOYLE C.M., FARFAN D.E., FRIS E.,
 RA GALLE R., GEORGE R.A., HARRIS N.L., HOSKINS R.A., EVANS-HOLM M.,
 RA HOUSTON K.A., HUMMASSTI S.R., KIM E., LI P., MOSHREFI M., PACTLE J.M.,
 RA PARK S., SEQUEIRA A., SETHI H., SNIR E., SYRSKAS R.R., WEINBURG T.,
 RA CELINKER S.E.;
 RT "Full length *Drosophila melanogaster* cDNA sequence.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF145687: AAD38662.1: -;
 SQ SEQUENCE 1146 AA: 124541 MW: 8DA1D02B CRC32;

Query Match 32.0%; Score 47; DB 5; Length 1146;
 Best Local Similarity 64.3%; Pred. No. 69;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 16 LDSFGLIIPQSPNE 29
 DB 330 LDSVGEKTPQPNK 343

RESULT 12

Q9Z330 PRELIMINARY; PRT; 1622 AA.

AC Q9Z330;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE MODIFICATION METHYLASE (EC 2.1.1.73) (CYTOSINE-SPECIFIC
 DE METHYLTRANSFERASE).
 OS *Rattus rattus* (black rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN, AND PLACENTA;
 RX MEDLINE: 99097263.
 RA KIMURA H., TAKEDA T., TANAKA S., OGAWA T., SHIOTA K.;
 RT "Expression of rat DNA (cytosine-5) methyltransferase (DNA MTase) in
 RT rodent trophoblast giant cells: molecular cloning and characterization
 RT of rat DNA MTase";
 RL Biochem. Biophys. Res. Commun. 253:495-501(1998).
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOSINE = S-
 CC ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.
 CC -1- SIMILARITY: STRONG, TO OTHER C5-DNA METHYLASES.
 DR EMBL: AB012214: BAA37118.1: -;
 DR PROSITE: PS00094: C5_MTASE_1; 1.
 DR PROSITE: PS00095: C5_MTASE_2; 1.
 KW transferase; Methyltransferase; Restriction system.

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 22:32:08 ; Search time 49.21 Seconds
(without alignments)
17.947 Million cell updates/sec

Title: US-09-104-340-3
Perfect score: 147
Sequence: 1 MDCQLSTLLSCSVLDSFGLIPQPSNE 29

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	100.0	983	EPB3_HUMAN	P29320 homo sapien
2	105	71.4	983	EPB3_MOUSE	P29319 mus musculu
3	94	63.9	984	EPB3_RAT	O08680 rattus norv
4	52.5	35.7	500	CAPA_MOUSE	P51942 mus musculu
5	51	34.7	224	Y091_NPVAC	P41479 autographa
6	51	34.7	983	EPB3_CHICK	P29318 gallus gall
7	47	32.0	1620	MTDM_MOUSE	P13864 mus musculu
8	46	31.3	189	INA1_PIG	P49879 sus scrofa
9	46	31.3	529	TDR_MOUSE	P09838 mus musculu
10	45	30.6	306	FAD1_YEAST	P38913 saccharomyc
11	45	30.6	370	PSPB_RABIT	P15385 oryctolagus
12	45	30.6	781	DROL_ARCFU	O29753 archaocytob
13	45	30.6	810	SYRB_STRY3	P74296 synecocyst
14	45	30.6	908	MGR8_HUMAN	O00222 homo sapien
15	44.5	30.3	438	FIBG_XENLA	P17634 xenopus lae
16	44.5	30.3	1039	ATHL_HUMAN	P54707 homo sapien
17	43	29.3	80	CALT_BOVIN	P06833 bos taurus
18	43	29.3	585	PTRR_DIDMA	P25107 dideiphis m
19	43	29.3	3801	LYST_HUMAN	O99698 homo sapien
20	42.5	28.9	509	CPYL_BRARE	O42145 brachydanio
21	42.5	28.9	575	YFBR_ECOLI	P76481 escherichia
22	42.5	28.9	716	RRP2_LAGU2	P13167 influenza a
23	42	28.6	125	NUIM_ARBLI	O33756 arbacia ilk
24	42	28.6	189	INAI_BOVIN	P07348 bos taurus
25	42	28.6	189	INAB_BOVIN	P05008 bos taurus
26	42	28.6	189	INAD_BOVIN	P05010 bos taurus
27	42	28.6	189	INAF_BOVIN	P49876 bos taurus
28	42	28.6	189	INAG_BOVIN	P49877 bos taurus
29	42	28.6	189	INAH_BOVIN	P49878 bos taurus
30	42	28.6	234	GU45_RAT	P35898 rattus norv
31	42	28.6	257	FENR_AOVI	O44332 azocobacter
32	42	28.6	322	NUIM_STRPU	P15548 strongyloce
33	42	28.6	331	YOFA_BACSU	P54466 bacillus su
34	42	28.6	340	GLN2_STRHY	P22878 streptomyce

35	42	28.6	345	1	LEU3_THERH	P00351 thermus aqu
36	42	28.6	376	1	PSPB_RAT	P23255 rattus norv
37	42	28.6	558	1	AGP3_YEAST	P43548 saccharomyc
38	42	28.6	855	1	ENV_FIVT2	O02282 feline limu
39	42	28.6	908	1	MGR8_MOUSE	P47743 mus musculu
40	42	28.6	908	1	MGR8_RAT	P70579 rattus norv
41	42	28.6	1071	1	PR16_YEAST	P15938 saccharomyc
42	42	28.6	1133	1	SREL_CRIGR	O60416 criceturmu
43	41.5	28.2	246	1	MOS_MOUSE	O61885 mus musculu
44	41.5	28.2	351	1	WNT4_MOUSE	P22724 mus musculu
45	41.5	28.2	648	1	TALA_POVMK	P24597 mouse polyo

ALIGNMENTS

RESULT 1
ID EPB3_HUMAN STANDARD: PRT; 983 AA.
AC P29320:
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (HEK).
GN EPB3 OR ETK1 OR ETK OR HEK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RX MEDLINE: 92179233.
RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed by human lymphoid tumor cell lines."
RT Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
RN [2]
RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
RX MEDLINE: 92147681.
RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A., Welch K., Loudovaris M., Rockman S., Busmanis I.;
RT "Isolation and characterization of a novel receptor-type protein tyrosine kinase (hek) from a human pre-B cell line."
RT J. Biol. Chem. 267:3262-3267(1992).
CC - FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID FUNCTION.
CC - CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - TISSUE SPECIFICITY: RESTRICTED TO LYMPHOID TUMOR CELL LINES.
CC - SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sid.ch/announce/](http://www.isb-sib.ch/announce/) or send an email to license@sib-sib.ch).

CC EMBL: M83941; AAA58633.1; -
CC EMBL: A28003; CAA01906.1; -
CC PIR: A38224; A38224.
CC HSSP: P00523; 2PTK.
CC KIM: I79611; -
CC PRINTS: PR00014; FNTYPEI1.
CC PRINTS: PR00109; TYRKINASE.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00069; PKinase; 1.
 DR PFAM; PF00336; SAM; 1.
 DR PFAM; PF01404; EPH_Lbd; 1.
 KW Transferase; tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 983 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 21 541 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 542 565 POTENTIAL.
 FT DOMAIN 566 983 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 21 320 CYS-RICH.
 FT DOMAIN 321 431 FIBRONECTIN TYPE-III.
 FT DOMAIN 432 528 FIBRONECTIN TYPE-III.
 FT DOMAIN 529 882 FIBRONECTIN TYPE-III.
 FT NP_BIND 621 882 PROTEIN KINASE.
 FT BINDING 627 635 ATP (BY SIMILARITY).
 FT BINDING 633 635 ATP (BY SIMILARITY).
 FT ACT_SITE 746 746 BY SIMILARITY.
 FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 232 232 POTENTIAL.
 FT CARBOHYD 337 337 POTENTIAL.
 FT CARBOHYD 391 391 POTENTIAL.
 FT CARBOHYD 404 404 POTENTIAL.
 FT CARBOHYD 493 493 POTENTIAL.
 FT CONFLICT 507 507 F -> L (IN CAA01906).
 FT CONFLICT 724 724 V -> L (IN CAA01906).
 SO SEQUENCE 983 AA; 110086 MW; B8D900FA80FF5121 CRC64;

Query Match 100.0%; Score 147; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 3; 9e-14;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDCOLSTLLSCSVDSFEGELIPSPNE 29
 DB 1 MDCOLSTLLSCSVDSFEGELIPSPNE 29

RESULT 2
 ID EPHA3_MOUSE STANDARD; PRT; 983 AA.
 AC P29319;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, last sequence update)
 DT 01-NOV-1997 (Rel. 35, last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR ETK1) (MEK4).
 GN EPHA3 OR ETK1 OR MEK4 OR TYRO4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ICR X SWISS WEBSTER; TISSUE-EMBRYO;
 RX MEDLINE; 92031278.
 RA Sajjadi F.G., Pasquale E.B., Subramani S.;
 RT Identification of a new eph-related receptor tyrosine kinase gene
 RT from mouse and chicken that is developmentally regulated and encodes
 RT at least two forms of the receptor.";
 RL New Biol. 3:769-778(1991).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: A SECRETED VARIANT WITHOUT THE TRANSMEMBRANE
 CC REGION AND THE KINASE DOMAIN IS PRODUCED BY ALTERNATIVE SPLICING
 CC OF THE SAME GENE.
 CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE
 CC BRAIN.

CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch)
 CC -----
 DR EMBL; M68513; AAA39521.1; -; ALT_SEQ.
 DR EMBL; M68515; AAA39522.1; ALT_SEQ.
 DR PIR; A45583; A45583.
 DR HSSP; P16109; 1FSB.
 DR MGD; MGI:99612; EPHA3.
 DR PRINTS; PRO0014; ENTPEPIL.
 DR PRINTS; PRO0109; TYRKINSE.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00069; PKinase; 1.
 DR PFAM; PF00336; SAM; 1.
 DR PFAM; PF01404; EPH_Lbd; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 983 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 21 540 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 541 564 POTENTIAL.
 FT DOMAIN 565 983 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 21 320 CYS-RICH.
 FT DOMAIN 321 431 FIBRONECTIN TYPE-III.
 FT DOMAIN 432 528 FIBRONECTIN TYPE-III.
 FT DOMAIN 529 882 FIBRONECTIN TYPE-III.
 FT NP_BIND 621 882 PROTEIN KINASE.
 FT BINDING 627 635 ATP (BY SIMILARITY).
 FT BINDING 633 635 ATP (BY SIMILARITY).
 FT ACT_SITE 746 746 BY SIMILARITY.
 FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 231 231 POTENTIAL.
 FT CARBOHYD 336 336 POTENTIAL.
 FT CARBOHYD 390 390 POTENTIAL.
 FT CARBOHYD 403 403 POTENTIAL.
 FT CARBOHYD 492 492 POTENTIAL.
 FT VARSPIC 530 983 MISSING (IN SHORT ISOFORM).
 SO SEQUENCE 983 AA; 109955 MW; BE44A655D8107A2 CRC64;

Query Match 71.4%; Score 105; DB 1; Length 983;
 Best Local Similarity 72.4%; Pred. No. 7; 1e-08;
 Matches 21; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 MDCOLSTLLSCSVDSFEGELIPSPNE 29
 DB 1 MDCOLSTLLSCSVDSFEGELIPSPNE 29

RESULT 3
 ID EPHA3_RAT STANDARD; PRT; 984 AA.
 AC O08650;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 15-FEB-2000 (Rel. 39, last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR REK4).
 GN EPHA3 OR REK4.
 OS Rattus norvegicus (Rat).

CC Eukaryota;Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGE-DAMELEY;
RA LI Y.Y., McIernan C.F., Feldman A.M.;
RT "Il-1 beta alters the expression of the receptor tyrosine kinase gene
RL Am. J. Physiol. 274:H331-H341(1998)."
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC -1- EPHRIN-A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U69278; AAC06273.1; -.
DR HSSP; P16109; IFSB.
DR PRINTS; PR00014; FNTYPEPITI.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR. 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM. 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V.1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V.2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN.1.
DR PFM; PFM0041; fn3; 2.
DR PFM; PFM0069; Pkinase; 1.
DR PFM; PFM00536; SAM; 1.
DR PFM; PFM01404; EPH_lbd; 1.
KW Transferase; tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 984
FT DOMAIN 21 541
FT TRANSSEM 542 565
FT DOMAIN 566 984
FT DOMAIN 321 321
FT DOMAIN 322 432
FT DOMAIN 433 529
FT DOMAIN 622 883
FT NP_BIND 628 656
FT BINDING 654 654
FT ACCT_SITE 747 747
FT MOD_RES 780 780
FT CARBOHYD 232 232
FT CARBOHYD 337 337
FT CARBOHYD 391 391
FT CARBOHYD 404 404
FT CARBOHYD 493 493
FT SEQUENCE 984 AA; 110227 MW; F170C49312E7A0AB CRC64;
CC -----

Query Match	63.9%	Score 94	DB 1	Length 984
Best Local Similarity	65.5%	Pred. No.	3.1e-06	
Matches 19	Conservative 1	Mismatches 9	Indels 0	Gaps 0

QY 1 MDCQSLILLSCSVLDSEFGELIPQPSNE 29
||| ||| : | | | | |
Db 1 MDCHSLILIFGCVLSCSRELSPPQPSNE 29

RESULT	4			
ID	CAMA_MOUSE	STANDARD;	PRT;	500 AA.
AC	P51942;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).			
GN	MATN1 OR CRTM OR CMP.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-C57BL/6 X CBA; TISSUE-CARTILAGE;			
RX	MEDLINE; 962/0751.			
RA	Aszodi A., Hauser N., Studer D., Paulsson M., Hirtl L., Bosze Z.;			
RT	"Cloning, sequencing and expression analysis of mouse cartilage			
RT	matrix protein cDNA."			
RL	Eur. J. Biochem. 236:970-977(1996).			
CC	-1- FUNCTION: CARTILAGE MATRIX PROTEIN IS A MAJOR COMPONENT OF THE			
CC	EXTRACELLULAR MATRIX OF NONARTICULAR CARTILAGE. IT BINDS TO			
CC	COLLAGEN.			
CC	-1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).			
CC	-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/isb-sib.ch).			
CC	or send an email to license@isb-sib.ch .			
CC	-----			
DR	EMBL; U35035; AAB06521.1; -.			
DR	HSSP; P05099; 1A05.			
DR	MGD; MGI:106591; MATN1.			
DR	PRINTS; PR00453; VWFADOMAIN.			
DR	PROSITE; PS00022; EGF_1; FALSE_NEG.			
DR	PROSITE; PS01186; EGF_2; 1.			
DR	PFAM; PF00008; EGF; 1.			
DR	PFAM; PF00092; vwa; 2.			
KW	EGF-like domain; Signal; Glycoprotein; Cartilage; Repeat; Coiled coil.			
FT	SIGNAL	1	29	POTENTIAL.
FT	CCHAIN	30	500	POTENTIAL.
FT	REPEAT	30	226	CARTILAGE MATRIX PROTEIN.
FT	DOMAIN	227	267	CMP 1.
FT	REPEAT	268	457	EGF-LIKE.
FT	DOMAIN	471	499	CMP 2.
FT	DISULFID	39	225	COILED COIL (POTENTIAL).
FT	DISULFID	231	242	POTENTIAL.
FT	DISULFID	238	251	BY SIMILARITY.
FT	DISULFID	253	266	BY SIMILARITY.
FT	DISULFID	269	456	POTENTIAL.
FT	CARBOHYD	80	80	POTENTIAL.
FT	CARBOHYD	348	348	POTENTIAL.
SO	SEQUENCE	500 AA;	54446 MW;	57460287ELLFFA6 CRC64;

Query Match	35.7%	Score 52.5;	DB 1;	Length 500;
Best Local Similarity	54.2%;	Pred. No.2,3;		
Matches 13; Conservative	2;	Mismatches	8;	Indels 1; Gaps 1;

```
QY      3 CQLSILLLLSCSVLDSEFGEIPQP 26
          | | : | | | | | | | | | |
Db     12 CSLLLLLLLLLLQVPDSL-SLVPQP 34
```

RESULT	5		
Y091_NPVAC			
ID	Y091_NPVAC	STANDARD;	PRT; 224 AA
AC	P41479;		
DT	01-NOV-1995 (Rel. 32, Created)		


```

RN [2]
RP REVISIONS TO N-TERMINUS.
RX MEDLINE: 97094871.
RA Yoder J.A., Yen R.C., Vertino P.M., Bestor T.H., Baylin S.B.;
RT "New 5' regions of the murine and human genes for DNA (cytosine-5)-
RT methyltransferase."
RL J. Biol. Chem. 271:31092-31097(1996).
CC -1- FUNCTION: METHYLATES CG RESIDUES.
CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA = S-ADENOSYL-L-
CC HOMOCYSTEINE + DNA CONTAINING 5-METHYLCYTOSINE.
CC -1- SIMILARITY: HIGH TO OTHER EUKARYOTIC DNA METHASE.
CC -1- SIMILARITY: SOME TO BACTERIAL RESTRICTION SYSTEMS
CC METHYLTRANSFERASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X14805; CAA32910.1; -.
CC PIR: S01845; S01845.
CC REBASE: RB02813; M.Mmu1.
CC MGD: MGI:94912; Dmmt.
CC PRINTS: PR00105; C5METHFRASE.
CC PROSITE: PS00094; C5_MTASE_1; 1.
CC PROSITE: PS00095; C5_MTASE_2; 1.
CC PFM: PF00145; DNA_methylase; 3.
CC PFM: PF01426; BAH; 2.
CC KW Transferrase; Methyltransferase; DNA-binding.
CC FT DOMAIN 651 693 CYS/ARG/LYS-RICH.
CC FT ACT SITE 1229 1229 BY SIMILARITY.
CC SQ SEQUENCE 1620 AA; 183286 MW; F73710AD0043E709 CRC64;

Query Match 32.0%; Score 47; DB 1; Length 1620;
Best Local Similarity 33.3%; Pred. No. 51;
Matches 8; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 DCQSLILILSCSYLDSFGELIPQ 25
ID 1193 DCNVLTKLVAGETVNSLQGLPQ 1216
DB 1193 DCNVLTKLVAGETVNSLQGLPQ 1216

RESULT 8
ID INAL_PIG STANDARD; PRT; 189 AA.
AC P49879;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERFERON ALPHA-1 PRECURSOR (IFN-ALPHA-1).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DOMESTICA; TISSUE=LIVER;
RX MEDLINE: 92193689.
RA Lefevre F., la Bonnardiere C., Mege D.;
RT "The porcine family of interferon-omega: cloning, structural
RT analysis, and functional studies of five related genes."
RL J. Interferon Res. 11:341-350(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 87035119.
RA Lefevre F., la Bonnardiere C.;
RT "Molecular cloning and sequencing of a gene encoding biologically
RT active porcine alpha-interferon."
RL J. Interferon Res. 6:349-360(1986).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL

```

```

CC CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC -1- A PROTEIN KINASE AND AN OLIGODENYATE SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X57191; CAA40477.1; -.
CC DR EMBL: M28623; AAA31053.1; -.
CC DR HSP: P01563; IITP.
CC DR PRINTS: PR00266; INTERFERONAB.
CC PROSITE: PS00252; INTERFERON_A_B_D; 1.
CC PFM: PF00143; Interferon; 1.
CC KW Cytokine; Antiviral; Multigene family; Signal.
CC FT SIGNAL 1 23 POTENTIAL.
CC FT CHAIN 24 189 INTERFERON ALPHA-1.
CC FT DISULFID 24 122 BY SIMILARITY.
CC FT DISULFID 52 162 BY SIMILARITY.
CC SQ SEQUENCE 189 AA; 21433 MW; 8C8B8ABDEAAE3334 CRC64;

Query Match 31.3%; Score 46; DB 1; Length 189;
Best Local Similarity 47.6%; Pred. No. 7;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 5 LSLILILSCSYLDSFGELIPQ 25
ID 8 LFLVLILSCNALSGLGDLIPQ 28
DB 8 LFLVLILSCNALSGLGDLIPQ 28

RESULT 9
ID TDT_MOUSE STANDARD; PRT; 529 AA.
AC P09838;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE DNA NUCLEOTIDYLTRANSFERASE (PC 2.7.7.31) (TERMINAL ADDITION ENZYME)
DE (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TDT) (TERMINAL TRANSFERASE).
GN TDT OR TDT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86286588.
RA Koiwai O., Yokota T., Kageyama T., Hirose T., Yoshida S., Arai K.;
RT "Isolation and characterization of bovine and mouse terminal
RT deoxynucleotidyltransferase cDNAs expressible in mammalian cells."
RL Nucleic Acids Res. 14:5777-5792(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=THYMUS;
RX MEDLINE: 93219079.
RA Doyen N., Pantou D'Andon M., Bentolila L.A., Nguyen T.O., Rougeon F.;
RT "Differential splicing in mouse thymus generates two forms of
RT terminal deoxynucleotidyl transferase."
RL Nucleic Acids Res. 21:1187-1191(1993).
RN [3]
RP CHARACTERIZATION OF ALTERNATIVE FORMS.
RX MEDLINE: 96016194.
RA Bentolila L.A., Pantou D'Andon M., Nguyen T.O., Martinez O.,
RA Rougeon F., Doyen N.;
RT "The two isoforms of mouse terminal deoxynucleotidyl transferase
RT differ in both the ability to add N regions and subcellular
RT localization."
RL EMBO J. 14:4221-4229(1995).

```

CC -1- FUNCTION: TEMPLATE-INDEPENDENT DNA POLYMERASE WHICH CATALYZES THE
CC RANDOM ADDITION OF DEOXYNUCLEOSIDE 5'-TRIPHOSPHATE TO THE 3' END OF
CC A DNA INITIATOR. ONE OF THE IN-VIVO FUNCTION OF THIS ENZYME IS THE
CC ADDITION OF NUCLEOTIDES AT THE JUNCTION (N REGION) OF REARRANGED
CC IG HEAVY CHAIN AND T CELL RECEPTOR GENE SEGMENTS DURING THE
CC MATURATION OF B AND T CELLS.
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE + (DEOXY
CC NUCLEOTIDE)(N) = N PYROPHOSPHATE + (DEOXYNUCLEOTIDE)(N+1).
CC -1- COFACTOR: REQUIRES MAGNESEIUM.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (TDT-S) OR CYTOPLASMIC (TDT-L).
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS; TDT-L(LARGE) (SHOWN HERE) AND
CC TDT-S(SMALL) ARE PRODUCED BY ALTERNATIVE SPLICING. THE TDT-S FORM
CC IS THE MAJOR FORM. THE TWO FORMS DIFFER IN SUBCELLULAR LOCATION
CC AND IN ACTIVITY AS THE LONG CYTOPLASMIC FORM CAN NOT ACT ON N
CC REGIONS.
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-X FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X04123; CAA27735.1; -;
DR EMBL; X68670; CAA48634.1; -;
DR PIR; B23595; B23595.
DR MGI; 98659; TDT.
DR PRINTS; PR00869; DNAPOIX.
DR PRINTS; PR00871; DNAPOIXDT.
DR PROSITE; PS00522; DNA_POLYMERASE_X; 1.
DR PFM; PF00533; BRC1; 1.
DR PFM; PF00966; DNA_Polymerase; 1.
KW Transferase; Nucleotidyltransferase; Terminal addition; Magneslum;
KW Alternative splicing; Nuclear protein.
FT VARSPIC 482 501 MISSING (IN ISOFORM TDT-S).
FT CONFLICT 26 26 M -> T (IN REF. 1).
FT CONFLICT 99 99 F -> L (IN REF. 1).
FT CONFLICT 193 193 R -> G (IN REF. 1).
FT CONFLICT 287 287 Q -> K (IN REF. 1).
FT CONFLICT 309 309 E -> O (IN REF. 1).
FT CONFLICT 367 367 D -> H (IN REF. 1).
FT CONFLICT 441 444 DRAS -> ECAC (IN REF. 1).
SQ SEQUENCE 529 AA; 60179 MW; DE949PD7CE3A9562 CRC64;

Query Match 31.3%; Score 46; DB 1; Length 529;
Best Local Similarity 47.6%; Pred. No. 23;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 9 LLLSCVLSFGLIPQPSNE 29
||| :|:| | ||| :
Db 374 LLLYCDLLESTFEKPKSRK 394

RESULT 10
FAD1_YEAST
ID FAD1_YEAST STANDARD; PRT; 306 AA.
AC P38913;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE FAD SYNTHETASE (EC 2.7.7.2) (FMN ADENYLYLTRANSFERASE) (FAD
DE PYROPHOSPHATASE) (FLAVIN ADENINE DINUCLEOTIDE SYNTHETASE).
GN FAD1 OR YDL045C OR D2702.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
CC [1]
RN SEQUENCE FROM N.A.
RP STRAIN-W303-1A / D273-10B;
RX MEDLINE; 95098000.

RA Wu M., Repetto B., Glemum D.M., Tzagoloff A.;
RT "Cloning and characterization of FAD1, the structural gene for flavin
RT adenine dinucleotide synthetase of *Saccharomyces cerevisiae*.";
RL Mol. Cell. Biol. 15:264-271(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RA Paulin L., Saren A.M., Laamanen P.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ADENYLATES FMN TO FAD.
CC -1- CATALYTIC ACTIVITY: ATP + FMN = DIPHOSPHATE + FAD.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: SOME, TO BACTERIAL SULFATE ADENYLATE TRANSFERASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U12331; AA65730.1; -;
DR EMBL; Z71781; CAA96444.1; -;
DR EMBL; Z74093; CAA96604.1; -;
DR PIR; S47906; S47906.
DR SGD; L0000598; FAD1.
DR PFM; PF01507; PAPS_reduct; 1.
KW Transferase; Nucleotidyltransferase; FAD; FMN
SQ SEQUENCE 306 AA; 35546 MW; 55BBB830163A457F CRC64;

Query Match 30.6%; Score 45; DB 1; Length 306;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DCQVLLLYLSC 13
||| :|:| |||
Db 65 DCQVLLLYLSC 76

RESULT 11
PSPB_RABIT
ID PSPB_RABIT STANDARD; PRT; 370 AA.
AC P15285;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PULMONARY SURFACTANT-ASSOCIATED PROTEIN B PRECURSOR (SP-B) (6 KD
DE PROTEIN) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(PHE)).
GN SFRPB OR SFRP3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RX MEDLINE; 89228033.
RA Xu J., Richardson C., Ford C., Spencer T., Li-Juan Y., Mackie G.,
RA Hammond G., Possmayer F.;
RT "Isolation and characterization of the cDNA for pulmonary surfactant-
RT associated protein-B (SP-B) in the rabbit.";
RL Biochem. Biophys. Res. Commun. 160:325-332(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE;
RX MEDLINE; 95208794.
RA Margana R.K., Boggaram V.;
RT "Transcription of rabbit surfactant protein B gene.";
RL Am. J. Physiol. 268:L481-L490(1995).
RN [3]
RP SEQUENCE OF 1-34 FROM N.A.

```

RA Kleink H.P., Clayton R.A., Tomb J.F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Cavin M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Krelavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.R., Badger J.H., Glodak A., Zhou L.,
RA Overbeek R., Gocayne J.D., Meldrum J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spiggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
CC N PYROPHOSPHATE + DNA(N).
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as their content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001070; AAB90741.1; -.
DR TIGR; AF0497; -.
DR PRINTS; PR00106; DNAPOLB.
DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
DR PIRAM; PF00136; DNA_POL_B; 1.
DR Transferrase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding.
SQ SEQUENCE 781 AA; 89850 MW; 761C7B18FC66188B CRC64;

Oy 8 LLLISCVDLSFGLIPQPSNE 29
Db 164 MLVFDCEMLSSFG--MPEKED 183

RESULT 13
SYTB_SYNT3
ID SYTB_SYNT3 STANDARD: PRT; 810 AA.
AC P74296;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PHENYLALANYL--TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.20) (PHENYLALANINE--
DE TRNA LIGASE BETA CHAIN) (PHERS).
GN PHE1 OR SLI153.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
[1]
RA SEQUENCE FROM N.A.
RA MEDLINE; 97061201.
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraiki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpō S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: ATP + L-PHENYLALANINE + TRNA(PHE) = AMP +
CC PYROPHOSPHATE + L-PHENYLALANYL--TRNA(PHE).
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains
CC (by similarity).

```

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: D90913; BAA18390.1; -.
DR HSSP: P27002; 1PYS.
DR PFAM: PF01588; tRNA_bind. 2.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SQ SEQUENCE 810 AA; 87887 MW; 4D1416874C12BE9 CRC64;

Query Match 30.6%; Score 45; DB 1; Length 810;
Best Local Similarity 54.5%; Pred. No. 50;
Matches 12; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 10 LISC--SVLDFSGELIPQPSNE 29
DB 660 LLSCTVGLRGFGQLHPLRRE 681
||||:|||||
MGR8_HUMAN STANDARD; PRT; 908 AA.
ID MGR8_HUMAN
AC 000222; 015493;
DT 01-NOV-1997 (Rel. 35 Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 15-FEB-2000 (Rel. 39; Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN GRM8 OR MGLUR8.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eukaryota; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98141892.
RA Wu S., Wright R.A., Rokey P.K., Burgett S.G., Arnold J.S.,
RA Rosebeck P.R., Jr., Johnson B.G., Schoepp D.D., Belagaje R.M.,
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RT pharmacological properties in RGT cells.";
RT J. Neurosci. 19: 388-397 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97446143.
RA Scherer S.W., Soder S., Duvoisin R.M., Huizenga J.J., Tsui L.C.,
RT "The human metabotropic glutamate receptor 8 (GRM8) gene: a
RT disproportionately large gene located at 7q31.3-q32.1.";
RT Genomics 44:232-236(1997).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: U92459; AAB5164.1; -.
DR EMBL: U95025; AAB72040.1; -.
DR GCRDB: GCR_1889; -.
DR GCRDB: GCR_2604; -.
DR MIM: 601116; -.
CC -----

DR PRINTS: PR00248; GPCRMR.
DR PRINTS: PR00593; MTABOTROPICR.
DR PRINTS: PR01058; MTABOTROPICR.
DR PROSITE: PS00979; G_PROTEIN_RECPE_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECPE_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECPE_F3_3; 1.
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction.
FT SIGNAL 1 33
FT CHAIN 34 908
FT DOMAIN 34 583
FT DOMAIN 584 608
FT DOMAIN 609 620
FT DOMAIN 621 641
FT DOMAIN 642 647
FT TRANSMEM 648 668
FT TRANSMEM 669 695
FT TRANSMEM 696 716
FT TRANSMEM 717 746
FT TRANSMEM 747 768
FT TRANSMEM 769 781
FT TRANSMEM 782 803
FT TRANSMEM 804 818
FT TRANSMEM 819 843
FT TRANSMEM 844 908
FT CARBOHYD 95 95
FT CARBOHYD 298 298
FT CARBOHYD 452 452
FT CARBOHYD 480 480
FT CARBOHYD 565 565
FT CARBOHYD 565 565
FT CONFLICT 194 194
FT CONFLICT 460 460
FT CONFLICT 642 642
FT CONFLICT 768 768
FT CONFLICT 904 904
SQ SEQUENCE 908 AA; 101741 MW; 95C2D0886E743905 CRC64;

Query Match 30.6%; Score 45; DB 1; Length 908;
Best Local Similarity 37.9%; Pred. No. 56;
Matches 11; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 3 COL--SVLDFSGELIPQPSNE 29
DB 751 CSLGSLIMLVCTVYANKRGVPEFNE 779
||||:|||||
FIBG_XENLA STANDARD; PRT; 438 AA.
ID FIBG_XENLA
AC P17634;
DT 01-AUG-1990 (Rel. 15 Created)
DT 01-AUG-1990 (Rel. 15; Last sequence update)
DT 15-JUL-1999 (Rel. 38; Last annotation update)
DE FIBRINOGEN GAMMA CHAIN PRECURSOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90241882.
RA Pastori R.L., Moskalts J.E., Smith L.H., Jr., Schenberg D.R.,
RT "Estrogen regulation of Xenopus laevis gamma-fibrinogen gene
RT expression.";
RT Biochemistry 29:2599-2605(1990).
RN [2]
RN SEQUENCE OF 1-58 FROM N.A.
RP TISSUE=LIVER;
RX MEDLINE: 91146806.
RA Bhattacharya A., Shepard A.R., Moser D.R., Holland L.J.;

```

RT "Isolation and characterization of cDNA clones for the gamma subunit
RT of xenopus fibrinogen, the product of a coordinately regulated gene
RT family";
RL Mol. Cell. Endocrinol. 72:213-220(1990).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
-----
DR EMBL: J02894; AAA49709.1; -
DR EMBL: M35548; AAA03247.1; -
DR PIR: A32670; A32670.
DR HSSP: P02679; LFIC.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
DR PFAM: PF00147; fibrinogen_C; 1.
KW Blood coagulation; Glycoprotein; Calcium; Plasma; Platelet; Signal.
FT SIGNAL 1 25
FT CHAIN 26 438 FIBRINOGEN GAMMA CHAIN.
FT DISULFID 32 32 INTERCHAIN (WITH C-33') (BY SIMILARITY).
FT DISULFID 33 33 INTERCHAIN (WITH C-32') (BY SIMILARITY).
FT DISULFID 43 43 INTERCHAIN (WITH BETA) (BY SIMILARITY).
FT DISULFID 47 47 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 158 158 INTERCHAIN (WITH BETA) (BY SIMILARITY).
FT DISULFID 162 162 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 176 205 BY SIMILARITY.
FT DISULFID 349 362 BY SIMILARITY.
FT CARBOHYD 76 76 POTENTIAL.
SQ SEQUENCE 438 AA; 50064 MW; 69B1F01BB6716F60 CRC64;

```

```

Query Match 30.3%; Score 44.5; DB 1; Length 438;
Best Local Similarity 47.8%; Pred. No. 31;
Matches 11; Conservative 4; Mismatches 7; Indels 1; Gaps 1;
QY 7 ILLLLSCSVLDS-FGEIIPQPSN 28
:| | | | : : | | | | |
Db 9 LLLLSIALLSAFAGNIIPTNDN 31

```

Search completed: May 9, 2000, 22:32:11
Job time: 2402 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 22:27:16 ; Search time 64.29 Seconds
(without alignments)
26.447 Million cell updates/sec

Title: US-09-104-340-3
Perfect score: 147
Sequence: 1 MDCQSLILLSCSVLDSFGELIPQPSNE 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues
Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	983	2	A38224
2	105	71.4	983	2	A45583
3	58.5	39.8	495	2	T18835
4	52.5	35.7	500	2	S65522
5	51	34.7	224	2	D72861
6	51	34.7	983	2	B45583
7	49.5	33.7	901	2	T01135
8	49	33.3	147	2	T28131
9	47	32.0	399	2	T20204
10	47	32.0	429	2	F69063
11	47	32.0	1622	2	JE0378
12	46	31.3	189	2	S23709
13	46	31.3	431	2	T38260
14	46	31.3	529	2	B23595
15	46	31.3	793	2	T27133
16	45.5	31.0	526	2	T12313
17	45.5	31.0	528	2	T12309
18	45.5	31.0	975	2	T16073
19	45	30.6	79	2	S77428
20	45	30.6	223	2	T21437
21	45	30.6	306	2	S47906
22	45	30.6	369	2	I46531
23	45	30.6	370	1	LNRMB
24	45	30.6	563	1	C64420
25	45	30.6	781	2	A69312
26	45	30.6	810	2	S75931
27	45	30.6	1490	2	UC5145
28	45	30.6	3898	2	S58295
29	44.5	30.3	128	2	S13028
30	44.5	30.3	176	2	I41076

ALIGNMENTS

31	44.5	30.3	276	2	S31504	H+/K+-exchanging A
32	44.5	30.3	438	2	A32670	fibrinogen gamma c
33	44.5	30.3	591	2	T39195	probable amino aci
34	44.5	30.3	1039	2	I38401	ATP-driven ion pum
35	44	29.9	111	2	D72112	hypothetical prote
36	44	29.9	157	2	S58068	probable olfactory
37	44	29.9	411	2	S69735	hypothetical prote
38	44	29.9	191	2	T04987	hypothetical prote
39	44	29.9	482	2	A70963	hypothetical prote
40	44	29.9	1537	2	UC4172	DNA (cytosine-5'-)
41	43.5	29.6	364	2	T10174	hypothetical prote
42	43	29.3	80	2	A35572	seminaplasmn pre
43	43	29.3	94	2	B40506	pR27 protein - hum
44	43	29.3	117	2	T20888	hypothetical prote
45	43	29.3	130	1	JI0079	tg kappa chain pre

RESULT 1
A38224
protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C:Accession: A38224; B38224
R:Wicks, I.P.; Wilkinson, D.; Salvaris, E.; Boyd, A.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
A:Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expe
A:Reference number: A38224; MUID:92179233
A:Accession: A38224
A:Molecule type: mRNA
A:Residues: 1-983 <WIC>
A:Cross-references: GB:M83941; NID:g183931; PIDN:AAA5633.1; PID:g183932
A:Experimental source: pre-B-cell leukemia cell line LK63
A:Note: sequence extracted from NCBI backbone (NCBIP:86627)
A:Accession: B38224
A:Molecule type: protein
A:Residues: 21-39;810-860 <WIC>
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferas
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-983/Product: protein-tyrosine kinase hek #status experimental <TM>
F:547-565/Domain: transmembrane #status predicted <TM>
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif
F:232,337,391,404,493/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 147; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDCQSLILLSCSVLDSFGELIPQPSNE 29
|||||
|||||

RESULT 2
A45583
receptor tyrosine kinase Mek4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: A45583
R:Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
A:Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
A:Reference number: A45583; MUID:92031278
A:Accession: A45583
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-983 <SAJ>
A:Cross-references: GB:M8513; NID:g199119; PIDN:AAA39521.1; PID:g199120

A:Note: sequence extracted from NCBI backbone (NCBIN:62398, NCBI:62401)
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
 F:619-885/Domain: protein kinase homology <KIN>
 F:627-635/Region: protein kinase ATP-binding motif

Query Match 71.4%; Score 105; DB 2; Length 983;
 Best Local Similarity 72.4%; Pred. No. 1.8e-07;
 Matches 21; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 MNCQSLILLSCSYLDSPFGLIPQPSNE 29
 ||| ||||| ||| ||| |||||
 Db 1 MDCHSLITVLGCVLSCGSELSQPSPNE 29

RESULT 3
 T18835
 hypothetical protein C01G6.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T18835

R:Berk, M.
 submitted to the EMBL Data Library, August 1994
 A:Reference number: Z19029
 A:Accession: T18835
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-495 <M11>
 A:Cross-references: EMBL:Z35595; PIDN:CAA84634.1; GSPDB:GN00020; CESP:C01G6.3
 A:Experimental source: clone C01G6
 C:Genetics:
 A:Gene: CESP:C01G6.3
 A:Map position: 2
 A:Introns: 47/1: 303/3; 344/3

Query Match 39.8%; Score 58.5; DB 2; Length 495;
 Best Local Similarity 36.4%; Pred. No. 0.62;
 Matches 16; Conservative 6; Mismatches 3; Indels 19; Gaps 2;

QY 1 MNCQSLILLSCSYLDSPFGLIPQ 25
 :||: ||||| :||| |||||
 Db 105 IDQMKLILLICSAFSTCVLDFRANGIEFYVGEGLIPE 148

RESULT 4
 S66522
 cartilage matrix protein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
 C:Accession: S66522
 R:Ascoli, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hirtl, L.; Bosze, Z.
 Eur. J. Biochem. 226, 970-977, 1996

A:Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein c
 A:Reference number: S66522; MUID:96270751
 A:Accession: S66522
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-500 <ASZ>
 A:Cross-references: EMBL:U35035; NID:g1163178; PIDN:AAB06521.1; PID:g1163179
 C:Genetics:
 A:Gene: CMP

C:Superfamily: von Willebrand factor type A repeat homology; EGF homology
 F:1-39/Domain: signal sequence status predicted <SIG>
 F:30-500/Product: cartilage matrix protein #status predicted <MAT>
 F:43-210/Domain: von Willebrand factor type A repeat homology <WMA1>
 F:231-266/Domain: EGF homology <EGF>
 F:277-441/Domain: von Willebrand factor type A repeat homology <WMA2>

Query Match 35.7%; Score 52.5; DB 2; Length 500;
 Best Local Similarity 34.2%; Pred. No. 4.8;

Matches 13; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
 QY 3 COLSTILLSCSYLDSPFGLIPQ 26
 | | |||| | | | ||||
 Db 12 CSLILLILLQVPSL-SIVQP 34

RESULT 5
 D72861
 ACOF-91 protein - Autographa californica nuclear polyhedrosis virus
 C:Species: Autographa californica nuclear polyhedrosis virus, ACNPV
 A:Note: dsDNA virus
 C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
 C:Accession: D72861
 R:Avres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
 Virology 202, 586-605, 1994
 A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis vir
 A:Reference number: A72850; MUID:94303173
 A:Accession: D72861
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-224 <AVP>
 A:Cross-references: GB:L22858; NID:g510708; PIDN:AAA66721.1; PID:g559160
 C:Genetics:
 A:Gene: ACOF-91

Query Match 34.7%; Score 51; DB 2; Length 224;
 Best Local Similarity 45.5%; Pred. No. 3.6;
 Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 5 ISILLSCSYLDSPFGLIPQ 26
 | |||: || | | | |
 Db 16 LFIILLTKILIDDQGLYPNP 37

RESULT 6
 B45583
 receptor tyrosine kinase Cerk - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
 C:Accession: B45583
 R:Sajjad, F.G.; Pasquale, E.B.; Subraman, S.
 New Biol. 3, 769-778, 1991
 A:Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
 A:Reference number: A45583; MUID:92031278
 A:Accession: B45583
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-983 <SA>
 A:Cross-references: GB:M68514; NID:g454809; PIDN:AAA48666.1; PID:g211447
 A:Note: sequence extracted from NCBI backbone (NCBIN:62405, NCBI:62411)
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
 C:Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
 F:619-885/Domain: protein kinase homology <KIN>
 F:627-635/Region: protein kinase ATP-binding motif

Query Match 34.7%; Score 51; DB 2; Length 983;
 Best Local Similarity 32.4%; Pred. No. 16;
 Matches 11; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 9 LLLSCSYLDSPFGLIPQPSNE 29
 ||| | | | | | | | |
 Db 8 LLLCNAAGSAGRLSARPENE 28

RESULT 7
 T01135
 hypothetical protein F26B6.11 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 30-Apr-1999
 C:Accession: T01135

us-09-104-340-3.rpt

A: Introns: 87/1; 115/3; 189/1; 210/3; 266/3; 331/2

[illegible]

C:\date_05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:\accession: F69603
R\Smith, D.R.: Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Alredge, T.
Qiu, D.; Spedalora, R.; Vicaltre, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Javan,
K.I., S.; Church, G.M.; Daniels, C.S.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
#title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func

```
A>Status: pretranslary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-429 <MTH>
A:Cross-references: GB:AE000908; GB:AE000666; NID:g2622579; PIDN:AAB85951.1; PID:g2622579
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1476
C:Superfamily: tryptophan synthase beta chain; tryptophan synthase beta chain homolog F_30-422/Domain: tryptophan synthase beta chain homology <TRPB>

Query Match          32.0%; Score 47; DB 2; Length 429;
Best Local Similarity 28.6%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 6; Indels 24; Gaps 2;

OY      4 QLSLLISCSD-----SF-----GELIQPSN 28
           |   | :|::|   ||
Ddb     137 QMGTAISLACSLMDLQCKVYAVRVSFNQKPRKRIMQLGGVEVPSPSN 185
```

```

JE0378      11
DNA (cytosine-5)-methyltransferase (EC 2.1.1.37) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: JE0378
R:Kamura, H., Takeda, T., Tanaka, S., Ogawa, T., Shiota, K.
B:Biochem. Biophys. Res. Commun. 253, 495-501, 1998
A:Title: Expression of rat DNA (cytosine-5) methyltransferase (DNA MTase) in rodent t
A:Reference number: JE0378
A:Accession: JE0378
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1622 <RIM>
A:Cross-references: DDBJ:AB012214
C:Keywords: methyltransferase

Query Match          32.0%  Score 47;  DB 2;  Length 1622;
Best Local Similarity 33.3%;  Pred. No. 1e+02;
Matches      8;  Conservative      8;  Mismatches      8;  Indels      0;  Gaps      0;

OY      2  DCOLSTLLLSCTVLDSPGRLIPQ 25
|| : : |::: | : | : ||
Db      1195 DCAVLLKLVNAGEVTNSLDGRLPQ 1218

```

S23709
Interferon alpha-1 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S23709; I46589
R:Mege, D.; Lefevre, F.; Labonnardiere, C.
J. Interferon Res. 11, 341-350, 1991
A:Title: The porcine family of interferon-omega: cloning, structural analysis, and function
A:Reference number: S23709; MUID:92193689
A:Accession: S23709
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <MEC>
A:Cross-references: EMBL:X57191; NID:92062; PIDN:CAA0477.1; PID:92063
R:Lefevre, F.; La Bonnardiere, C.
J. Interferon Res. 6, 349-360, 1986
A:Title: Molecular cloning and sequencing of a gene encoding biologically active porcine
A:Reference number: I46589; MUID:87035119
A:Accession: I46589
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-189 <LEF>
A:Cross-references: GB:M28623; NID:g164498; PIDN:AA31053.1; PID:g164499
C:Genetics:
A:Gene: PolrN-alpha-1
C:Superfamily: Interferon alpha

Query Match 31.3%; Score 46; DB 2; Length 189;
Best Local Similarity 47.6%; Pred. No. 16;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 5 LILLSCSVLDSFGELIPQ 25
||:||||:|:|:|:
DB 8 LTAIVLSCNATCSLGCDDLPQ 28

RESULT 13
T38260
hypohectical protein SPAC23C4.05c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38260
R:Harrell, D.; Squares, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: 221782
A:Accession: T38260
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-431 <HAR>
A:Cross-references: EMBL:299753; PIDN:CAB16876.1; GSPDB:GN00066; SPDB:SPAC23C4.05c
C:Genetics:
A:Experimental source: strain 972h-; cosmid C23C4
A:Gene: SPDB:SPAC23C4.05c
A:Map position: 1
A:introns: 23/1

Query Match 31.3%; Score 46; DB 2; Length 431;
Best Local Similarity 72.7%; Pred. No. 37;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 16 LDFSGELIPQ 26
|:||||:|:
DB 375 LDFSGELIPQ 385

RESULT 14
B23595
DNA nucleotidylexotransferase (EC 2.7.7.31) - mouse
N:Alternate names: terminal addition enzyme; terminal deoxynucleotidyltransferase (T
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 18-Jun-1999

C:Accession: B23595; S30235
R:Kolwa, O.; Yokota, T.; Kageyama, T.; Hirose, T.; Yoshida, S.; Arai, K.
Nucleic Acids Res. 14, 5777-5792, 1986
A:Title: Isolation and characterization of bovine and mouse terminal deoxynucleotidyl
A:Reference number: A93633; MUID:66286588
A:Accession: B23595
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-529 <KOI>
A:Cross-references: GB:X04123; NID:954765; PIDN:CAA27735.1; PID:954766
R:Doyen, N.; d'Adon, M.F.; Bentolila, L.A.; Nguyen, Q.T.; Rougeon, F.
Nucleic Acids Res. 21, 1187-1191, 1993
A:Title: Differential splicing in mouse thymus generates two forms of terminal deoxyn
A:Reference number: S30235; MUID:93219079
A:Accession: S30235
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-25, 'M', 27-98, 'F', 100-192, 'R', 194-286, 'Q', 288-308, 'E', 310-366, 'D', 368-44
A:Cross-references: EMBL:X66670; NID:9287808; PIDN:CAA48634.1; PID:9287809
C:Superfamily: DNA nucleotidylexotransferase
C:Keywords: alternative splicing; magnesium; nucleotidyltransferase; nucleus

Query Match 31.3%; Score 46; DB 2; Length 529;
Best Local Similarity 47.6%; Pred. No. 46;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 9 LLLSCSVLDSFGELIPQ 29
|||:|:|:|:|:
DB 374 LLLYCDLIESFTEKQPSRK 394

RESULT 15
T27133
hypohectical protein Y53C12B.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27133
R:Kershaw, J.; Lennard, N.
submitted to the EMBL Data Library, September 1997
A:Reference number: 220316
A:Accession: T27133
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-793 <WIL>
A:Cross-references: EMBL:299278; PIDN:CAB16490.1; GSPDB:GN00020; CESP:Y53C12B.1
A:Experimental source: clone Y53C12B
C:Genetics:
A:Gene: CESP:Y53C12B.1
A:Map position: 2
A:introns: 51/2; 320/3; 464/2; 686/3

Query Match 31.3%; Score 46; DB 2; Length 793;
Best Local Similarity 34.0%; Pred. No. 69;
Matches 16; Conservative 5; Mismatches 8; Indels 18; Gaps 3;

OY 1 MDCCOL-----SIL-----LLSCSVLDS--FGELIPQ 29
|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
DB 351 LDCQILRHGTHSVSVPTWDTSLASCSKDNSTLTFRLVTSFEND 397

Search completed: May 9, 2000, 22:27.18
Job time: 4157 sec .

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 22:25:59 ; Search time 44.2 Seconds
(without alignments)
9.490 Million cell updates/sec

Title: US-09-104-340-3

Perfect score: 147
Sequence: 1 MDCQLSTLLTSCSYLDSFGELIPQPSNE 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 143561 seqs, 14463640 residues

Total number of hits satisfying chosen parameters: 143561

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents, AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	100.0	983	1 US-08-167-919A-10	Sequence 10, Appl
2	147	100.0	983	2 US-08-449-645A-21	Sequence 21, Appl
3	147	100.0	983	2 US-08-702-367A-21	Sequence 21, Appl
4	147	100.0	983	3 US-08-715-106-10	Sequence 10, Appl
5	147	100.0	983	4 PCT-US95-04681-21	Sequence 21, Appl
6	51	34.7	982	2 US-08-673-789-4	Sequence 4, Appl
7	51	34.7	983	1 US-08-162-809-16	Sequence 16, Appl
8	47	32.0	14	1 US-08-167-919A-2	Sequence 2, Appl
9	47	32.0	14	3 US-08-715-106-2	Sequence 2, Appl
10	47	32.0	19	1 US-08-167-919A-3	Sequence 3, Appl
11	47	32.0	19	3 US-08-715-106-3	Sequence 3, Appl
12	45	30.6	128	1 US-08-476-275-4	Sequence 4, Appl
13	44	29.9	129	4 PCT-US95-07372-12	Sequence 12, Appl
14	44	29.9	316	2 US-08-837-281A-2	Sequence 2, Appl
15	43.5	29.6	448	1 US-08-207-904-2	Sequence 2, Appl
16	43.5	29.6	448	2 US-08-207-904-2	Sequence 2, Appl
17	43	29.3	128	4 PCT-US95-07302-2	Sequence 1, Appl
18	43	29.3	235	2 US-08-303-569B-5	Sequence 5, Appl
19	43	29.3	235	2 US-08-116-247-5	Sequence 5, Appl
20	43	29.3	585	1 US-08-468-249A-18	Sequence 18, Appl
21	43	29.3	585	1 US-08-142-439A-6	Sequence 6, Appl
22	43	29.3	585	2 US-08-142-511B-125	Sequence 125, Appl
23	43	29.3	585	2 US-08-869-477-6	Sequence 6, Appl
24	43	29.3	585	2 US-08-468-249A-19	Sequence 19, Appl
25	43	29.3	3672	2 US-08-832-445-12	Sequence 12, Appl
26	43	29.3	3801	2 US-08-832-445-10	Sequence 10, Appl
27	42	28.6	128	1 US-07-634-278-31	Sequence 31, Appl
28	42	28.6	128	1 US-07-946-421-26	Sequence 26, Appl
29	42	28.6	128	1 US-08-477-728-31	Sequence 31, Appl

ALIGNMENTS

30	42	28.6	128	1 US-08-474-040-31	Sequence 31, Appl
31	42	28.6	128	1 US-08-487-200-31	Sequence 31, Appl
32	42	28.6	128	3 US-08-444-644-15	Sequence 15, Appl
33	42	28.6	128	3 US-08-444-644-25	Sequence 25, Appl
34	41	27.9	277	1 US-08-118-270-68	Sequence 68, Appl
35	41	27.9	277	4 PCT-US93-08528-68	Sequence 68, Appl
36	41	27.9	339	1 US-08-396-357A-4	Sequence 4, Appl
37	41	27.9	687	2 US-08-449-645A-29	Sequence 29, Appl
38	41	27.9	687	2 US-08-702-367A-29	Sequence 29, Appl
39	41	27.9	915	1 US-08-453-862-2	Sequence 2, Appl
40	41	27.9	915	2 US-08-452-734A-2	Sequence 2, Appl
41	41	27.9	915	4 PCT-US94-14989-2	Sequence 2, Appl
42	41	27.9	1242	2 US-08-680-326-33	Sequence 33, Appl
43	40.5	27.6	40	2 US-08-194-981E-14	Sequence 14, Appl
44	40.5	27.6	158	2 US-08-729-103-1	Sequence 1, Appl
45	40.5	27.6	158	2 US-08-468-413-2	Sequence 2, Appl

RESULT 1
US-08-167-919A-10
; Sequence 10, Application US/08167919A
; Patent No. 5674691
; GENERAL INFORMATION:
; APPLICANT: Boyd, Andrew W.
; APPLICANT: Simpson, Richard J.
; APPLICANT: Wicks, Ian
; APPLICANT: Ward, Larry D.
; APPLICANT: Wilkinson, David
; TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,919A
; FILING DATE: 18-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK6841 (AU)
; FILING DATE: 21-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK6992 (AU)
; FILING DATE: 12-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU92/00294
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9159
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELECOMMUNICATION INFORMATION:
; TELETYPE: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-167-919A-10

Query Match 100.0%; Score 147; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.2e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCCQSLILLSCSVLDSFGELIPQPSNE 29
|||||
DB 1 MDCCQSLILLSCSVLDSFGELIPQPSNE 29

RESULT 2

US-08-449-645A-21
; Sequence 21, Application US/08449645A
; Patent No. 5981245
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; KINASES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,645A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-645A-21

Query Match 100.0%; Score 147; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.2e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCCQSLILLSCSVLDSFGELIPQPSNE 29
|||||
DB 1 MDCCQSLILLSCSVLDSFGELIPQPSNE 29

RESULT 3

US-08-702-367A-21
; Sequence 21, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; KINASES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,367A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 983 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-702-367A-21

Query Match 100.0%; Score 147; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.2e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCCQSLILLSCSVLDSFGELIPQPSNE 29
|||||
DB 1 MDCCQSLILLSCSVLDSFGELIPQPSNE 29

RESULT 4

US-08-715-106-10
; Sequence 10, Application US/08715106
; Patent No. 6020306
; GENERAL INFORMATION:
; APPLICANT: Boyd, Andrew W.
; APPLICANT: Simpson, Richard J.
; APPLICANT: Wicks, Ian
; APPLICANT: Ward, Larry D.
; APPLICANT: Wilkinson, David
; TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715,106
; FILING DATE: 18-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/167,919
; FILING DATE: 18-APR-1994
; APPLICATION NUMBER: PK6841 (AU)
; FILING DATE: 21-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK9992 (AU)
; FILING DATE: 12-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU92/00294
; FILING DATE: 19-JUN-1992

ATTORNEY/AGENT INFORMATION:
NAME: DIGILLO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-715-106-10

Query Match 100.0%; Score 147; DB 3; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.2e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDQQLSILLSCSVLDSFGELIPQSPNE 29
DB 1 MDQQLSILLSCSVLDSFGELIPQSPNE 29

RESULT 5
PCT-US95-04681-21
Sequence 21, Application PC/TUS9504681
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-21

Query Match 100.0%; Score 147; DB 4; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.2e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDQQLSILLSCSVLDSFGELIPQSPNE 29
DB 1 MDQQLSILLSCSVLDSFGELIPQSPNE 29

RESULT 6

US-08-673-789-4
Sequence 4, Application US/08673789
Patent No. 5814479

GENERAL INFORMATION:
APPLICANT: ZHOU, RENDING; SCHULZ, NICHOLAS,
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994

ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GROUPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 982
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
US-08-673-789-4

Query Match 34.7%; Score 51; DB 2; Length 982;
Best Local Similarity 52.4%; Pred. No. 8.7;
Matches 11; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 9 LLLSCSVLDSFGELIPQSPNE 29
DB 8 LLLSCSVLDSFGELIPQSPNE 28

RESULT 7
US-08-162-809-16
Sequence 16, Application US/08162809
Patent No. 5457048

GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America

US-08-162-809-16
Sequence 16, Application US/08162809
Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-809-16

Query Match 34.7%; Score 51; DB 1; Length 983;
Best Local Similarity 52.4%; Pred. No. 8.7;
Matches 11; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 9 LILSCVLDSEGLIPQPSNE 29
|||:|||||:|
Db 8 LILCALGAGRLSARPGNE 28

RESULT 8
US-08-167-919A-2
Sequence 2, Application US/08167919A
Patent No. 5674691
GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,919A
FILING DATE: 18-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992

ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-167-919A-2

Query Match 32.0%; Score 47; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ELIPQPSNE 29
|||||||
Db 1 ELIPQPSNE 9

RESULT 9
US-08-715-106-2
Sequence 2, Application US/08715106
Patent No. 6020306
GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-715-106-2

Query Match 32.0%; Score 47; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ELIPOPSNE 29
|||||
DB 1 ELIPOPSNE 9

RESULT 10
US-08-167-919A-3
Sequence 3, Application US/08167919A
Patent No. 5674691
GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,919A
FILING DATE: 18-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-167-919A-3

Query Match 32.0%; Score 47; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ELIPOPSNE 29
|||||
DB 1 ELIPOPSNE 9

RESULT 11
US-08-715-106-3
Sequence 3, Application US/08715106
Patent No. 6020306
GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-715-106-3

Query Match 32.0%; Score 47; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.37;

ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,291A
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: GP50001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-827-291A-2

Query Match 29.9%; Score 44; DB 2; Length 316;
Best Local Similarity 42.9%; Pred. No. 27;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 3 CQLSTILLSCVLDSPFGLI 23
DB 179 CELPSILLISCNDTSTIFEXVI 199

RESULT 15
US-08-207-904-2
Sequence 2, Application US/08207904
Patent No. 5477002
GENERAL INFORMATION:
APPLICANT: Tuttle, AnnMarie
APPLICANT: Crossland, Lyle D.
TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,904
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/908,242
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: CGC 1624

TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-207-904-2

Query Match 29.6%; Score 43.5; DB 1; Length 448;
Best Local Similarity 31.0%; Pred. No. 48;
Matches 9; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

OY 1 MDQSTILLSCV--LDSFGELIPQ 26
DB 87 LDQNSGIYLMETAEKLDLDGDFSPSP 115

Search completed: May 9, 2000, 22:26:00
Job time: 4149 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 21:52:03 ; Search time 50.71 Seconds

(without alignments)
13.546 Million cell updates/sec

Title: US-09-104-340-3

Perfect score: 147

Sequence: 1 MDCOLSTLLSLSCVSLDSFGELIPSPNE 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 08
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	983	1 R31466	HEK polypeptide, R
2	55	37.4	288	1 W88378	Human sperm-specific
3	55	37.4	323	1 W88380	Human sperm-specific
4	51	34.7	983	1 R75711	Eph-related PTK Ce
5	48.5	33.0	2458	1 R07640	Deduced protein se
6	48.5	33.0	2458	1 R04031	Full length T4 enc
7	47.5	32.3	242	1 W58379	Human immunoglobul
8	46	31.3	189	1 W83902	Porcine interferon
9	46	31.3	189	1 W73231	Porcine interferon
10	45.5	31.0	490	1 R72361	Human cytochrome P
11	45.5	31.0	490	1 R81465	Human cytochrome P
12	45.5	31.0	490	1 R31168	Human derived cyto
13	45	30.6	114	1 W27850	Human cytochrome P
14	45	30.6	128	1 R55214	Staphylococcus aur
15	45	30.6	908	1 W41568	Murine variable re
16	44	29.9	129	1 R8108	Human metabotropic
17	44	29.9	129	1 W75960	Murine anti-Protei
18	43.5	29.6	448	1 R47475	Human olfactory OL
19	43.5	29.6	448	1 R46929	Polypeptide encode
20	43	29.3	128	1 R90690	Tobacco Ant32 geno
21	43	29.3	129	1 P82937	Mouse 5C7.29 monoc
22	43	29.3	129	1 P70626	Variable region of
23	43	29.3	129	1 W10241	Sequence encoded b
24	43	29.3	129	1 W16342	Variable region of
25	43	29.3	129	1 W10587	L6 antibody-Y-kapp
26	43	29.3	129	1 W47512	V region of the L6
27	43	29.3	129	1 W41069	Mouse L6 antibody
28	43	29.3	129	1 W47519	Mouse L6 antibody
29	43	29.3	129	1 W89537	Anti-cancer antio
30	43	29.3	135	1 R08347	Monoclonal antibody
31	43	29.3	235	1 R13060	Humanised light ch
32	43	29.3	235	1 W41410	Humanised light ch
33	43	29.3	515	1 R27704	Opssum kidney PTH
34	43	29.3	515	1 R92275	Opssum kidney PTH

35	43	29.3	515	1 W73314	Parathyroid hormon
36	43	29.3	565	1 R76700	Elert enterotoxin e
37	43	29.3	565	1 R76699	Shen2 enterotoxin e
38	43	29.3	585	1 R27705	Opssum kidney PTH
39	43	29.3	585	1 R27705	Opssum kidney PTH
40	43	29.3	585	1 R92276	Opssum kidney PTH
41	43	29.3	611	1 W83428	Parathyroid hormon
42	43	29.3	1763	1 W83431	Munc13-1-interacti
43	43	29.3	2001	1 W23596	Rat Munc13-1. Scra
44	43	29.3	3672	1 W31950	Human LXR1 longer
45	43	29.3	3801	1 W31949	Human bg protein a

ALIGNMENTS

RESULT 1	
R31466	R31466 standard; Protein; 983 AA.
ID	R31466;
AC	24-MAY-1993 (first entry)
DE	HEK polypeptide.
KW	Primer; expression vector; extracellular domain; human; HEK;
KW	eph/ek-like; kinase; pre-B; cell; T; tumour; lymphoid; IK63;
KW	lila-1; JM; epithelial; HeLa; receptor-type; thymidine kinase;
KW	TK; ligand; B;cellular response; growth; differentiation.
OS	Homo sapiens.
PH	Key
FT	peptide
FT	/note= "Signal peptide"
FT	protein
FT	/note= "Purified HEK protein #1"
FT	protein
FT	/note= "Purified HEK protein #2"
FT	modified_site
FT	/note= "N-link glycosylation"
FT	modified_site
FT	/note= "N-link glycosylation"
FT	modified_site
FT	/note= "N-link glycosylation"
FT	modified_site
FT	/note= "N-link glycosylation"
FT	modified_site
FT	/note= "N-link glycosylation"
FT	domain
FT	/note= "Transmembrane domain"
FT	binding_site
FT	/note= "Arp binding site"
FT	binding_site
FT	/note= "Arp binding site"
FT	binding_site
FT	/note= "Arp binding site"
FT	modified_site
FT	/note= "Putative autophosphorylation site"
PD	W09300425-A.
PD	07-JAN-1993.
PD	19-JUN-1992; AU00294.
PD	21-JUN-1991; AU-006841.
PD	12-DEC-1991; AU-009992.
PD	(HALT-) HALT INSTR MEDICAL RES WALTER & ELIZA.
PD	Boyd AD, Simpson R, Ward LD, Wicks I, Wilkinson D;
PD	WPI: 93-036373/04.
PD	P-PSDB: R31466.
PD	Receptor-type tyrosine kinase reactive with monoclonal antibody
PD	III-A4 - is Eph-Elk-like kinase, useful for phosphorylating
PD	proteins in modulating pre-B, B and T cell function, in cancer
PD	therapy etc.
PD	Claim 6, Fig 1: 58pp: English.
PD	This sequence represents human eph/ek-like kinase (HEK). HEK is
PD	expressed in both pre-B cells and T cell lines and in a number of
PD	tumours of human origin, eg. lymphoid tumours IK63, lila-1 and JM,
PD	and the epithelial tumour HeLa. This receptor-type thymidine kinase
PD	(TK) and/or its ligands are useful as agents in modulation of the

CC production and/or function of pre-B, B and T cells. The TK and its
 CC analogues have activity in transducing signals or in stimulating
 CC cellular responses such as growth and/or differentiation.
 SQ Sequence 983 AA;

Query Match 100.0%; Score 147; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 6, 2e-14;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDCQLSTLLSCSVLDSFGEILPOPSNE 29
 ID 1 MDCQLSTLLSCSVLDSFGEILPOPSNE 29

RESULT 2

ID W88378 standard; Protein; 288 AA.

AC W88378; 26-APR-1999 (first entry)

DT 26-APR-1999 (first entry)

DE Human sperm-specific antigen 4.1 (partial sequence).

KW Sperm-specific antigen 4.1; vaccine; contraceptive; human.

OS Homo sapiens.

PN WO9858954-A2.

PD 30-DEC-1998; E04016.

PF 17-JUN-1998; EP-201863.

PR 19-JUN-1997; EP-201863.

PA (ALKU) AKZO NOBEL NV.

PI Aitken RJ, Grootenhuis AJ, Van Duin M;

DR WPI: 99-095361/08.

DR N-PSDB; X06777.

PT New sperm proteins 4.1 and 6.7 - useful as a contraceptive vaccine

PS Claim 8; Page 28-29; 44pp; English.

CC This is a partial sequence of human sperm specific antigen 4.1.

CC The sequence was deduced from a cDNA clone (see X06777) isolated

CC from a human testicular cDNA library using marmoset 4.1 cDNA

CC as probe. A full-length sequence for protein 4.1 is provided in

CC W88380. Human and marmoset sperm proteins 4.1 and 6.7 (see

CC W88373-80) and nucleotide sequences (see X06772-79) encoding them

CC are new. The proteins are sperm specific and can be used in a

CC contraceptive vaccine to prevent or reduce fertility in a subject

CC without the autoimmune reactions that are a serious side-effect of

CC prior art female contraceptive vaccines. Expression vectors and

CC host cells used in production of recombinant sperm proteins are

CC provided.

CC Sequence 288 AA;

SQ Sequence 288 AA;

Query Match 37.4%; Score 55; DB 1; Length 288;
 Best Local Similarity 58.3%; Pred. No. 0.88;

Matches 14; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

OY 6 SILLLS--CSVLDSFGEILPOPS 27
 ID 6 SILLLS--CSVLDSFGEILPOPS 27

DB 26 SYLLALPAMCRVLETFLELIQOPS 49

RESULT 3

ID W88380 standard; Protein; 323 AA.

AC W88380; 26-APR-1999 (first entry)

DT 26-APR-1999 (first entry)

DE Human sperm-specific antigen 4.1.

KW Sperm-specific antigen 4.1; vaccine; contraceptive; human.

OS Homo sapiens.

PN WO9858954-A2.

PD 30-DEC-1998; E04016.

PF 17-JUN-1998; EP-201863.

PR 19-JUN-1997; EP-201863.

PA (ALKU) AKZO NOBEL NV.

PI Aitken RJ, Grootenhuis AJ, Van Duin M;

DR WPI: 99-095361/08.

DR N-PSDB; X06779.

PT New sperm proteins 4.1 and 6.7 - useful as a contraceptive vaccine

PS Claim 8; Page 32-33; 44pp; English.

CC This is a full-length sequence of human sperm specific antigen 4.1.

CC The sequence was deduced from a cDNA clone (see X06777) isolated

CC from a human testicular cDNA library using marmoset 4.1 cDNA

CC as probe. Human and marmoset sperm proteins 4.1 and 6.7 (see

CC W88373-80) and nucleotide sequences (see X06772-79) encoding them

CC are new. The proteins are sperm specific and can be used in a

CC contraceptive vaccine to prevent or reduce fertility in a subject

CC without the autoimmune reactions that are a serious side-effect of

CC prior art female contraceptive vaccines. Expression vectors and

CC host cells used in production of recombinant sperm proteins are

CC provided.

CC Sequence 323 AA;

Query Match 37.4%; Score 55; DB 1; Length 323;
 Best Local Similarity 58.3%; Pred. No. 1;

Matches 14; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

OY 6 SILLLS--CSVLDSFGEILPOPS 27
 ID 6 SILLLS--CSVLDSFGEILPOPS 27

DB 61 SYLLALPAMCRVLETFLELIQOPS 84

RESULT 4

ID R75711 standard; Protein; 983 AA.

AC R75711; 11-NOV-1995 (first entry)

DT 11-NOV-1995 (first entry)

DE Epn-related PTK Cck4.

KW Cck4; Epn; protein tyrosine-kinase; PTK; cancer; diagnosis;

KW prognosis.

OS Gallus sp.

PN WO9515375-A.

PD 08-JUN-1995.

PF 07-SEP-1994; U10140.

PR 03-DEC-1993; US-162809.

PA (LJOL-) LA JOLLA CANCER RES FOUND.

PI Pasquale EB, Sajjad FG;

DR WPI: 95-215256/28.

DR N-PSDB; Q90659.

PT Epn-related protein tyrosine kinase(s) - for monitoring and diagnosing

PT cancer.

PS Disclosure; Page 85-89; 129pp; English.

CC Probes derived from the EPN-related PTKs Cck4 (Q90659) and Cck5

CC (Q90660) were used to isolate novel cDNA clones (Q90652-58,

CC Q90661-62) from chicken embryo and embryonic brain libraries.

CC Cck4 is highly expressed in the chicken developing brain and

CC embryonic tissues and also in the adult brain and retina.

SQ Sequence 983 AA;

Query Match 34.7%; Score 51; DB 1; Length 983;
 Best Local Similarity 52.4%; Pred. No. 14;

Matches 11; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 9 LLLSCSVLDSFGEILPOPSNE 29
 ID 9 LLLSCSVLDSFGEILPOPSNE 29

DB 8 LLLLCALGSGARLSAPGNE 28

RESULT 5

ID R07640 standard; Protein; 2458 AA.

AC R07640; 20-DEC-1990 (first entry)

DT 20-DEC-1990 (first entry)

DE Deduced protein sequence of p170-2 comprising T4.

KW plasmid p170-2; soluble T4 protein; AIDS; ARC; HIV.

FT Key location/Qualifiers

FT protein 400..858

FT /label=T4 surface glycoprotein

PN WO9008198-A.

PD 26-JUL-1990.
 PF 18-JAN-1990; 000358.
 PR 18-JAN-1989; US-300096.
 PA (HARD) HARVARD COLLEGE.
 PI Letvin NA;
 DR WPI; 90-234040/33.
 DR N-PSDB; 005607.
 PT treating or preventing AIDS, ARC or HIV infection - by
 PT administering an immunologically effective amt. of soluble T4
 protein.
 PS Disclosure: Fig 1; 121pp; English.
 CC Entire sequence from T4-encoding plasmid p170-2. It is almost
 CC identical to the sequence published by Madden et al.(1985) with the
 CC exception of three codon changes. At T4 amino acid residue 3,
 CC (posn.403 of entire sequence) Lys is encoded in stead of Asn. At
 CC posn. 64, (posn.464) Arg replaces Trp and at posn. 231, (posn. 631)
 CC Ser replaces Phe.
 CC Soluble T4 can be produced by truncating the CDS to remove the
 CC transmembrane and cytoplasmic domains. The soluble forms may be
 CC modified to increase their immunogenicity by addition of an adjuvant
 CC such as incomplete Freund's adjuvant. The T4 interferes with HIV/T4
 CC interaction and elicits anti-soluble T4 antibody production.
 CC See also 005608.
 SQ Sequence 2458 AA;

Query Match 33.0%; Score 48.5; DB 1; Length 2458;
 Best Local Similarity 50.0%; Pred. No. 95;
 Matches 13; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 4 QLSILLSCSVLDSEGLI-POPSN 28

DB 2268 QHCIIILSCHPXDAFLXIVSTQPSH 2293

RESULT 6
 ID R04031
 AC R04031;
 DT 29-MAY-1990 (first entry)
 DE Full length T4 encoded by plasmid p170-2.
 KM Soluble T4; p170-2; anti-retroviral agent; AIDS; ARC; HIV; AZT.
 FH Key Location/Qualifiers
 FT misc_difference 425
 FT /note="Aasp of Madden et al replaced by Lys"
 FT misc_difference 423
 FT /note="Trp of Madden et al replaced by Arg"
 FT misc_difference 653
 FT /note="Phe of Madden et al replaced by Ser"
 PN W08911860-A.
 PD 14-DEC-1989.
 PF 08-JUN-1989; 002453.
 PR 10-JUN-1988; US-204645.
 PR 20-APR-1989; US-341080.
 PA (GENO-) General Hospital Corp. (BIOJ) Biogen Inc.
 PI Fisher RA, Schooley RT, Hirsch MS, Johnson VA, Walker BD;
 DR WPI; 90-007302/01.
 DR N-PSDB; 003005
 PT Combinations of soluble T4 protein and anti-retroviral agent -
 PT having synergistic activity in treatment and prevention of AIDS,
 PT ARC and HIV infection.
 PS Disclosure: fig 1; 100pp; English.
 CC The sequence differs from that determined by PJ Madden et al., [Cell, 42
 CC pp. 93-104 (1985)] in three places due to three nucleotide substitutions.
 CC The Asp reported at position 3 by Madden et al. was the result of a
 CC sequencing error [DR Littman et al. Cell, 55, p.541 (1988)].
 CC X = stop codon.
 CC The sequence was deduced from the cDNA insert of p170-2.
 CC Soluble T4 constructs may be produced by truncating this sequence to give
 CC fragments from position 400 to 799, removing the transmembrane and
 CC intracytoplasmic domains whilst retaining the extracellular region
 CC responsible for HIV binding. The sol. T4 is combined with an anti-viral
 CC agent such as AZT.

CC See also 003006.
 SQ Sequence 2458 AA;

Query Match 33.0%; Score 48.5; DB 1; Length 2458;
 Best Local Similarity 50.0%; Pred. No. 95;
 Matches 13; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 4 QLSILLSCSVLDSEGLI-POPSN 28

DB 2268 QHCIIILSCHPXDAFLXIVSTQPSH 2293

RESULT 7
 ID W58379 standard; Protein: 242 AA.
 AC W58379;
 DT 08-SEP-1998 (first entry)
 DE Human immunomodulatory protein BL-1.3.
 KM Human; BL-1; immunotherapy; vaccine; immunomodulatory protein; HIV;
 KW infection; cancer; autoimmune disease.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_difference 1.242
 FT /note="the protein is decoded from the third reading
 FT frame of BL-1 cDNA and so contains stop codons
 FT (i.e. all X's are stop codons)"
 PN W09817799-A1.
 PD 30-APR-1998.
 PF 23-OCT-1997; 019502.
 PR 23-OCT-1996; US-028613.
 PA (APOL-) APOLLON INC.
 PA (UNYP-) UNIV PENNSYLVANIA.
 PI Bagarazzi ML, Boyer JD, Kim JJ, Wang B, Weiner DB;
 DR WPI; 98-261495/23.
 DR N-PSDB; V30915.
 PT New compositions for immuno-therapy and protection - comprise
 PT nucleotide sequences encoding an immuno-modulating protein and an
 PT antigen, used for e.g. infections, cancer or auto-immune diseases
 PS Example 6; Fig 14; 136pp; English.
 CC The present sequence represents the protein from the third reading
 CC frame of human immunomodulatory protein BL-1 encoding cDNA (given in
 CC V30915). The present invention describes a plasmid which comprises a
 CC nucleotide sequence (NS) that encodes:(a) an immunomodulating protein
 CC selected from interleukin (IL)-12, granulocyte-macrophage colony
 CC stimulating factor (GM-CSF), IL-1, tumour necrosis factor (TNF)-alpha,
 CC TNF-beta, IL-2, IL-4, IL-5, IL-10, IL-15, IL-18 and BL-1 operably
 CC linked to regulatory elements. Products of the present invention can be
 CC used to induce an immune response to an antigen such as a pathogen
 CC antigen, a hyperproliferative disease-associated antigen, and antigen
 CC linked to cells associated with autoimmune diseases or an allergen.
 CC They can be used for immunotherapy or to provide a protective immune
 CC response. In particular, they can be used for treating subjects with
 CC an allergic reaction, pathogen infection, hyperproliferative disease
 CC such as cancer or psoriasis or autoimmune diseases e.g. rheumatoid
 CC arthritis, multiple sclerosis, Sjogren's syndrome, sarcoidosis, insulin
 CC dependent diabetes mellitus, autoimmune thyroiditis, ankylosing
 CC spondylitis, scleroderma, polymyositis, dermatomyositis, psoriasis,
 CC vasculitis, Wegener's granulomatosis, Crohn's disease and ulcerative
 CC colitis, Grave's disease, autoimmune thrombocytopenia, asthma and
 CC pernicious anaemia.
 SQ Sequence 242 AA;

Query Match 32.3%; Score 47.5; DB 1; Length 242;
 Best Local Similarity 50.0%; Pred. No. 9.6;
 Matches 13; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 4 QLSILLSCSVLDSEGLI-POPSN 28

DB 149 QHCIIILSCHPXDAFLXIVSTQPSH 174

```

RESULT      8
W83902
ID    W83902 standard; Protein; 189 AA.
AC    W83902.
DT    15-FEB-1999   (first entry)
DE    Porcine Interferon-alpha 1.
KW    Interferon-alpha 1; Leukocyte Interferon; virucide; antiviral;
KM    antitumour; pig.
OS
SUS scrofa.
FH Key                                     Location/Qualifiers
FT Peptide                               1..23
                                         /label= sig_peptide
FT Protein                              24..189
                                         /label= Mat_protein
                                         /note= "Claim 1"
FN US5831023-A.
PD 03-NOV-1998.
PE 19-MAY-1995; 444A54.
PR 02-OCT-1987; US-104461.
PR 08-MAR-1982; US-355298.
PR 01-NOV-1982; US-438128.
PR 23-AUG-1991; US-749371.
PR 21-SEP-1992; US-949327.
PR 19-MAY-1995; US-444A54.
PA (GETH ) GENENTECH INC.
PI Capon DJ, Goeddel DV.
PT N-Psdb; V68167.
DR Animal interferon polypeptides - useful as antiviral and antitumour agents
PS Claim 1; Fig 14A; 48bp; English.
CC This is the amino acid sequence of porcine interferon alpha-1, as deduced from the open reading frame of a cDNA clone (see V68167). The invention provides bovine, murine, porcine, feline, laprine and rat mature alpha, beta and gamma interferons and their cDNAs (see W83895-905, W83918 and W70582-85). Recombinant DNA methods can be utilised to prepare these non-human animal interferons in amounts sufficient to enable the determination of their biochemical properties and bioactivities, and hence to allow efficient production for commercial or biological exploitation. CC Interferons are useful as antiviral and antitumour agents. SO Sequence 189 AA.

Query Match          31.3%; Score 46; DB 1; Length 189;
Best Local Similarity 47.6%; Pred. No. 12;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0.

OY 5 LSIILLISGVDSFGELIPQ 25
     |:-|::|||:-:|-|:-||
DB 8 LTALVLSCNAICSLGCDLPQ 28

RESULT      9
ID    W73231 standard; Protein; 189 AA.
AC    W73231.
DT    01-MAR-1999   (first entry)
DE    Porcine Interferon-alpha 1.
KW    Interferon-alpha 1; Leukocyte Interferon; virucide; antiviral;
KM    antitumour; pig.
OS
SUS scrofa.
FH Key                                     Location/Qualifiers
FT Peptide                               1..23
                                         /label= sig_peptide
FT Protein                              24..189
                                         /label= Mat_protein
FN US5827694-A.
PD 27-OCT-1998.
PE 19-MAY-1995; 446I71.
PR 02-OCT-1987; US-104461.
PR 08-MAR-1982; US-395298.
PR 01-NOV-1982; US-438128.
```

	PR	23-AUG-1991;	US-749371.
	PR	21-SEP-1992;	US-949327.
	PR	19-MAY-1995;	US-446171.
	PA	(GETH) GENENTECH INC.	
	P1	Capon DJ, Goeddel DV,	
	DR	WPI; 98-593994/50.	
	DR	N-PSDB; V08184.	
PT	DNA encoding non-human interferon polypeptide(s) - useful for		
PT	producing recombinant polypeptide(s) to determine their		
PT	bioactivity		
PS	Claim 6; Fig 14A; 59pp; English.		
CC	This is the amino acid sequence of porcine interferon alpha-1,		
CC	deduced from a cDNA (see V08184). The invention provides		
CC	bovine, porcine, feline and rabbit mature interferons and their		
CC	propeptides (see W324-35). Recombinant DNA methods can be used		
CC	to prepare these non-human animal interferons in amounts sufficient		
CC	to enable the determination of their biochemical properties and		
CC	biocativities, and hence to allow efficient production for		
CC	commercial or biological exploitation. Interferons are useful as		
CC	antiviral and antitumour agents. A replicable expression vehicle		
CC	comprising claimed non-human animal interferon nucleic acid, a		
CC	process for producing such an interferon, and a microorganism		
CC	(especially Escherichia coli) or cell culture transfected with the		
CC	nucleic acid are claimed.		
SQ	Sequence 189 AA;		
OY	5 LSTLLLSGVDSFGELIPQ 25		
	: : : : : : : : : : : :		
Db	8 LTALVLSGNMAICSLGCDLPQ 28		
RESULT	10		
R72361	R72361 standard; Protein; 490 AA.		
ID	R72361; (first entry)		
AC	10-NOV-1995		
DT	Human cytochrome P450 molecular species 2C9 protein.		
DE	Human cytochrome P450; amplification; PCR; primer; expression vector;		
KM	yeast NADPH-P450 reductase; safety; fusion protein; metabolite;		
KW	carcinogen; mutagen; liver metabolism.		
OS	Homo sapiens.		
PN	EP-644267-A.		
PD	22-MAR-1995		
PF	20-JUL-1994; 111298.		
PR	20-JUL-1993; JP-201120.		
PR	21-JUL-1993; JP-180246.		
PR	30-JUL-1993; JP-208279.		
PA	(HAYA/) HAYASHI K.		
PA	(SUMO) SUMITOMO CHEM CO LTD.		
F1	Hayashi K, Kaneko H, Komai K, Nakatsuka I, Sakaki T;		
F1	Yabusaki Y;		
DR	WPI; 95-116991/16.		
DR	N-PSDB; Q87715.		
PT	Evaluation of safety of a chemical cpd. - using recombinant yeast		
PT	expressing human cytochrome p450 and a yeast NADPH-P450 reductase		
PS	Examples; Page 23-25; 124pp; English.		
CC	The amino acid sequence of the human cytochrome P450 species 2C9. The		
CC	cDNA was amplified by PCR using the primers Q87735-8. The product was		
CC	cloned into the yeast expression vectors PAH5N or PAHR to produce the		
CC	vectors pPC9 for the expression of the cytochrome P450 alone or p2C9R		
CC	for co-expression with the yeast NADPH-P450 reductase.		
CC	The vectors are used in a method for evaluating the safety of a chemical		
CC	compound by reacting the chemical compound with recombinantly produced		
CC	human cytochrome P450 molecular species 1A2 (Q87714), 2C9 , 2E1 (Q87716)		
CC	or 3A4 (Q87717), or their auxiliary species and variants (Q87718-32), and		
CC	yeast NADPH-P450 reductase, either as a fused protein or in cell		
CC	extracts, and analysing the resulting metabolite to assess the safety of		
CC	the chemical compound. The method is useful for determining whether the		

CC Chemical compound, or its metabolite, will be converted into a
 CC carcinogenic or mutagenic form through metabolism in the liver.
 SQ Sequence 490 AA;

Query Match 31.0%; Score 45.5; DB 1; Length 490;
 Best Local Similarity 38.2%; Pred. No. 43;
 Matches 13; Conservative 6; Mismatches 8; Indels 7; Gaps 1;

OY 1 MDCQSLILLSCSYLDSF-----GELIPQPS 27
 ||:::|||||:|:|:|:
 DB 1 MDSTVSLVCLSCILLSLIMROSSGRKLPPEPT 34

RESULT 11

R81465
 ID R81465 standard; Protein: 490 AA.

AC R81465;
 DT 01-AUG-1996 (first entry)
 DE Human derived cytochrome P4502C9.
 KW Human derived cytochrome; P4502C9; commercial cDNA library; yeast;
 KW transfection; recombinant production; expression vector; mammal;
 KW immunisation; sensitisation; antibody; determination; detection;
 KW non-cross reactive.
 OS Homo sapiens.
 PN J08027196-A.
 PD 30-JAN-1996.
 PE 13-JUL-1994; 161551.
 PR 13-JUL-1994; JP-161551.
 RA (SUMO) SUMITOMO CHEM CO LTD.
 DR WPI; 96-136337/14.
 DR N-PSDB; T17404.
 PT Antibody recognising human derived cytochrome P4502C9 - allows
 PT specific detection of cytochrome P450 species in humans
 PS Example 1: Pages 11-13; 13pp; Japanese.
 CC The present sequence is the human derived cytochrome (HDC)
 CC P4502C9, which was obtd. from a commercial cDNA library. Yeast
 CC were transfected with an expression vector contg. the HDC cDNA,
 CC cultured and then disrupted to give a microsomal fraction. The
 CC HDC was purified from the fraction, and used to immunise and
 CC sensitise a mammal. Blood was drawn from the mammal, and an
 CC anti-HDC antibody isolated. The antibody obtd. recognises HDC
 CC P4502C9, partic. at a serum dilution rate of 1:10000, and is
 CC substantially without cross reaction to other HDC P450 spp.
 SQ Sequence 490 AA;

Query Match 31.0%; Score 45.5; DB 1; Length 490;
 Best Local Similarity 38.2%; Pred. No. 43;
 Matches 13; Conservative 6; Mismatches 8; Indels 7; Gaps 1;

OY 1 MDCQSLILLSCSYLDSF-----GELIPQPS 27
 ||:::|||||:|:|:|:
 DB 1 MDSTVSLVCLSCILLSLIMROSSGRKLPPEPT 34

RESULT 12

R93168
 ID R93168 standard; Protein: 490 AA.

AC R93168;
 DT 11-OCT-1996 (first entry)
 DE Human cytochrome P450 amplified species 2C9 protein.
 KW Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
 KW liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter;
 KW evaluation; safety; fusion protein; metabolite; detoxification;
 KW carcinogenic.
 OS Homo sapiens.
 PN J08056695-A.
 PD 05-MAR-1996.
 PE 15-JUL-1994; 164184.
 PR 20-JUL-1993; JP-201120.
 PR 30-JUL-1993; JP-208279.
 PR 17-JUN-1994; JP-136053.

PA (SUMO) SUMITOMO CHEM CO LTD.
 DR WPI; 96-182311/19.
 DR N-PSDB; T28381.

PT Novel method for the evaluation of the safety of a cpd. - using a
 PT human cytochrome P450 and yeast NADPH reductase to determine whether
 PT the analyte cpd. is detoxified or metabolised to a carcinogen
 PS Example 1; Page 20-22; 74pp; Japanese.
 CC This is the amino acid sequence of the human cytochrome P450 molecular
 CC species 2C9 protein. The corresp. gene was amplified from a human liver
 CC derived cDNA library as 2 fragments of 0.9 and 0.6 kb using primers
 CC T26925-8. The prod. was cloned into the yeast expression vector PAH5N
 CC to generate plasmid p2C9 for prodn. of the cytochrome only or into the
 CC vector PAHRR to generate the plasmid p2C9R for co-prodn. with the yeast
 CC NADPH-P450 reductase. The sequence is placed under control of the yeast
 CC ADH gene promoter and terminator.
 CC The vectors are used in a method for evaluating the safety of a cpd. by
 CC reacting the test cpd. with recombinantly produced human cytochrome P450
 CC mol. species 1A2 (T28380), 2C9, 2E1 (T28382), 3A4 (T28383) or their
 CC variants (T28384-98) together with yeast NADPH-P450 reductase (either as
 CC a fused protein or as a cell extract) and analysing the resultant
 CC metabolite. The cpd. is considered "safe" if it is detoxified or not
 CC rendered carcinogenic or "unsafe" if it is not detoxified or is
 CC metabolised to a carcinogenic cpd.
 SQ Sequence 490 AA;

Query Match 31.0%; Score 45.5; DB 1; Length 490;
 Best Local Similarity 38.2%; Pred. No. 43;
 Matches 13; Conservative 6; Mismatches 8; Indels 7; Gaps 1;

OY 1 MDCQSLILLSCSYLDSF-----GELIPQPS 27
 ||:::|||||:|:|:|:
 DB 1 MDSTVSLVCLSCILLSLIMROSSGRKLPPEPT 34

RESULT 13

W27850
 ID W27850 standard; Protein: 114 AA.

AC W27850;
 DT 21-JUL-1998 (first entry)
 DE Staphylococcus aureus protein of unknown function.
 KW Staphylococcus aureus protein; ribozyme; antisense sequence; control;
 KW Staphylococcal gene; regulatory element; bacterial gene expression;
 KW vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
 KW toxic shock syndrome.
 OS Staphylococcus aureus.
 FH Key Location/Qualifiers
 FT Misc_difference 111
 FT Misc_difference 111
 FT Misc_difference 112 /note= "not specified"
 FT Misc_difference 112 /note= "not specified"
 FT W09730070-A1.
 PN W09730070-A1.
 PD 21-AUG-1997.
 PE 19-FEB-1997; U02318.
 PR 20-FEB-1996; US-011888.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,
 PI Pratt JM, Reichard RW, Rosenberg M, Ward JM.
 DR WPI; 97-424969/39.
 DR N-PSDB; T83813.
 PT Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used
 PT to isolate antimicrobial compounds, and in vaccines against S.
 PT aureus infection
 PS Claim 6; Pages 309-310; 989pp; English.
 CC The present sequence represents a Staphylococcus aureus protein of
 CC unknown function. The DNA sequence was isolated from a library of
 CC clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can
 CC be used in the construction of ribozymes and antisense sequences to
 CC control the expression of Staphylococcal genes. The DNA sequence is
 CC also useful as a source of regulatory elements for the control of
 CC bacterial gene expression. The present protein may be used to produce
 CC vaccines to enable a host to produce specific antibodies with
 CC antibacterial action. These vaccines and antibodies would protect

CC a host against invasion by *S. aureus*, and conditions relating to
CC Staphylococcal infection, e.g. Staphylococcal food poisoning, scalded
CC skin syndrome, and toxic shock syndrome.
SQ Sequence 114 AA;

Query Match	30.6%	Score 45;	DB 1;	Length 114;
Best Local	Similarity 57.1%;	Pred No. 9.6;		
Matches	8;	Conservative	3;	Mismatches 3;
				Indels 0;
				Gaps 0

```

Qy      12 SC$VLD$F$GELIPQ 25
          | | | | | | | |
Db      97 SASILDIFGRLLPR 110

```

RESULT	14
R55214	
ID	R55214 standard; Protein; 128 AA
NC	R55214.

DT 01-FEB-1995 (first entry)
DE Murine variable region light chain from 2B5.
KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
KW cell lysate.
OS Mus musculus.
PN W09411026-A.
PD 26-MAY-1994.
PE 12-NOV-1993. U10953.
PR 13-NOV-1992; US-978891.
PR 03-NOV-1993; US-149099.
PA (IDEC-) IDEC PHARM CORP.
PI Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH;
PI Refine; 94-183162/22.
DR WPI: 94-183162/22.
DR N-PSBD: Q65630.
PT Treating B cell lymphoma with chimeric antibody - against CD20,
PT causing rapid depletion of peripheral B cells, also new
PT antibodies and hybridomas
PS Disclosure: Fig 4: 101pp: English.
CC The sequence is the murine variable region light chain derived from
CC murine anti-CD20 monoclonal antibody 2B5.
CC See also Q65629-35.
CC Sequence 128 AA;
SQ

Query Match	30.6%	Score 45	DB 1	Length 128
Best Local Similarity	44.0%	Pred. No. 11		
Matches 11, Conservative	7	Mismatches 5	Indels 2	Gaps 1

```
QY      1 MDCQLSIL--LLSCSVLDSFGELI 23
        |||::|||::|||::|||::
DB      1 MDFOVQIIISFLLISASVIMSRGQIV 25
```

RESULT	15
W41568	
ID	W41568 standard; Protein; 908 AA

DT 22-JUN-1998 (first entry)
 DE Human metabotropic glutamate receptor.
 KW Metabotropic glutamate receptor; mGluR8; human; agonist; antagonist;
 KW neurodegenerative disease; antipsychotic; anticonvulsant; analgesic;
 KW anxiolytic; antidepressant; antileptic; therapy.
 OS Homo sapiens.
 PN EP-816498-A2.
 PD 07-JAN-1998.
 PF 02-JUL-1997; 304821.
 PR 03-JUL-1996; US-021243.
 PA (ELIL) LILLY & CO ELI.
 PI Belagaje RM, Wu S;
 DR WPI; 98-054913/06.
 DR N-PSDB: V04206-07.
 PT Human metabotropic glutamate receptor protein - agonists and
 PT antagonists of which are useful to treat neurodegenerative diseases

PS Claim 1, Page 46-48: 56pp: English.
CC This protein comprises a novel human metabotropic glutamate
CC receptor, designated mgluR8. Its amino acid sequence was deduced
CC from cDNA clones isolated from a human foetal retina cDNA library.
CC The metabotropic glutamate receptors are linked to multiple second
CC messenger pathways. They function to modulate the presynaptic
CC release of glutamate, and the postsynaptic sensitivity of the
CC neuronal cell to glutamate excitation. Host cells transfected with
CC an expression vector comprising nucleic acids encoding mgluR8,
CC especially RGR-18 host cells transfected with pgr-h-mgluR8, are
CC claimed. They can be used in claimed methods for evaluating the
CC effectiveness of a test compound for the treatment or prevention of
CC a condition associated with a deficiency or excess of stimulation of
CC of the human mgluR8 receptor. mgluR agonists and antagonists can
CC be used to treat neurodegenerative diseases, or as antidepressant, and
CC anticonvulsant, analgesic, anxiolytic, antidepressant and
CC antileptic agents.
CC Sequence 908 AA:

Query Match	30.68	Score 45	DB 1	Length 908
Best Local Similarity	37.98	Pred. No. 1e+02		
Matches 11; Conservative	7	Mismatches	9	Indels 2; Gaps 1

```
QY      3  CQL--SILLLSCVLDSEFGLIPQPSNE 29
          | | ||||:::| | : :| |
Db      751 CSLGYSLIMVCTCTVYANKTRGPETENE 779
```

Search completed: May 9, 2000, 21:52:05
Job time: 3757 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 22:31:13 ; Search time 71.69 Seconds
(without alignments)
262.094 Million cell updates/sec

Title: US-09-104-340-4
Percent score: 1466
Sequence: 1 MCOQLSILLLLSCSVLDSFG.....VPIGKSCSNANGYERGFMCQ 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 6934122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL_12.*

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	977	66.6	985	13	091694 xenopus lae
2	977	66.6	986	13	091845 xenopus lae
3	934.5	63.7	993	13	042422 gallus gall
4	851.5	58.1	981	13	013146 brachydanio
5	838.5	57.2	880	13	073879 brachydanio
6	768.5	52.4	985	13	091571 xenopus lae
7	767	52.3	1055	4	043477 homo sapien
8	739.5	50.4	943	4	043569 homo sapien
9	724.5	49.4	984	4	095142 xenopus lae
10	724.5	49.4	974	13	091735 xenopus lae
11	713.5	48.7	973	4	095143 homo sapien
12	679	46.3	988	13	007498 gallus gall
13	594.5	40.6	952	13	007494 gallus gall
14	589	40.2	938	11	060669 mus musculu
15	563.5	38.4	902	13	091736 xenopus lae
16	534	36.4	976	13	073878 brachydanio
17	528.5	36.1	1006	4	015197 homo sapien
18	524.5	35.8	1014	11	008644 mus musculu
19	407.5	27.8	1035	5	09x216 drosophila
20	407.5	27.8	1080	5	09y110 drosophila

ALIGNMENTS

RESULT 1
ID 091694 PRELIMINARY; PRT; 985 AA.

AC 091694;
DT 01-NOV-1996 (TRENDEL. 01, Created)
DT 01-NOV-1996 (TRENDEL. 01, Last sequence update)
DT 01-NOV-1999 (TRENDEL. 12, Last annotation update)
DE TYROSINE-PROTEIN KINASE RECEPTOR PAG PRECURSOR (EC 2.7.1.112) (PAGLIACCIO).
GN PAG.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae.
CC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-NEURAL CREST;
RX MEDLINE; 95001564.
RA WINNING R.S., SARGENT T.D.;
RT "Pagliaccio, a member of the Eph family of receptor tyrosine kinase genes, has localized expression in a subset of neural crest and neural tissues in Xenopus laevis embryos."
RT Mech. Dev. 46:219-229(1994).
RL -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY (BY STIMILARITY). MAY PLAY A ROLE IN THE DIFFERENTIATION OF CRANIAL NEURAL CREST AND OTHER TISSUES.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: LOCALIZED EXPRESSION IN A SUBSET OF NEURAL CREST AND NEURAL TISSUES IN EMBRYOS.
CC -1- DEVELOPMENTAL STAGE: PRESENT TRANSIENTLY IN VISCERAL ARCH 3, ALSO EXPRESSED IN THE FOREBRAIN, RHOMBOMERES R3 AND R5 OF THE HINDBRAIN AND IN THE PROMPHOS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPH FAMILY.
DR EMBL; U26099; AAA64464.1; -.
DR HSSP; P00523; 2PTK.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR_1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

RESULT	ID	PRELIMINARY:	PRT:	993 AA.
042422	042422			
AC	042422;			
AD	01-JAN-1998 (Tremblrel. 05, Created)			
DT	01-JAN-1998 (Tremblrel. 05, last sequence update)			
DT	01-NOV-1999 (Tremblrel. 12, last annotation update)			
DE	EPH-LIKE RECEPTOR TYROSINE KINASE PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEPHA7).			
GN	CEPHA7.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
OC	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EMBRYO:			
RX	MEDLINE; 98092111.			
RA	ARUOD M., NIEHO M.A.:			
RT	"The expression of chick EphA7 during segmentation of the central and peripheral nervous system.";			
RT	Mech. Dev. 68:173-177(1997)."			
RL	-1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN FAMILY.			
CC	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM, EXPRESSION IS RESTRICTED TO PROSOMERES 1 AND 2 IN THE DIOCEPHALON AND ALL THE RHOMOMERES IN THE HINDBRIN DURING SEGMENTATION STAGES. LATER ON A SUPERIMPOSED PATTERN APPEARS THAT CORRELATES WITH THE FORMATION OF SEVERAL AXONAL TRACTS. IN THE SOMATIC MESODERM, THE EXPRESSION CORRELATES WITH SEGMENTATION AND THE GUIDANCE OF BOTH NEURAL CREST AND MOTOR AXONS THROUGH THE SCLEROTOMES.			
CC	-1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
DR	EMBL; Y14271; CAA74643.1; -.			
DR	HSSP; P00523; 2PTK.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.			
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.			
DR	PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.			
DR	PFAM; PF00041; fn3; 2.			
DR	PFAM; PF00069; pkinase; 1.			
DR	PFAM; PF00536; Sam; 1.			
DR	PFAM; PF01404; EPH_Lbd; 1.			
DR	PRINTS; PR00109; TYRKINASE.			
DR	PRINTS; PR00014; ENTPEPIL.			
KM	Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain.			
FT	SIGNAL	1	30	POTENTIAL.
FT	CHAIN	31	993	EPH-LIKE RECEPTOR TYROSINE KINASE.
FT	DOMAIN	31	551	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	552	572	POTENTIAL.
FT	DOMAIN	573	993	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	677	116	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	192	328	CYS-RICH.
FT	DOMAIN	329	438	FIBRONECTIN TYPE-III (BY SIMILARITY).
FT	DOMAIN	439	536	FIBRONECTIN TYPE-III (BY SIMILARITY).
FT	DOMAIN	628	889	FIBRONECTIN TYPE-III (BY SIMILARITY).
FT	NP_BIND	634	642	ATP (BY SIMILARITY).
FT	DISULFID	74	109	ATP (BY SIMILARITY).
FT	ACT_BINDING	660	660	ATP (BY SIMILARITY).
FT	MOD_SITE	753	753	BY SIMILARITY.
FT	ACT_SITE	753	753	BY SIMILARITY.
FT	MOD_RES	786	786	PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	CARBOHYD	343	343	POTENTIAL.
FT	CARBOHYD	410	410	POTENTIAL.
QO	SEQUENCE	993 AA;	111366 MM;	66B6FD17 CRC32;

Query Match

63.7%; Score 934.5; DB 13; Length 993;

Best Local Similarity 65.4%; Pred. No. 2,4e-79;
Matches 176; Conservative 43; Mismatches 41; Indels 9; Gaps

```
QY      10 LILCSV-----LDSGELIPDPSNVNLLDSTKTIGELGMISTYSHGWEEISGDENHTPI 65
           ::::| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       11 IMLCSWMLRFRAHNGE--AQAKAEVILLDSKAOQTLEWMISSPENGWEELISGLDENHTPI 68
QY      66 RTYOVCNNMHDSONNMWLRTMNVPNSAKIYVELKFLRDCNSTPLVLGCKETFNLYYM 125
           ||||| | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db       69 RTYOVCQVMESNONNMWLTMTNIASMQRLFVELKFLTRDCNSTLPGLCTKEFFNLYY 128
QY     126 ESDDHGVKFEEHFQFKDTIAADESTOMDLGRILKLWTEIREVPVNKKGFYLAFOD 183
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     129 ETVDITGNIRPENRYVKIDITIADESTOGDLGERAKKLNTVEAIEPLSKGFYLAFO 188
QY     186 VGCALVALSVRVYEKKCPFTYKNLAMEPDIVP-MDSOSLIVEKRSQVNSKE--EDPPRM 242
           ||||| | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db     189 VGACIALVSXVVYKKCKMSIENLAIFPDIVTGEFSFLVEVRGTQVSAADEEAENS PKM 248
QY      243 YCSTEGEWLVPIGKCSNAGYEENFGMCQ 271
           ::||| | | | | | | | | | | | | | | | | | | | | | | | |
Db     249 HCSAGEWLVPIGKCICKACKAGYQKGPCE 277

RESULT    4
013146    PRELIMINARY;          PRT;   981 AA.
ID         013146
AC         013146;
DT      01-JUL-1997 (TREMBLrel. 04, Created)
DI      01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT      01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE      Eph-like kinase 1 precursor (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ZEK1).
DN
GN        ZEK1.
OS        Brachydanio rerio (Zebrafish) (Zebra danio).
OC        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinidae; Rasbora; Danio.
RC        [1]
RP        SEQUENCE FROM N.A.
RX        MEDLINE: 97329578.
RA        BOVENKAMP D.E., GREER P.;
RT        "Novel Eph-family receptor tyrosine kinase is widely expressed in the developing zebrafish nervous system.";
RL        Dev. Dyn. 209:166-181(1997).
CC        -1 FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. MAY PLAY A ROLE IN EARLY PATTERN FORMATION WITHIN THE DEVELOPING NERVOUS SYSTEM.
CC        -1 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.
CC        -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC        -1 TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE DEVELOPING ZEBRAFISH NERVOUS SYSTEM.
CC        -1 SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC        -1 SIMILARITY: CONTAINS 1 IMMUGLOBULIN-LIKE C2-TYPE DOMAIN.
CC        -1 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR        EMBL: U98295; AAC60220.1; -.
DR        HSSP: P00523; 2PTR.
DR        ZFIN: ZDB-GENE-990415-58; zek1.
DR        PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR        PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR        PROSITE: PS00790; RECEPTOR_TYR_KIN_V.1; 1.
DR        PROSITE: PS00790; RECEPTOR_TYR_KIN_V.2; FALSE_NEG.
DR        PFAM: PF00069; Pkinase; 1.
DR        PFAM: PF00536; SAM; 1.
DR        PFAM: PF01404; Eph_Ibd; 1.
DR        PFAM: PF00041; fn3; 2.
DR        PRINTS: PR00109; TYRKINASE.
DR        PRINTS: PR00014; TRYPEPTII.
KW        Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain.
XT        SIGNAL
            1
            20
BY SIMILARITY.
```

FT SIGNAL

20 BY SIMILARITY

coprotein; signal; immunoglobulin domain.
BY SIMILARITY.

```

FT CHAIN 21 981 EPH-LIKE KINASE 1.
FT DOMAIN 21 345 EXTRACELLULAR (POTENTIAL).
FT TRAMSEM 546 566 POTENTIAL.
FT DOMAIN 567 981 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 64 113 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 192 325 CYS-RICH.
FT DOMAIN 326 438 FIBRONECTIN TYPE-III.
FT DOMAIN 439 532 FIBRONECTIN TYPE-III.
FT DOMAIN 626 887 PROTEIN KINASE.
FT NP_BIND 632 640 ATP (BY SIMILARITY).
FT DISULFID 71 106 ATP (BY SIMILARITY).
FT BINDING 658 658 ATP (BY SIMILARITY).
FT ACT_SITE 751 751 BY SIMILARITY.
FT MOD_RES 784 784 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 340 340 POTENTIAL.
FT CARBOHYD 410 410 POTENTIAL.
FT CARBOHYD 435 435 POTENTIAL.
FT CARBOHYD 485 485 POTENTIAL.
FT VARIANT 141 141 S->N.
SQ SEQUENCE 981 AA; 109654 MW; 10D38182 CRC32;

```

Query Match Best Local Similarity 58.1%; Score 851.5; DB 13; Length 981;

Matches 156; Conservative 44; Mismatches 57; Indels 9; Gaps 2;

```

QY 9 LLTSCSVLDSFGELIPQSPNEVNLDSKTIQELGWSYPSHGWEISGVDEHYTPRTY 68
DB 15 ILVLCQALRRY-----PDNEVTLTLDMSAPAGDLGWEAYSEGEWEISVDEHNIPRTY 68
QY 69 QVCNVNDHSGNNMLRTNWPVRNSAKIYVELKFTLRDONSIPLYLCKTETNLYVESD 128
DB 69 QVCNVNEANQNNMLRTGLQREGAORYVEIKFTLRDONSIPGVGCKETFNMYHESN 128
QY 129 DDHGV---KFEHQFTKIDTIADESEFTQMDLDRILKLTETREVGVPKKGFTYAFOD 185
DB 129 NAAAPLPHRTRESQYIKIDTIADESTQTDVGDWRKMLTEVRDLSGSKRGILYAFOD 188
QY 186 VGACVALVSRYVFKKCPFTVKNLAMFPDTPVNDOSLVEVRSGCVNNSKEEDPPRMVCS 245
DB 189 LGACIALVSRYVFKKCPFTVKNLAMFPDTPVNDOSLVEVRSGCVNNSKEEDPPRMVCS 248
QY 246 TEGEWLVPYIKKSCNMGYERGFMCQ 271
DB 249 ADGGWLVPYIGRCVCRPGFEEDGHQ 274

```

```

RESULT 5
073879 PRELIMINARY; PRT; 880 AA.
AC 073879;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE EPH-LIKE RECEPTOR TYROSINE KINASE RTK4 (FRAGMENT).
GN RTK4.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinoidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RA COOKE J.E.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA COOKE J.E.; XU Q.; WILSON S.W.; HOLDER N.;
RL Dev. Genes. Evol. 206:515-531(1997).
DR EMBL; AU050303; CA065303.1; -.
DR HSSP; P00523; 2PTK.
DR ZFIN; ZDB-GENE-990415-61; rtk4.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

```

```

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PFAM; PF01404; Eph_Lbd; 1.
DR PFAM; PF00069; pkinase; 1.
DR PFAM; PF00041; f3; 2.
FT NON_TER 1 880
FT NON_TER 880 880
SQ SEQUENCE 880 AA; 98862 MW; 7C139606 CRC32;

```

Query Match Best Local Similarity 57.2%; Score 838.5; DB 13; Length 880;

Matches 149; Conservative 36; Mismatches 33; Indels 1; Gaps 1;

```

QY 54 EISGVDEHYTPRTYQVCNVNDHSGNNMLRTNWPVRNSAKIYVELKFTLRDONSIPLYL 113
DB 1 EVISIMDEKNIPRTYQVCNVNDSQNNMLRTNHPHIGQAQRIYELKFTLRDONSIPGYI 60
QY 114 GTCKETFNLYMESDDHGVKREHQFTKIDTIADESEFTQMDLDRILKLTETREVGVP 173
DB 61 GTCKETFNLYMESDDHGVKREHQFTKIDTIADESEFTQMDLDRILKLTETREVGVP 120
QY 174 VNKKGFTYAFODVGACVALVSRYVFKKCPFTVKNLAMFPDTPVNDOSLVEVRSGCVN 232
DB 121 LSRAGFTYAFODVGACIALVSRYVFKKCPFTVKNLAMFPDTPVNDOSLVEVRSGCVN 180
QY 233 NSKEDPPRMVCSKEDEWLVPIKSCNMGYERGFMCQ 271
DB 181 HSEGEVPMKYGADDEWLVPIKNCNMGYERNGCQ 219

```

```

RESULT 6
091571 PRELIMINARY; PRT; 985 AA.
AC 091571;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR XEK PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR XEK).
GN XEK.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodidae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 95215070.
RA JONES T.L.; KARAVANOVA I.; MAENO M.; ONG R.C.; KUNG H.-F.; DAAR I.O.;
RT "Expression of an amphibian homolog of the Eph family of receptor
RT tyrosine kinases is developmentally regulated."
RL Oncogene 10:1111-1117(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. MAY PLAY A
CC ROLE IN THE DEVELOPMENT OR FUNCTION OF THE CENTRAL NERVOUS SYSTEM.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DEVELOPMENTAL STAGE: MATERNALLY EXPRESSED, IT DECREASES AT MID
CC BLASTULA TRANSITION AND REAPPEARS AT LATE NEURULATION. EXPRESSED
CC AT HIGHER LEVELS IN THE ANTERIOR AND DORSAL REGIONS OF EMBRYONIC
CC STAGES 16, 24 AND 37. IN ADULT IT APPEARS TO BE UBQUITOUSLY
CC EXPRESSED WITH HIGHER EXPRESSION IN BRAIN AND OVARY. EXPRESSION IN
CC THE BRAIN, BRACHIAL ARCHES, TRIGEMINAL FACIAL GANGLION, AND THE
CC RETINA OF SWIMMING Tadpole STAGE OF DEVELOPMENT.
CC -1- SIMILARITY: NO OTHER PROTEIN TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR EMBL; U14164; AAA74888.1; -.
DR HSSP; P00523; 2PTK.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

```


DR PRAM: PR01404; EPH_1bd. 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRINTS; PR0014; ENTPEIIT.
 SQ SEQUENCE 943 AA; 105291 MW; C4C78A21 CRC32;

Query Match 50.4%; Score 739.5; DB 4; Length 943;
 Best Local Similarity 50.7%; Pred. No. 4, 4e-61;
 Matches 138; Conservative 53; Mismatches 64; Indels 17; Gaps 5;

QY 7 ILLILCSVLDSFGELLIPPSNEVNLDSKTIGELGMISYPHSGWEISGVDEHYPIR 66
 DB 7 LLLILLESAY-----AAEETLMDTRATATLGMTANPAGSWEVSGYDENLMTIR 56
 QY 67 TYQVCNVMDSQNNWMLRTNWPFRNSAOKIYVELKFTLRDCNSIPLYVGTCKEFTNLYME 126
 DB 57 TYQVCNVEEPNWNMLTFTLRNGARIRISEMFTYRDCSSLNVPVGSCKEFTNLYME 116
 QY 127 SDDDHGK----FREHOFKIDITIADEFTQMDLGRILKLTETREVGPNKKGFTYLA 182
 DB 117 TDSVIATKSAFSEAPYLVDTIADESFQVDFRGLKLVNTEVRSFGPLTFNGFTYLA 176
 QY 183 FQDVGACVALSVYVYFKKCPFTYKNLAMPDPVTP-MDSQSLVEVRGSCVNNKSEDDP- 241
 DB 177 FQDYGACMILLSVYVFEKKCPSTIVQNFVPEPTMTGAEISTLYIARGTCLPNAEEVDVPI 236
 QY 241 RMYCTEGEWLVPIGKCSNAGYE-ERGFMQ 271
 DB 237 KLYCNGDEMMVPIGRCTCKRGPENSVACK 268

RESULT 9
 095142 ID 095142 PRELIMINARY; PRT; 984 AA.
 AC 095142;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE EPH-LIKE RECEPTOR TYROSINE KINASE HEPHBI.
 GN HEPHBI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA STEIN E., HUYNH-DO U., LANE A., CERRETTI D.P., DANIEL T.O.;
 RT "Nck recruitment to Eph receptor, Ephbi/ELK, couples ligand activation
 RT to c-Jun kinase.";
 RL J. Biol. Chem. 0:0-0(1997).
 DR EMBL: AF037331; AAD02030.1; -.
 DR HSSP: P00523; 2PTK.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 KW Receptor; kinase.
 SQ SEQUENCE 984 AA; 110041 MW; DF5C8ED3 CRC32;

Query Match 50.4%; Score 739.5; DB 4; Length 984;
 Best Local Similarity 50.7%; Pred. No. 4, 7e-61;
 Matches 138; Conservative 53; Mismatches 64; Indels 17; Gaps 5;

QY 7 ILLILCSVLDSFGELLIPPSNEVNLDSKTIGELGMISYPHSGWEISGVDEHYPIR 66
 DB 7 LLLILLESAY-----AAEETLMDTRATATLGMTANPAGSWEVSGYDENLMTIR 56
 QY 67 TYQVCNVMDSQNNWMLRTNWPFRNSAOKIYVELKFTLRDCNSIPLYVGTCKEFTNLYME 126
 DB 57 TYQVCNVEEPNWNMLTFTLRNGARIRISEMFTYRDCSSLNVPVGSCKEFTNLYME 116
 QY 127 SDDDHGK----FREHOFKIDITIADEFTQMDLGRILKLTETREVGPNKKGFTYLA 182
 DB 117 TDSVIATKSAFSEAPYLVDTIADESFQVDFRGLKLVNTEVRSFGPLTFNGFTYLA 176

QY 183 FQDVGACVALSVYVYFKKCPFTYKNLAMPDPVTP-MDSQSLVEVRGSCVNNKSEDDP- 241
 DB 177 FQDYGACMILLSVYVFEKKCPSTIVQNFVPEPTMTGAEISTLYIARGTCLPNAEEVDVPI 236
 QY 241 RMYCTEGEWLVPIGKCSNAGYE-ERGFMQ 271
 DB 237 KLYCNGDEMMVPIGRCTCKRGPENSVACK 268

RESULT 10
 091735 ID 091735 PRELIMINARY; PRT; 974 AA.
 AC 091735;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE EPHRIN TYPE-B RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR) (TCK).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
 OC Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96068901.
 RA SCALES J.B., WINNING R.S., RENAUD C.S., SHEA L.J., SARGENT T.D.;
 RT "Novel members of the eph receptor tyrosine kinase subfamily expressed
 RT during xenopus development";
 RL Oncogene 11:1745-1752(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN PRE-SOMITIC
 CC MESODERM, CAUDAL SOMITES, MIDBRAIN, AND CEMENT GLAND. MOST
 CC ABUNDANT IN ADULT BRAIN, EYE, HEART, LUNG AND OVARY. LOWER LEVELS
 CC IN INTESTINE, KIDNEY, OVIDUCT AND PHARYNX.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 DR EMBL: I43620; AAA93526.1; -.
 DR HSSP: P00523; 2PTK.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00780; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PIRAM: PF00041; fn3; 2.
 DR PIRAM: PF00069; PKINASE; 1.
 DR PIRAM: PF00536; SAM; 1.
 DR PRAM: PR01404; EPH_1bd; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRINTS; PR00014; ENTPEIIT.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain.
 FT CHAIN 1 16
 FT SIGNAL 17 974
 FT DOMAIN 17 334
 FT DOMAIN 17 534
 FT TRANSMEM 535 555
 FT DOMAIN 535 555
 FT DOMAIN 535 555
 FT DOMAIN 53 102
 FT DOMAIN 178 315
 FT DOMAIN 316 423
 FT DOMAIN 424 520
 FT DOMAIN 424 520
 FT DOMAIN 609 872
 FT NF_BIND 615 623
 FT DISULFID 60 95
 FT BINDING 641 641
 FT ACT_SITE 734 734
 FT MOD_RES 768 768
 FT PHOSPHORYLATION (AUTO-) (POTENTIAL).

KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain.
 FT NON_TER 1 1
 FT DOMAIN <1 459
 FT TRANSMEM 460 480
 FT DOMAIN 481 902
 FT DOMAIN <1 21
 FT DOMAIN 101 237
 FT DOMAIN 238 347
 FT DOMAIN 348 445
 FT DOMAIN 537 800
 FT NP_BIND 543 551
 FT DISULFID ? 14
 FT BINDING 569 569
 FT ACT_SITE 662 662
 FT MOD_RES 696 696
 FT CARBOHYD 252 252
 FT CARBOHYD 344 344
 FT CARBOHYD 398 398
 SQ SEQUENCE 902 AA; 100850 MW; C096D006 CRC32;

Query Match 38.4%; Score 563.5; DB 13; Length 902;
 Best Local Similarity 55.1%; Pred. No. 1.4e-44;
 Matches 102; Conservative 42; Mismatches 34; Indels 7; Gaps 4;

QY 94 KIYELKFTLRDCNSIPVLGTCRKETFNLYMESDDDHGVK----FREHOFKIDITIAAD 149
 DB 2 RYVYEMRTVADCCSLRPVPGCKETFNLYYEDNSIDNKISTFWNESPLYKVDITIAAD 61
 QY 150 ESFTQMDLGDRILKLNTEIREVGPVNRKGFYLAQDVAGACVALVSVRYFRKCPETVKNL 209
 DB 62 ESFSQVDVFGGRIMKVNTEVRFSFGPLTRSGFYLAQDYGACMSLSLVRYFRKCPVQNF 121
 QY 210 AMEPDTPV-MDSQSLVEVRGSCVNNKSEDDPP-RMYGSTEGEMLYPIQKSCNAGYE-ER 266
 DB 122 AVPEPTMGAEISTLVLAGTICIPNAEEVDVPIRLKLCNGDGMVPIGCTCKAGYEPEN 181
 QY 267 GFMCQ 271
 DB 182 HVVCK 186

Search completed: May 9, 2000, 22:31:15
 Job time: 2380 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 22:32:11 ; Search time 49.21 Seconds
(without alignments)
167.716 Million cell updates/sec

Title: US-09-104-340-4

Perfect score: 1466
Sequence: 1 MDCQLSTLLDSCSVLDISFG.....VPIGKSCSNAGYERGFMCQ 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues
Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1466	100.0	983	1	EPA3_HUMAN
2	1400.5	95.5	983	1	EPA3_MOUSE
3	1399	95.4	984	1	EPA3_RAT
4	1309	89.3	983	1	EPA3_CHICK
5	1003	68.4	948	1	EPA6_RAT
6	1002	68.3	1035	1	EPA6_MOUSE
7	998	68.1	986	1	EPA4_CHICK
8	990	67.9	986	1	EPA4_HUMAN
9	990	67.5	877	1	EPA5_MOUSE
10	985	67.2	1005	1	EPA5_RAT
11	984	67.1	1037	1	EPA5_HUMAN
12	980	66.8	986	1	EPA4_MOUSE
13	947	64.6	1013	1	EPA5_CHICK
14	927.5	63.3	998	1	EPA7_HUMAN
15	926.5	63.2	998	1	EPA7_MOUSE
16	925.5	63.1	998	1	EPA7_RAT
17	925.5	63.1	1004	1	EPA8_MOUSE
18	772	52.7	988	1	EPR2_HUMAN
19	767	52.3	986	1	EPR2_MOUSE
20	767	52.3	993	1	EPR2_MOUSE
21	760.5	51.9	984	1	EPR1_RAT
22	752.5	51.3	984	1	EPR1_HUMAN
23	740	50.5	987	1	EPR2_COTJA
24	698.5	47.6	977	1	EPA2_MOUSE
25	692	47.2	998	1	EPR3_HUMAN
26	681	46.5	993	1	EPR3_MOUSE
27	678	46.2	976	1	EPA2_HUMAN
28	623	42.5	1002	1	EPR5_CHICK
29	604	41.2	976	1	EPA1_HUMAN
30	528.5	36.1	1006	1	EPR6_HUMAN
31	510	34.8	987	1	EPR4_MOUSE
32	492	33.6	987	1	EPR4_HUMAN
33	99.5	6.8	982	1	MSHM_SARGL
34	90	6.1	3110	1	LMA2_HUMAN

35	88	6.0	1376	1	VG12_CVM4	P22432 murine coro
36	85	5.8	3106	1	LMA2_MOUSE	Q06075 mus musculu
37	84.5	5.8	380	1	I132_HUMAN	Q14627 homo sapien
38	84	5.7	788	1	ITB3_HUMAN	P05106 homo sapien
39	82.5	5.6	461	1	HMCS_ARATH	P54873 arabidopsis
40	82.5	5.6	1098	1	ITSL1_YEAST	P38427 saccharomyc
41	82	5.6	1029	1	YFC5_YEAST	P43571 saccharomyc
42	82	5.6	1376	1	VG12_CVM4	Q02385 murine coro
43	80.5	5.5	406	1	NPRA_BACST	P43130 bacillus st
44	80.5	5.5	897	1	SAP1_YEAST	P39955 saccharomyc
45	80	5.5	806	1	STL_HELPD	Q92j63 helicobacte

ALIGNMENTS

```

RESULT 1
EPA3_HUMAN          STANDARD;          PRT;          983 AA.
ID   EPA3_HUMAN
AC   P29320;
DT   01-DEC-1992 (Rel. 24, Created)
DI   01-DEC-1992 (Rel. 35, Last sequence update)
DR   01-NOV-1997 (Rel. 35, Last annotation update)
DE   EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE   KINASE RECEPTOR ETK1) (HEK).
OS   Homo sapiens (Human)
GN   EPHA3 OR ETK1 OR ETK OR HEK.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Carnivora; Hominoidea; Hominidae; Homo.
RN   [1]
RP   MEDLINE: 92147681.
RX   MEDLINE: 92179233.
RA   Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
RT   "Molecular cloning of HEK, the gene encoding a receptor tyrosine
RT   kinase expressed by human lymphoid tumor cell lines."
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
RN   [2]
RP   MEDLINE: 92147681.
RX   MEDLINE: 92147681.
RA   Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A.,
RA   Welch K., Loudovaris M., Rockman S., Busmanis I.;
RT   "Isolation and characterization of a novel receptor-type protein
RT   tyrosine kinase (hek) from a human pre-B cell line."
RL   J. Biol. Chem. 267:3262-3267(1992).
CC   -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC   EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID
CC   FUNCTION.
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC   PROTEIN TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: RESTRICTED TO LYMPHOID TUMOR CELL LINES.
CC   -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC   DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
-----
EMBL: M83941; AAA58633.1; -.
EMBL: A28003; CA01906.1; -.
PIR: A38224; A38224.
HSSP: P00523; 2PTR.
MIM: 179611; -.
PRINTS: PR00014; FNTRYPTIT.
PRINTS: PR00109; TYRKINASE.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

```

DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; pk_nase; 1.
DR PFAM: PF00536; SAM; 1.
DR PFAM: PF01404; Eph_Lbd; 1.
KW Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 983 EPHRIN TYPE-A RECEPTOR 3.
FT DOMAIN 21 541 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 542 565 POTENTIAL.
FT DOMAIN 566 983 POTENTIAL.
FT DOMAIN 21 320 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 321 431 FIBRONECTIN TYPE-III.
FT DOMAIN 432 528 FIBRONECTIN TYPE-III.
FT DOMAIN 621 882 PROTEIN KINASE.
FT NP_BIND 627 635 ATP (BY SIMILARITY).
FT BINDING 653 653 ATP (BY SIMILARITY).
FT ACT_SITE 746 746 BY SIMILARITY.
FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 232 232 POTENTIAL.
FT CARBOHYD 337 337 POTENTIAL.
FT CARBOHYD 381 381 POTENTIAL.
FT CARBOHYD 404 404 POTENTIAL.
FT CARBOHYD 493 493 POTENTIAL.
FT CONFLICT 507 507 F -> L (IN CAA01906).
FT CONFLICT 724 724 V -> L (IN CAA01906).
SQ SEQUENCE 983 AA; 110086 MW; BBD900FA80F5121 CRC64;

Query Match 100.0%; Score 1466; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 3.1e-122;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCQSILLLLSGVDSFSGELIPQSPNEVNLDSKTIGELGWSIPSHGWEISGVDE 60
DB 1 MCQSILLLLSGVDSFSGELIPQSPNEVNLDSKTIGELGWSIPSHGWEISGVDE 60
QY 61 HTPIPTYOVCNMDHSONNWLRTNWPNSAKIYVELKFTLDONSITLYVGTCKEPT 120
DB 61 HTPIPTYOVCNMDHSONNWLRTNWPNSAKIYVELKFTLDONSITLYVGTCKEPT 120
QY 121 NLYMESDDHGVKFEHQFTKIDITLADESFQMDLGDRIILKLNTEIRVGVNKKGFY 180
DB 121 NLYMESDDHGVKFEHQFTKIDITLADESFQMDLGDRIILKLNTEIRVGVNKKGFY 180
QY 181 LAFQDVGACVALSVRYEFKCPFTYKNTLAMPDTPVPMDSQSLVEYRGSCVNNKKEEDPP 240
DB 181 LAFQDVGACVALSVRYEFKCPFTYKNTLAMPDTPVPMDSQSLVEYRGSCVNNKKEEDPP 240
QY 241 RMVCSGEGEMLVPIGKCSNAGYEERGFMCQ 271
DB 241 RMVCSGEGEMLVPIGKCSNAGYEERGFMCQ 271

RESULT 2

EPH3_MOUSE STANDARD; PRT; 983 AA.

AC P29319;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (MEK4).
GN EPHA3 OR ETK1 OR MEK4 OR TYRO4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ICR X SWISS WEBSTER; TISSUE-EMBRYO;

RX MEDLINE: 92031278.
RA Sajjadi F.G., Pasquale E.B., Subramani S.;
RT "Identification of a new eph-related receptor tyrosine kinase gene
RT from mouse and chicken that is developmentally regulated and encodes
RT at least two forms of the receptor."
RL New Biol. 3:769-778(1991).
CC CC EPHRIN-A2, -A3, -A4 AND -A5.
CC CC CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC CC PROTEIN TYROSINE PHOSPHATE.
CC CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -1- ALTERNATIVE PRODUCTS: A SECRETED VARIANT WITHOUT THE TRANSMEMBRANE
CC CC REGION AND THE KINASE DOMAIN IS PRODUCED BY ALTERNATIVE SPLICING
CC CC OF THE SAME GENE.
CC CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE
CC CC BRAIN.
CC CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC CC DOMAIN, BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC CC -----
CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR EMBL: M68513; AAA39521.1; -;
DR EMBL: M68515; AAA39522.1; ALT_SEQ.
DR PIR: A45583; A45583.
DR HSP: P16109; IFSB.
DR MGI: 99612; EPHA3.
DR PRINTS: PR0014; ENTPEIIL.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; pk_nase; 1.
DR PFAM: PF00536; SAM; 1.
DR PFAM: PF01404; Eph_Lbd; 1.
KW Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 983 EPHRIN TYPE-A RECEPTOR 3.
FT DOMAIN 21 540 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 541 564 POTENTIAL.
FT DOMAIN 565 983 POTENTIAL.
FT DOMAIN 21 320 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 321 431 FIBRONECTIN TYPE-III.
FT DOMAIN 432 528 FIBRONECTIN TYPE-III.
FT DOMAIN 621 882 PROTEIN KINASE.
FT NP_BIND 627 635 ATP (BY SIMILARITY).
FT BINDING 653 653 ATP (BY SIMILARITY).
FT ACT_SITE 746 746 BY SIMILARITY.
FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 231 231 POTENTIAL.
FT CARBOHYD 336 336 POTENTIAL.
FT CARBOHYD 390 390 POTENTIAL.
FT CARBOHYD 403 403 POTENTIAL.
FT CARBOHYD 482 482 POTENTIAL.
FT VARSPIC 530 983 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 983 AA; 109955 MW; BE44A655D8107A2 CRC64;

Query Match 95.5%; Score 1400.5; DB 1; Length 983;
Best Local Similarity 95.9%; Pred. No. 2e-116;
Matches 260; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

```

QY 1 MDCQLSILLSCSYDSEGLIPDPSNEVNLDSKTIGELGWSYPSHGWEISGVDE 60
DB 1 MCHSLIYLIGCCVLSCESELSPSPSNEVNLDSKTIGELGWSYPSHGWEISGVDE 60
QY 61 HTPRTTYOVANMDSQNMWLTNTNVPNRSACKIYVELKFLTRDONSIPLVGCTKEF 120
DB 61 HTPRTTYOVANMDSQNMWLTNTNVPNRSACKIYVELKFLTRDONSIPLVGCTKEF 120
QY 121 NLYMESDDHGVKREHOFKIDITIADESFQMDLGRILKLNTEIREVGPVNNKGFY 180
DB 121 NLYMES-DDHGVKREHOFKIDITIADESFQMDLGRILKLNTEIREVGPVNNKGFY 179
QY 181 LAFQDYGACVALSVRYVRKRCFTYVKNLAMPDTPVPMDSQSLVEYRGSCVNNKEDDP 240
DB 181 LAFQDYGACVALSVRYVRKRCFTYVKNLAMPDTPVPMDSQSLVEYRGSCVNNKEDDP 239
QY 241 RMVCSFEGEMLVPIGKSCNAGYEEERGFCQ 271
DB 240 RMVCSFEGEMLVPIGKSCNAGYEEERGFCQ 270

```

RESULT 3

EPB3_RAT STANDARD: PRT: 984 AA.

AC 008680;

DT 01-NOV-1997 (Rel. 35, Created)

DT 15-FEB-2000 (Rel. 39, Last sequence update)

DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN

DE KINASE RECEPTOR REK4).

GN EPHA3 OR REK4.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY;

RA MEDLINE; 98120505.

RA L4 Y.Y., McTierman C.F., Feldman A.M.;

RT "IL-1 beta alters the expression of the receptor tyrosine kinase gene

RT r-Epha3 in neonatal rat cardiomyocytes."

RL Am. J. Physiol. 274:H331-H341(1998).

CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO

CC EPHRIN-A2, -A3, -A4 AND -A5.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +

CC PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation-

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to license@sib-sib.ch).

CC -----

DR EMBL; U69278; AAC06273.1; -

DR HSP; P16109; IFSB.

DR PRINTS; PR00014; FNTYPEI1.

DR PROSITE; PS00109; TYRKINASE.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00109; PROTEIN KINASE.

DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

DR PROSITE; PS01186; EGF_2; UNKNOWN_1.

DR PFAM; PF00041; fn3; 2.

DR PFAM; PF00069; pkinase; 1.

DR PFAM; PF00336; SAM; 1.

DR PFAM; PF01404; EPH_Lbd; 1.

```

KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 984
FT DOMAIN 21 541 EPHRIN TYPE-A RECEPTOR 3.
FT TRANSMEM 542 565 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 566 984 POTENTIAL.
FT DOMAIN 21 321 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 322 432 CYS-RICH.
FT DOMAIN 433 529 FIBRONECTIN TYPE-III.
FT DOMAIN 622 863 FIBRONECTIN TYPE-III.
FT NP_BIND 628 636 PROTEIN KINASE.
FT BINDING 654 654 ATP (BY SIMILARITY).
FT ACT_SITE 747 747 ATP (BY SIMILARITY).
FT MOD_RES 780 780 BY SIMILARITY.
FT CARBOHYD 232 232 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 337 337 POTENTIAL.
FT CARBOHYD 391 391 POTENTIAL.
FT CARBOHYD 404 404 POTENTIAL.
FT CARBOHYD 493 493 POTENTIAL.
SQ SEQUENCE 984 AA; 110227 MW; F170C49312F7A0AB CRC64;

```

Query Match

Best Local Similarity 95.4%; Score 1399; DB 1; Length 984;

Matches 258; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

```

QY 1 MDCQLSILLSCSYDSEGLIPDPSNEVNLDSKTIGELGWSYPSHGWEISGVDE 60
DB 1 MCHSLIYLIGCCVLSCESELSPSPSNEVNLDSKTIGELGWSYPSHGWEISGVDE 60
QY 61 HTPRTTYOVANMDSQNMWLTNTNVPNRSACKIYVELKFLTRDONSIPLVGCTKEF 120
DB 61 HTPRTTYOVANMDSQNMWLTNTNVPNRSACKIYVELKFLTRDONSIPLVGCTKEF 120
QY 121 NLYMESDDHGVKREHOFKIDITIADESFQMDLGRILKLNTEIREVGPVNNKGFY 180
DB 121 NLYMESDDHGVKREHOFKIDITIADESFQMDLGRILKLNTEIREVGPVNNKGFY 180
QY 181 LAFQDYGACVALSVRYVRKRCFTYVKNLAMPDTPVPMDSQSLVEYRGSCVNNKEDDP 240
DB 181 LAFQDYGACVALSVRYVRKRCFTYVKNLAMPDTPVPMDSQSLVEYRGSCVNNKEDDP 240
QY 241 RMVCSFEGEMLVPIGKSCNAGYEEERGFCQ 271
DB 241 RMVCSFEGEMLVPIGKSCNAGYEEERGFCQ 270

```

RESULT 4

EPB3_CHICK STANDARD: PRT: 983 AA.

AC P29318;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN

DE KINASE RECEPTOR ETK1) (CEK4).

GN EPHA3 OR ETK1 OR CEK4.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;

OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RP SEQUENCE FROM N.A.

RC MEDLINE; 92031278.

RA Sajjadi F.G., Pasquale E.B., Subramani S.;

RT "Identification of a new eph-related receptor tyrosine kinase gene

RT from mouse and chicken that is developmentally regulated and encodes

RT at least two forms of the receptor."

RL New Biol. 3:769-778(1991).

CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO

CC EPHRIN-A2, -A3, -A4 AND -A5.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +

CC PROTEIN TYROSINE PHOSPHATE.

```
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE
CC BRAIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions so long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL: M68514; AAA48666.1; -.
DR PIR: B45583; B45583.
DR HSP: P00523; 2PTR.
DR PRINTS: PRO0014; ENTPEIT1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; pkinase; 1.
DR PFAM: PF00536; SAM; 1.
DR PFAM: PF01404; EPH_Lbd; 1.
DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
DR Receptor; Transmembrane; Glycoprotein; Signal.
DR CHAIN 1 19
DR DOMAIN 20 983
DR TRANSMEM 541 540
DR DOMAIN 541 564
DR DOMAIN 565 983
DR DOMAIN 20 320
DR DOMAIN 321 431
DR DOMAIN 432 528
DR DOMAIN 621 882
DR NP_BIND 627 635
DR BINDING 653 653
DR ACT_SITE 746 746
DR MOD_RES 779 779
DR CARBOHYD 231 231
DR CARBOHYD 336 336
DR CARBOHYD 390 390
DR CARBOHYD 403 403
DR CARBOHYD 492 492
DR SEQUENCE 983 AA; 109910 MW; E8895F0BDF7651E CRC64;

Query Match 89.3%; Score 1309; DB 1; Length 983;
Best Local Similarity 91.6%; Pred. No. 2.6e-108;
Matches 241; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
```

```
QY 249 EMLVPIGKSCNAGYERGERGMCQ 271
DB 248 EMLVPIGKCLCNAGYERGERGFAQC 270

RESULT 5
EPA6_RAT STANDARD: PRT; 948 AA.
AC P54758;
DR 01-OCT-1996 (Rel. 34; Created)
DT 01-OCT-1996 (Rel. 34; Last sequence update)
DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EHK-2) (EPH HOMOLOG KINASE-2).
GN EPA6 OR EHK2 OR EHK-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE: 94067777.
RA Maisonneuve P.C., Barthezuela N.X., Yancopoulos G.D.;
RT EHK-1 and EHK-2: two novel members of the Eph receptor-like tyrosine
RT kinase family with distinctive structures and neuronal expression.
RL Oncogene 8:3277-3288(1993).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC HSP: P00523; 2PTR.
DR PRINTS: PRO0014; ENTPEIT1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00069; pkinase; 1.
DR PFAM: PF01404; EPH_Lbd; 1.
DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
DR Receptor; Transmembrane; Glycoprotein; Signal.
DR CHAIN 1 22
DR DOMAIN 23 948
DR TRANSMEM 550 570
DR DOMAIN 571 948
DR DOMAIN 630 943
DR NP_BIND 636 644
DR BINDING 662 662
DR ACT_SITE 797 797
DR CARBOHYD 342 342
DR CARBOHYD 396 396
DR CARBOHYD 409 409
DR SEQUENCE 948 AA; 106235 MW; A47DC78EBD2DEF30 CRC64;

Query Match 68.4%; Score 1003; DB 1; Length 948;
Best Local Similarity 65.7%; Pred. No. 3.3e-81;
Matches 180; Conservative 39; Mismatches 37; Indels 18; Gaps 3;
```

QY 113 LGCTKETENLYMESDDHGVKFRHFOFTKIDTIADESFTOMDGLDRILKINTEIREVG 172
 DB 117 LGCTKETENLYMESDHSHTGFKFSQYIKIDTIADESFTOMDGLDRILKINTEIREVG 176
 QY 173 PVNKGFTYLAODVGACALVALSVRYEFKCPFTVKNLAFDPDTPV-MDSQSLEYVSGSCV 231
 DB 177 PIERGFTYLAODIGACALVALSVRYEFKCPFTVKNLAFDPDTPV-MDSQSLEYVSGSCV 236
 QY 232 NNSKEDPEPRMTCSTEGEMVLPVIGKSCNAGYEE 265
 DB 237 KSEERDTPKLYCGADGMDLPLVLRGICSTGYEE 270

RESULT 6
 EPA6_MOUSE STANDARD: PRT: 1035 AA.
 AC 062413:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-2) (EPH HOMOLOG KINASE-2).
 GN EPHA6 OR EHK2 OR EHK-2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RA Lee A.M., Navarathnam D., Ichimiya S., Greene M.I., Davis J.G.;
 RT "Cloning of m-ehk2 from the murine inner ear, an eph family receptor tyrosine kinase expressed in the developing and adult cochlea."
 RL DNA Cell Biol. 15:817-825(1996).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U58332; AAB53836.1; -;
 DR HSSP: P00523; 2PTRK.
 DR MGD: MGI:108034; EPHA6.
 DR PRINTS: PRO0014; FNTYPEP11.
 DR PRINTS: PRO0109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE.
 DR PROSITE: PS00109; PROTEIN_KINASE_ATP. 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_TYR. 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1. 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2. 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PFM: PFM0041; fn3. 2.
 DR PFM: PFM0069; kinase. 1.
 DR PFM: PFM0036; SAM. 1.
 DR PFM: PFM01404; EPH_lbd. 1.
 KW transferase; tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 1035 EPHRIN TYPE-A RECEPTOR 6.
 FT DOMAIN 23 549 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 550 570 POTENTIAL.

FT DOMAIN 571 1035 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 630 943 PROTEIN KINASE.
 FT NP_BIND 636 644 ATP (BY SIMILARITY).
 FT BINDING 662 662 ATP (BY SIMILARITY).
 FT ACT_SITE 797 797 BY SIMILARITY.
 FT CARBOHYD 342 342 POTENTIAL.
 FT CARBOHYD 396 396 POTENTIAL.
 FT CARBOHYD 409 409 POTENTIAL.
 SQ SEQUENCE 1035 AA; 116137 MW; 560B264194A5E74 CRC64;

Query Match 68.3%; Score 1002; DB 1; Length 1035;
 Best Local Similarity 65.7%; Pred. No. 4.6e-81;
 Matches 180; Conservative 41; Mismatches 35; Indels 18; Gaps 3;

QY 3 COLSTLLISCVSDSFGELIP-----QPSNEVNLDSKTIQGLGISTPSHG 52
 DB 4 CEVREFLL-----QFGFELPLTAWTGDCSHVSNQVLLDTVTVMGELGWKTYPLNG 56
 QY 53 EHSIGVDHYPIRTYOVCMWDSQNNMLRTNWPFRSAQKIYVELKFTLPDCNSIPLY 112
 DB 57 DAITEDEHNRPIRTYOVCMWEPNNMLRTNWPFRSAQKIYVELKFTLPDCNSIPWY 116
 QY 113 LGCTKETENLYMESDDHGVKFRHFOFTKIDTIADESFTOMDGLDRILKINTEIREVG 172
 DB 117 LGCTKETENLYMESDHSHTGFKFSQYIKIDTIADESFTOMDGLDRILKINTEIREVG 176
 QY 173 PVNKGFTYLAODVGACALVALSVRYEFKCPFTVKNLAFDPDTPV-MDSQSLEYVSGSCV 231
 DB 177 PIERGFTYLAODIGACALVALSVRYEFKCPFTVKNLAFDPDTPV-MDSQSLEYVSGSCV 236
 QY 232 NNSKEDPEPRMTCSTEGEMVLPVIGKSCNAGYEE 265
 DB 237 KSEERDTPKLYCGADGMDLPLVLRGICSTGYEE 270

RESULT 7
 EPA4_CHICK STANDARD: PRT: 986 AA.
 AC 007496; Q90772;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK8).
 GN EPHA4 OR CEK8.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SPINAL CORD;
 RX MEDLINE: 96404128.
 RA Ohka K., Nakamura M., Hirokawa K., Tanaka S., Iwana A., Suda T.,
 RA "The receptor tyrosine kinase, Cek8, is transiently expressed on subtypes of motoneurons in the spinal cord during development."
 RL Mech. Dev. 54:59-69(1996).
 RN [2]
 RP SEQUENCE OF 138-986 FROM N.A.
 RC TISSUE-EMBRYO;
 RX MEDLINE: 93288394.
 RA Sajjadi F.G., Pasquale E.B.;
 RA "Five novel avian Eph-related tyrosine kinases are differentially expressed."
 RT Oncogene 8:1807-1813(1993).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A4 AND -A5. BINDS POORLY TO EPHRIN-A2 AND A-3.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

ID	EP#4 MOUSE	STANDARD;	PRT;	986 AA.
AC	Q03137;			
DT	01-OCT-1994	(Rel. 30,	Created)	
DT	01-OCT-1994	(Rel. 30,	Last sequence update)	

FT	DOMAIN	570	986	CYTOSOLASMIC (POTENTIAL).
FT	DOMAIN	325	435	FIBRONECTIN TYPE-III (BY SIMILARITY).
FT	DOMAIN	436	532	FIBRONECTIN TYPE-III (BY SIMILARITY).
FT	DOMAIN	621	882	PROTEIN KINASE.

```

FT NP_BIND 627 635 ATP (BY SIMILARITY).
FT BINDING 653 653 ATP (BY SIMILARITY).
FT ACT_SITE 746 746 BY SIMILARITY.
FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CARBOHYD 235 235 POTENTIAL.
FT CARBOHYD 340 340 POTENTIAL.
FT CARBOHYD 408 408 POTENTIAL.
FT CARBOHYD 423 423 POTENTIAL.
FT VARSPLIC 783 832 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 986 AA; 109801 MW; D16AD8B85668C80E CRC64;

Query Match 66.8%; Score 980; DB 1; Length 986;
Best Local Similarity 71.4%; Pred. No. 3,8e-79;
Matches 177; Conservative 35; Mismatches 34; Indels 2; Gaps 2;

QY 26 PSEVNLDSKITQIGELGMSYSP-SHGMETISGVDEHYPIRTYQVCNVDHSONNWLRT 84
DB 27 PANEVTLDSRSYQGLGWLASPLGEGWEVSTMDKNTPIRTYQVCNWEASONNWLRT 86
QY 85 NMYPRNSAKIYVELKFTLDCNSIPVLVGTCKETFNLYMESDDHGVFREHQFTKID 144
DB 87 DMTIRGAGRVYEIKFTLDCNSLPVGMCTCKETFNLYYESDNDKERTIRESQFKID 146
QY 145 TTADESFQMDLGDRIKLKNTIREVGVNKKGYLAQDVACVALVSRYVFKKCP 204
DB 147 TTADESFQVMDIGDRIKNTIREVGVNKKGYLAQDVACVALVSRYVFKKCP 206
QY 205 TYVNLAMPPTVP-MDSOSLYEVGSCVNNKEDPPRMVCSREGEMVTVIGKSCNAG 263
DB 207 TYVNLAMPPTVP-MDSOSLYEVGSCVNNKEDPPRMVCSREGEMVTVIGKSCNAG 266
QY 264 EERGFMCQ 271
DB 267 EERGFMCQ 274

RESULT 13
EPAS_CHICK
ID EPAS_CHICK STANDARD; PRT; 1013 AA.
AC P54755;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR CEK7).
GN EPHAS OR CEK7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BODY WALL;
RX MEDLINE; 95047429.
RA Steyer D.A., Verderrame M.F.;
RT Identification of a complete Cek7 receptor protein tyrosine kinase
RT coding sequence and cDNAs of alternatively spliced transcripts."
RL Gene 148:219-226(1994).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL; U03910; AAB60613.1; -
DR EMBL; U03910; AAB60614.1; -
DR EMBL; U03910; AAB60612.1; -
DR HSSP; P00523; 2PTK.
DR PRINTS; PR00014; ENTYPEIIL.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00069; PKINASE; 1.
DR PFAM; PF00536; SAM; 1.
DR PFAM; PF01404; EPH_Lbd; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 31
FT CHAIN 32 1013
FT DOMAIN 32 549
FT TRANSMEM 550 570
FT DOMAIN 571 1013
FT DOMAIN 651 912
FT NP_BIND 657 665
FT BINDING 683 683
FT ACT_SITE 776 776
FT CARBOHYD 240 240
FT CARBOHYD 275 275
FT CARBOHYD 345 345
FT CARBOHYD 399 399
FT CARBOHYD 412 412
FT CARBOHYD 437 437
FT VARSPLIC 280 443
FT VARSPLIC 573 595
SQ SEQUENCE 1013 AA; 112245 MW; AC36FD6AEB38382 CRC64;

Query Match 64.6%; Score 947; DB 1; Length 1013;
Best Local Similarity 64.6%; Pred. No. 3,4e-76;
Matches 170; Conservative 37; Mismatches 52; Indels 4; Gaps 2;

QY 10 LASCYVLSDFGELIPQPSNEVNLDSKITQIGELGMSYSHGMETISGVDEHYPIRTYQ 69
DB 20 LLLCALARS---LLASPGSEVNLDSRTYVAGDLGWATYPRKNGMEETIGEDENYAPHTYQ 76
QY 70 VCNVMDHSONNMLRTMNVWRNSAKIYVELKFTLRCCNSIPVLVGTCKETFNLYYESD 129
DB 77 VCNVMDHSONNMLRTMNVWRNSAKIYVELKFTLRCCNSIPVLVGTCKETFNLYYESD 136
QY 130 DHGKFRHQFTKIDITIADESFQMDLGDRIKLKNTIREVGVNKKGYLAQDVAC 189
DB 137 EDCRNIRNEMQIKIDITIADESFQMDLGDRIKLKNTIREVGVNKKGYLAQDVAC 196
QY 190 VALVSRYVFKKCPFTVKULAMPDTPV-MDSOSLYEVGSCVNNKEDPPRMVCSREG 248
DB 197 IALVSRYVFKKCPFTVKULAMPDTPV-MDSOSLYEVGSCVNNKEDPPRMVCSREG 256
QY 249 EMLVPTIGKSCNAGYERGFMCQ 271
DB 257 EMLVPTIGKSCNAGYERGFMCQ 279

RESULT 14
EPAT_HUMAN
ID EPAT_HUMAN STANDARD; PRT; 998 AA.
AC Q15375;
DT 01-NOV-1997 (Rel. 35, Created)

```

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR EHK-3) (EPH HOMOMLOGY KINASE-3) (RECEPTOR PROTEIN-
 DE TYROSINE KINASE HEK11).
 GN EPHA7 OR EHK3 OR HEK11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 95206782.
 RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
 RA Basu R., Weisner A.A.;
 RT "cDNA cloning and tissue distribution of five human EPH-like receptor
 RT protein-tyrosine kinases."
 RL Oncogene 10:897-905(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.jlb-sib.ch/announce/>
 CC or send an email to license@sib.ch).
 CC -----
 DR EMBL; L36642; AAA74243.1; -
 DR HSP; P00523; 2PTK.
 DR MIM; 602190; -
 DR PRINTS; PRO0014; FNTYPEIII.
 DR PRINTS; PRO0109; TYRKINASE.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM_1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PFM; PF00041; fn3; 2.
 DR PFM; PF00069; PKINASE_1.
 DR PFM; PF00536; SAM; 1.
 DR PFM; PF01404; EPH_1bd; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 1 24
 FT DOMAIN 25 556 EPHRIN TYPE-A RECEPTOR 7.
 FT TRANSHEM 557 577 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 578 998 POTENTIAL.
 FT DOMAIN 329 438 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 439 537 FIBRONECTIN TYPE-III.
 FT DOMAIN 633 937 FIBRONECTIN TYPE-III.
 FT NP_BIND 639 894 PROTEIN KINASE.
 FT BINDING 665 665 ATP (BY SIMILARITY).
 FT AC_SITE 758 758 ATP (BY SIMILARITY).
 FT MOD_RES 791 791 BY SIMILARITY.
 FT CARBOHYD 343 343 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 410 410 POTENTIAL.
 SQ SEQUENCE 998 AA; 112096 MW; 479B9CAD2B06EB CRC64;

Query Match 63.3%; Score 927.5; DB 1; Length 998;
 Best Local Similarity 68.4%; Pred. No. 1.8e-74;
 Matches 171; Conservative 39; Mismatches 37; Indels 3; Gaps 2;

QY 25 QPSNEVNLDSKTIQIGELGWISYPSHGWEISGVDEHYTPRTYQVCNMDHSONMLRT 84
 DQ 28 QAAREVLLDSKAQTELEWISSPPNGHEEISGDENTPRTYQVCNMDHSONMLRT 87
 QY 85 NWBPNSAKTIYELKFTLRDCNSIPYLGTCKETENLYMESDDHGKFRHQFTKID 144
 DQ 88 NMISGNARIFVELKFTLRDCNSLPGLVGTCKETENLYMETDYDGRNIRENLYKID 147
 QY 145 TIADESTQMDLDRIKLTLTEIREVGPVKKGFYLAFOVGCVALYVRYFKCP 204
 DQ 148 TIADESTQMDLDRIKLTLTEIREVGPVKKGFYLAFOVGCVALYVRYFKCP 207
 QY 205 TVKNLAMPDTPV-MDSQSLVEVSGCVNNSKE--EDPPRYCTEGEMLVPIKCSGNA 261
 DQ 208 IIEENLAIPTDVTSSSESLVEVAGTCVSAEELNAPRHACBEMLVPIKCSGNA 267
 QY 262 GYEERGFMCQ 271
 DQ 268 GYQCKDPTCE 277
 RESULT 15
 EPHA7_MOUSE STANDARD; PRT; 998 AA.
 AC 061772; 061773; 061774; 061505;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
 DE KINASE RECEPTOR EHK-3) (EPH HOMOMLOGY KINASE-3) (EMBRYONIC BRAIN
 DE KINASE) (EBK) (DEVELOPMENTAL KINASE 1) (MDK-1).
 GN EPHA7 OR EHK3 OR EBK OR MDK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE; 95124729.
 RA Closser T., Millauer B., Ulrich A.;
 RT "Identification of alternatively spliced mRNAs encoding variants of
 RT MDK1, a novel receptor tyrosine kinase expressed in the murine
 RT nervous system."
 RL Oncogene 10:97-108(1995).
 RN [2]
 RP SEQUENCE OF 431-998 FROM N.A. (ISOFORM MDK1).
 RC TISSUE-BRAIN;
 RX MEDLINE; 96081374.
 RA Ellis J., Liu O., Breitman M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling H.,
 RA Fletcher F.A., Ziegler S.F., Rogers J.H.;
 RT "Embryo brain kinase: a novel gene of the eph/elk receptor tyrosine
 RT kinase family."
 RL Mech. Dev. 52:319-341(1995).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN (MDK1, MDK1-1,
 CC MDK1-2, MDK1-T1 AND MDK1-T2) ARE PRODUCED BY ALTERNATIVE
 CC SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF
 CC MDK1.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN EMBRYO. IN ADULT,
 CC EXPRESSION RESTRICTED TO HIPPOCAMPUS, TESTIS AND SPLEEN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 22:27:18 / Search time 64.29 Seconds
(without alignments)
247.140 Million cell updates/sec

Title: US-09-104-340-4

Perfect score: 1466

Sequence: 1 MDCQLSTLLSCSVLDSFG.....VPIGKSCSNAGYERGFMCQ 271

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

PIR_63:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1466	100.0	983	2	A38224
2	1400.5	95.5	983	2	A45583
3	1309	89.3	983	2	B45583
4	1003	68.4	948	2	S51605
5	995	67.9	986	2	I78844
6	990	67.5	877	2	I48967
7	988	67.4	988	2	S47489
8	985	67.2	893	2	S51603
9	985	67.2	981	2	S51604
10	985	67.2	1005	2	S49015
11	984	67.1	991	2	I78843
12	980	66.8	986	2	S78059
13	977	66.6	985	2	I51549
14	947	64.6	1013	2	I50615
15	927.5	63.3	998	2	I58351
16	926.5	63.2	605	2	JC3673
17	926.5	63.2	610	2	I48612
18	926.5	63.2	626	2	I48612
19	926.5	63.2	998	2	JC5672
20	772	52.7	995	2	A56599
21	768.5	52.4	985	2	I51672
22	767	52.3	970	2	I78842
23	760.5	51.9	984	2	A39753
24	698.5	47.6	977	2	S49004
25	692	47.2	998	2	S37627
26	681	46.5	993	2	I48653
27	679	46.3	988	2	I50611
28	678	46.2	976	2	A38355
29	662	45.2	975	2	I48974
30	604	41.2	984	1	A34076

31	594.5	40.6	952	2	I50612	protein-tyrosine k
32	589	40.2	938	2	I49071	protein kinase - m
33	569.5	38.8	849	2	I50617	protein-tyrosine k
34	528.5	36.1	1006	2	JC3526	kinase-defective E
35	510	34.8	987	2	I48953	eph-related recept
36	510	34.8	987	2	I48953	mouse developmenta
37	493	33.6	987	2	A54092	protein-tyrosine k
38	397.5	27.1	1019	2	T13039	tyrosine kinase re
39	250.5	17.1	1122	2	T42400	Eph receptor tyros
40	96	6.5	698	2	H71401	probable A6 antier
41	93.5	6.4	982	2	S58881	mults protein homol
42	89.5	6.1	668	2	T05803	hypothetical prote
43	88	6.0	1376	1	VG1HJ2	E2 glycoprotein pr
44	87.5	6.0	788	2	I51530	integrin beta-3 su
45	86	5.9	919	2	T29581	hypothetical prote

ALIGNMENTS

```

RESULT 1
A38224
protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C:Accession: A38224; B38224
R:Wicks, I.P.; Wilkinson, D.; Salvaris, E.; Boyd, A.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
A:Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expe
A:Reference number: A38224; MUID:92179233
A:Accession: A38224
A:Molecule type: mRNA
A:Residues: 1-983 <WIC>
A:Cross-References: GB:M83941; NID:9183931; PID:AAA58633.1; PID:9183932
A:Experimental source: pre-B-cell leukemia cell line LK63
A:Note: sequence extracted from NCBI backbone (NCBI:86627)
A:Accession: B38224
A:Molecule type: protein
A:Residues: 21-39;810-860 <W12>
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferas
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-983/Product: protein-tyrosine kinase hek #status experimental <MAT>
F:542-556/Domain: transmembrane #status predicted <TM>
F:619-883/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif
F:232,337,391,404,493/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1466; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.9e-122;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCQLSTLLSCSVLDSFGELIPQSNVNLDSKTQIGELTSPSHGEETISGVE 60
DB 1 MDCQLSTLLSCSVLDSFGELIPQSNVNLDSKTQIGELTSPSHGEETISGVE 60
QY 61 HYPTRTYQVCNVMDHSONNWLRTNWPVPRNSAQKIYELKFTLRDONSIPLYGTCKEKF 120
DB 61 HYPTRTYQVCNVMDHSONNWLRTNWPVPRNSAQKIYELKFTLRDONSIPLYGTCKEKF 120
QY 61 HYPTRTYQVCNVMDHSONNWLRTNWPVPRNSAQKIYELKFTLRDONSIPLYGTCKEKF 120
DB 61 HYPTRTYQVCNVMDHSONNWLRTNWPVPRNSAQKIYELKFTLRDONSIPLYGTCKEKF 120
QY 121 NIYYESDDHGVKRRHOFTKIDITIADESFQMDLGRILKLTETREVPVNRKGFY 180
DB 121 NIYYESDDHGVKRRHOFTKIDITIADESFQMDLGRILKLTETREVPVNRKGFY 180
QY 121 NIYYESDDHGVKRRHOFTKIDITIADESFQMDLGRILKLTETREVPVNRKGFY 180
DB 121 NIYYESDDHGVKRRHOFTKIDITIADESFQMDLGRILKLTETREVPVNRKGFY 180
QY 181 LAFQDYGACVALVSVRYFKKCFYKTNLAMPDPVPMDSQSLVYRGSCVNNKSEEDP 240
DB 181 LAFQDYGACVALVSVRYFKKCFYKTNLAMPDPVPMDSQSLVYRGSCVNNKSEEDP 240
QY 241 RMYCSTEGEMLVPIGKSCSNAGYERGFMCQ 271
DB 241 RMYCSTEGEMLVPIGKSCSNAGYERGFMCQ 271

```

RESULT 2
A45583
receptor tyrosine kinase Mek4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: A45583
R:Sajjadi, F.G.; Pasquale, E.B.; Subramanli, S.
New Biol.. 3, 769-778, 1991
A:Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse and
A:Reference number: A45583; MUID:92031278
A:Accession: A45583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-983 <SMA>
A:Cross-references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A>Note: sequence extracted from NCBI backbone (NCBI:62398, NCBI:62401)
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C:Keywords: Arp; autophosphorylation; phosphoprotein; transmembrane protein
F:619-885/domain: protein kinase homology <KIN>
F:627-635/region: protein kinase ATP-binding motif

Query Match	95.5%;	Score 1400.5;	DB 2;	Length 983;
Best Local Similarity	95.9%;	Pred. No. 1.9e-116;		
Matches 260; Conservative	3;	Mismatches 7;	Indels 1;	Gaps 1.

Qy	1	MDCCSILLLLSCSYLDSFGELIPQPSNEVNLDSKTIQIGELGWSYPSHGMEISGVD	60
Db	1	MDCHSILVLLCGCVLSCGSELSQPSNEVNLDSKTIQIGELGWSYPSHGMEISGVD	60
Qy	61	HTPTPTTYVCVNMDSQNNMLFTNNVPRNSAQIYELKFTLDCNSIPLVGTCKETE	120
Db	61	HTPTPTTYVCVNMDSQNNMLFTNNVPRNSAQIYELKFTLDCNSIPLVGTCKETE	120
Qy	121	NIYYMESDDDHGKFEHQFTKIDTIAADESFQOMDGDRIILKNTIREYGPVNNKGFY	180
Db	121	NIYYMES-DDHGKFEHQFTKIDTIAADESFQOMDGDRIILKNTIREYGPVNNKGFY	179
Qy	181	IAFDVGVACVALSVRYRFRKCPFTVKNLAMPDTPVMDQSILVEYVSGCVNNKKEBDP	240
Db	180	IAFDVGVACVALSVRYRFRKCPFTVKNLAMPDTPVMDQSILVEYVSGCVNNKKEBDP	239
Qy	241	RMVCSGEEMVLPVIGKCSNAGYEERGFQO	271
Db	240	RMVCSGEEMVLPVIGKCTCNAGYEERGFQO	270

```

RESULT      3
B45583
receptor tyrosine kinase Cerk1 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: B45583
R:SaJJadi, F.G.; Pasquale, E.B.; Subraman1, S.
New Biol. 3, 769-778, 1991
A:Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
A:Reference number: A45583; MUID:92031278
A:Accession: B45583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-983 <SA>
A:Cross-references: GB:M68514; NID:g454809; PIDN:AAA48666.1; PID:g211447
A:Note: sequence extracted from NCBI backbone (NCBIN:62405; NCBIRef:62411)
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C:Keywords: Atp; autophosphorylation; phosphoprotein; transmembrane protein
F:615-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif

```

Query Match	89.3%	Score 1309;	DB 2;	Length 983;
Best Local Similarity	91.6%	Pred. No. 2.6e-108;		
Matches 241; Conservative	8;	Mismatches 14;	Indels 0;	Gaps 0

QY	9	LLISCVSIFSGEIIPOPSNEVLLDLSKIOGELGWSYPSGWEIISGVDEHYPIRTY	68
Db	8	LLILCALSGAGSLNRPNGEVNLLDLSKIOGELGWSYPSGWEIISGVDEHYPIRTY	67
QY	69	QVCNVMDHSONNMLRTNWPVRNSAOKIYVELKFTLDCNSIDLVLGTCKEFTNLYMESD	128
Db	68	QESVNVMDHSONNMLRTNWPVRNSAOKIYVELKFTLDCNSIDLVLGTCKEFTNLYMESD	127
QY	129	DDHGVPKREHQFKIPDIADSEFTOMDGLDRILKNTIRREVPVNNKGFLATODVGA	188
Db	128	DDHLAKREHQFKIPDIADSEFTOMDGLDRILKNTIRREVGVSKKGFLLAQDVGA	187
QY	189	CVALSVRYVYFKKCPFTVKNLAFPTDTPMDSQSLVEVNGSCVNNSKEDDPKMYCSTEG	248
Db	188	CVALSVRYVYFKKCPFTVKNLAFPTDTPMDSQSLVEVNGSCVNNSKKEEPPKMYCSTEG	247
QY	249	EMLVPIKSGSCNNGVEERGPMCO 271	
Db	248	EMLVPIKICLCCNNGVEERGPMCO 270	

RESULT 4

receptor-like tyrosine kinase Enk-2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C:Accession: S51605
R:Matsonpijerre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Enk-1 and Enk-2: two novel members of the Eph receptor-like tyrosine kinase
A:Reference number: S49015; MUID:94067777
A:Accession: S51605
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-948 <MAI>
A:Cross-references: EMBL:S68030
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repe
C:Keywords: ATP; transmembrane protein
E:628-936/Domains: protein kinase homology <KIN>
E:636-644/Region: protein kinase ATP-binding motif

Query Match	68.4%;	Score 1003;	DB 2;	Length 948;
Best Local Similarity	65.7%;	Pred. No. 4.1e-81;		
Matches 180;	Conservative 39;	Mismatches 37;	Indels 18;	Gaps 3

[illegible]

RESULT
I78844

receptor protein-tyrosine kinase - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999

A:Accession: S51603
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-893 <MA1>
A:Cross-references: EMBL:S68028
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:563-829/Domain: protein kinase homology <Kin>
F:571-579/Region: protein kinase ATP-binding motif

Query Match 67.2%; Score 985; DB 2; Length 893;
Best Local Similarity 65.8%; Pred. No. 1.5e-79;

Matches 173; Conservative 45; Mismatches 41; Indels 4; Gaps 2;

QY 10 LILCALALRT---LLASPSNEVNLLDSRTYGLDGLWIAFPKNGWEEIGEDENAPPIHTYQ 69
DB 46 LILCALALRT---LLASPSNEVNLLDSRTYGLDGLWIAFPKNGWEEIGEDENAPPIHTYQ 102
QY 70 VCNVMDHSONNMLRTNMVPRNSAQKIYVELKFTLRDCNSIPVLGTCKETFNLYMESDD 129
DB 103 VCKVMEQNONNMLLTSMISNEGASRIPIELKFTLRDCNSLPGLGTCKETFNMYFESDD 162
QY 130 DHGKRFREHOFTKIDITIADESTQMDLGRILKLTETREVGPNKKGFYLAFODVGAC 189
DB 163 ENGRNKNQYIKIDITIADESEFTELDGRVAKLTETREVDGVPILSKKGFYLAFODVGAC 222
QY 190 VALSVRYVYFKKCPFTVKNLAMFPDTPV-MDSQSLVEVSGCVNNSKEEDPPRMKCSAEG 248
DB 223 IALVSRYVYFKKCPSVYRRLAVFPDITITGADSSQLLEVSQCVNHSVTDPPRMKCSAEG 282
QY 249 EMLVPIGKCSNAGYEERGFMCQ 271
DB 283 EMLVPIGKCMCKRAGYEERKNGTCQ 305

RESULT 9

S51604
receptor-like tyrosine kinase Etk-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C:Accession: S51604
R:Maizompleire, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A:Reference number: S49015; MUID:94067777
A:Accession: S51604
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-981 <MA1>
A:Cross-references: EMBL:S68029
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:651-911/Domain: protein kinase homology <Kin>
F:659-667/Region: protein kinase ATP-binding motif

Query Match 67.2%; Score 985; DB 2; Length 981;
Best Local Similarity 65.8%; Pred. No. 1.7e-79;

Matches 173; Conservative 45; Mismatches 41; Indels 4; Gaps 2;

QY 10 LILCALALRT---LLASPSNEVNLLDSRTYGLDGLWIAFPKNGWEEIGEDENAPPIHTYQ 69
DB 46 LILCALALRT---LLASPSNEVNLLDSRTYGLDGLWIAFPKNGWEEIGEDENAPPIHTYQ 102
QY 70 VCNVMDHSONNMLRTNMVPRNSAQKIYVELKFTLRDCNSIPVLGTCKETFNLYMESDD 129
DB 103 VCKVMEQNONNMLLTSMISNEGASRIPIELKFTLRDCNSLPGLGTCKETFNMYFESDD 162
QY 130 DHGKRFREHOFTKIDITIADESTQMDLGRILKLTETREVGPNKKGFYLAFODVGAC 189
DB 163 ENGRNKNQYIKIDITIADESEFTELDGRVAKLTETREVDGVPILSKKGFYLAFODVGAC 222

DB 163 ENGRNKNQYIKIDITIADESEFTELDGRVAKLTETREVDGVPILSKKGFYLAFODVGAC 222
QY 190 VALSVRYVYFKKCPFTVKNLAMFPDTPV-MDSQSLVEVSGCVNNSKEEDPPRMKCSAEG 248
DB 223 IALVSRYVYFKKCPSVYRRLAVFPDITITGADSSQLLEVSQCVNHSVTDPPRMKCSAEG 282
QY 249 EMLVPIGKCSNAGYEERGFMCQ 271
DB 283 EMLVPIGKCMCKRAGYEERKNGTCQ 305

RESULT 10

S49015
receptor tyrosine kinase Etk-1 - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999

C:Accession: S49015; S51602
R:Maizompleire, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase
A:Reference number: S49015; MUID:94067777
A:Accession: S51602
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1005 <MA1>
A:Cross-references: EMBL:S68024
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:673-941/Domain: protein kinase homology <Kin>
F:683-691/Region: protein kinase ATP-binding motif

Query Match 67.2%; Score 985; DB 2; Length 1005;
Best Local Similarity 65.8%; Pred. No. 1.7e-79;
Matches 173; Conservative 45; Mismatches 41; Indels 4; Gaps 2;

QY 10 LILCALALRT---LLASPSNEVNLLDSRTYGLDGLWIAFPKNGWEEIGEDENAPPIHTYQ 69
DB 46 LILCALALRT---LLASPSNEVNLLDSRTYGLDGLWIAFPKNGWEEIGEDENAPPIHTYQ 102
QY 70 VCNVMDHSONNMLRTNMVPRNSAQKIYVELKFTLRDCNSIPVLGTCKETFNLYMESDD 129
DB 103 VCKVMEQNONNMLLTSMISNEGASRIPIELKFTLRDCNSLPGLGTCKETFNMYFESDD 162
QY 130 DHGKRFREHOFTKIDITIADESTQMDLGRILKLTETREVGPNKKGFYLAFODVGAC 189
DB 163 ENGRNKNQYIKIDITIADESEFTELDGRVAKLTETREVDGVPILSKKGFYLAFODVGAC 222
QY 190 VALSVRYVYFKKCPFTVKNLAMFPDTPV-MDSQSLVEVSGCVNNSKEEDPPRMKCSAEG 248
DB 223 IALVSRYVYFKKCPSVYRRLAVFPDITITGADSSQLLEVSQCVNHSVTDPPRMKCSAEG 282
QY 249 EMLVPIGKCSNAGYEERGFMCQ 271
DB 283 EMLVPIGKCMCKRAGYEERKNGTCQ 305

Query Match 67.2%; Score 985; DB 2; Length 1005;
Best Local Similarity 65.8%; Pred. No. 1.7e-79;

Matches 173; Conservative 45; Mismatches 41; Indels 4; Gaps 2;

QY 10 LILCALALRT---LLASPSNEVNLLDSRTYGLDGLWIAFPKNGWEEIGEDENAPPIHTYQ 69
DB 46 LILCALALRT---LLASPSNEVNLLDSRTYGLDGLWIAFPKNGWEEIGEDENAPPIHTYQ 102
QY 70 VCNVMDHSONNMLRTNMVPRNSAQKIYVELKFTLRDCNSIPVLGTCKETFNLYMESDD 129
DB 103 VCKVMEQNONNMLLTSMISNEGASRIPIELKFTLRDCNSLPGLGTCKETFNMYFESDD 162
QY 130 DHGKRFREHOFTKIDITIADESTQMDLGRILKLTETREVGPNKKGFYLAFODVGAC 189
DB 163 ENGRNKNQYIKIDITIADESEFTELDGRVAKLTETREVDGVPILSKKGFYLAFODVGAC 222
QY 190 VALSVRYVYFKKCPFTVKNLAMFPDTPV-MDSQSLVEVSGCVNNSKEEDPPRMKCSAEG 248
DB 223 IALVSRYVYFKKCPSVYRRLAVFPDITITGADSSQLLEVSQCVNHSVTDPPRMKCSAEG 282
QY 249 EMLVPIGKCSNAGYEERGFMCQ 271
DB 283 EMLVPIGKCMCKRAGYEERKNGTCQ 305

RESULT 11

I78843
receptor protein-tyrosine kinase - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999

C:Accession: I78843
R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welch
Oncogene 10, 897-905, 1995
A:Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 06:01:17 ; Search time 1358.94 Seconds
(without alignments)
2424.883 Million cell updates/sec

Title: US-09-104-340-5
Perfect score: 813
Sequence: 1 atgattgtcagctcccat.....aaagaggtttatgtgcacaa 813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*

45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_est45:*
80: gb_est46:*
81: gb_est47:*
82: gb_gss1:*
83: gb_gss2:*
84: gb_gss3:*
85: gb_gss4:*
86: em_gss1:*
87: em_gss2:*
88: em_gss3:*
89: em_gss4:*
90: gb_gss5:*
91: gb_gss6:*
92: gb_gss7:*
93: gb_gss8:*
94: gb_gss9:*
95: em_gss5:*
96: em_gss6:*
97: em_gss7:*
98: em_gss8:*
99: em_gss9:*
100: em_gss10:*
101: em_gss11:*
102: gb_gss10:*
103: gb_gss11:*
104: em_gss12:*
105: gb_gss12:*
106: gb_gss13:*
107: gb_gss14:*
108: gb_gss15:*
109: gb_gss16:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

	Db	429 c	429	
	RESULT	2		
	AU080921			
	LOCUS	835 bp mRNA EST	20-OCT-1999	
	DEFINITION	Sugano mouse brain mncb Mus musculus CDNA clone MNCB-6241		
	ACCESSION	5' mRNA sequence.		
	VERSION	AU080921		
	KEYWORDS	AU080921.1 GI:6085675		
	SOURCE	EST.		
	ORGANISM	house mouse. Mus musculus		
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
	AUTHORS	I (bases 1 to 835) Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M., Suzuki,Y., Sasaki,M. and Sugano,S. Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capting method Unpublished (1999)		
JOURNAL COMMENT		On May 18, 1998 this sequence version replaced gi:3137227. Contact: Katsuyuki Hashimoto Division of Genetic Resources National Institute of Infectious Diseases 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan Email: khsh@nih.go.jp URL: http://www.nih.go.jp/yoken/genbank/ Location/Qualifiers		
FEATURES		Source		
		1..835		
	/organism=	"Mus musculus"		
	/strain=	"C57BL"		
	/db_xref=	"taxon:10090"		
	/clone_1id=	MNcb-6241"		
	/clone_2lib=	"Sugano mouse brain mncb"		
	/sex=	"female"		
	/dev_stage=	"adult"		
	/lab_host=	"TOP10"		
	/note=	"Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTCGTTTTTT] double-stranded cDNA was ligated to a DraIII adaptor (TGTTGGCACTAG), digested and cloned into distinct DraIII sites of the pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugeno et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTTCTGCCTTAAGAAGTCGCC]"		
BASE COUNT	202 a	182 c	230 g 190 t 31 others	
ORIGIN				
	Query Match	36.6%; Score 297.6; DB 69;	Length 835;	
	Best Local Similarity	63.2%;	Pred. No. 4.2e-80;	
	Matches 469;	Conservative 0;	Mismatches 265; Indels 8; Gaps 2	
Oy	16	tccaccctccttccttgcagcgatggtttcgacagtctgggaacctgatccgccag	75	
Dd	75	TTCATCCCTCTTTCGTTTCCTTTCATTGGAAATTTGGACGCGTCACC GGTTCTAAGGATAAC	134	
Oy	76	cctccaatgaagcaattacttgatatcaaaacaattcaaaggagctggctgcatc	135	
Dd	135	CCCCGAATGAGTAGTTACTTTATTGATGCCAGATCTGTCCAGGAGAGCTGGTGATG	194	
Oy	136	tcttatcat---cacatgygtgysagaagatcagcygtgtygatygaattacaacc	192	
Dd	195	GCAAGCCCCTCTGGAAGAGAGGTGGGGAGATGACATATTATGATGAGAAAATAACACCG	254	
Oy	193	atcaggacttacaggctgycgaatgycatgcagaccacagaccaaatggctgtagaga	252	
Dd	255	ATCCGAACCTACAGAGTGTCCAACGTGATGAGAACCAAGCACCAACAACATGCTGCGAACT	314	

FEATURES	source
RESULT 3	
LOCUS	AM175051
DEFINITION	AM175051 572 bp mRNA EST 16-NOV-1999
ACCESSION	AM175051
VERSION	1
KEYWORDS	EST
SOURCE	zebrafish.
ORGANISM	Danio rerio.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinidae; Rasbora; Danio.
AUTHORS	1 (bases 1 to 572)
TITLE	Sugano, S., Kawakami, K., Johnson, S., Li, F., Marra, M., Eddy, S., Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucada, T., Martin, J., Pape, D., Stepien, M., Underwood, K., Theising, B., Rutter, E., Bowers, T., Wylie, T., Waterston, R., and Wilson, R.
JOURNAL	Washu zebrafish EST Project 1999
COMMENT	Unpublished (1999)
	On Jun 5, 1998 this sequence version replaced gi:3189572.
	Other: ESTs: f131g02.x1
	Contact: S.L. Johnson
	Washington University School of Medicine
	444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
	Tel: 314 286 1800
	Fax: 314 286 1810
	Email: est@wustl.wustl.edu
	Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center
	Seq primer: T3 EF from Amersham
	High quality sequence stop: 485.
	Location/Qualifiers
	1..572
	/organism="Danio rerio"

```

/strain="AB"
/db_xref="taxon:7955"
/clone="2639282"
/clone_lib="Sugano Kawakami zebrafish DBA"
/sex="mixed (one male and one female, including
unfertilized eggs)"
/dev_stage="adult"
/lab_host="DH10B (phage resistant)"
/notes="Vector: pME18S-FL3; site_1: DraIII (CACGTG);
site_2: DraIII (CACATG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[GTGTGGCTACTG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTG, 3' site
CACATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science) and
kindly donated by Dr. Koichi Kawakami. Custom primers for
sequencing: 5' end primer CTCTGCTCTTAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGACACA."
BASE COUNT      169 a      136 c      160 g      104 t      3 others
ORIGIN

```

```

Query Match      24.8%; Score 201.6; DB 74; Length 572;
Best Local Similarity 68.6%; Pred. No. 8e-51;
Matches 306; Conservative 0; Mismatches 136; Indels 4; Gaps 2;

```

```

QY 74 agcctccatgaagcattctactgattcaaaacattcaaggagcctggactga 133
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 113 accctcttaataaagtaagacactgctgactcgaaactgtgcamaagagattgaatggg 172
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 134 tctcttatcacac--acatgggtgggaagagatcagtggtgtggaattacattcacac 190
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 173 ttgcaagcccgacgagagagagaggtggagagtgatgcatgattgagaaatagcc 232
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 191 ccatca-aggattaccagggtgtgcaatgtcatgtaccacagtcacaaatgtgctgaga 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 233 caatcagggagctccacangtgcacacgtaatggaacccagccagaaacaaatggctccga 292
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 250 acaaatgtgtccccaggaacatcagctcagaagattatgtgagctcaagtcaactca 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 293 accgactgattccccctggcgagctcagcggtgttaactgagatcaaaattcacccctgc 352
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 310 cgaagctgcaatagcattcattgttttaggaacttgcaagagagacattcaacctgtac 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 353 cctgactgcaacagctcctcagagagtcattggaacctgcgaagagaccttttaattttac 412
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 370 tacatggagctctgatacatatgggtgtgaaatttcagagagcatcattcaaaagatt 429
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 413 tattatgactcacaacaaatgacaagaagcattacatccgaaanaacagttcaccaaatc 472
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 430 ggcacatggcagctgataaagattcactcaaatgagctcgtggagacctattctgaag 489
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 473 gacaccattgacgctgataaagcttcacgacagtgtagacataggaagacgcattcatgaag 532
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 490 cccaacacgagattagagaagtagg 515
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 533 ctgaacacngaggtgagagatgtggg 558
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 4
AI011631      474 bp      mRNA      EST      31-JAN-1999
LOCUS      EST206082 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
DEFINITION ROVA55 3' end, mRNA sequence.
ACCESSION  AI011631
VERSION     AI011631.1 GI:3225463
KEYWORDS   EST.
SOURCE     Rattus sp.
ORGANISM   Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

```

```

REFERENCE
AUTHORS      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
              1 (bases 1 to 474)
              Lee,N.H., Gloder,A., Chandra,I., Mason,T.M., Quackenbush,J.,
              Kerlavage,A.R. and Adams,M.D.
TITLE         Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
              Gene Index
JOURNAL       Unpublished (1998)
COMMENT       On Jan 19, 1998 this sequence version replaced gi:2153373.
              ATCC
              Contact: Lee, NH

```

```

FEATURES
source
    The Institute for Genomic Research
    9712, Medical Center Drive, Rockville, MD 20850, USA
    Tel: (301)-838-3529
    Fax: (301)-838-0208
    Email: nhlee@tigr.org
    Seq primer: M13-21.
    Location/Qualifiers
        1..474
        /organism="Rattus sp."
        /db_xref="ATCC (lnhost):2021827"
        /db_xref="taxon:10118"
        /clone="ROVA55"
        /clone_lib="Normalized rat ovary, Bento Soares"
        /note="Organ: ovary; Vector: pT73pac; Site_1: EcoRI;
        Site_2: NotI"

```

```

BASE COUNT      117 a      129 c      135 g      93 t
ORIGIN

```

```

Query Match      18.1%; Score 147.4; DB 41; Length 474;
Best Local Similarity 57.1%; Pred. No. 2.8e-34;
Matches 268; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

```

```

QY 71 cgcacctccatgaatcaatcactgattcaaaacattcaaggagcctggact 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4  cgaacagggcaaaagattgtttgctgacttcgacatgaaagggagaaactcgact 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 131 ggaatcttatccatcacatggtgtggaagatcagtggtgtgataacattcacac 190
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 64 ggctcacaacacccctacggaagaggtggagacctatgcacaaacatctgatatgcatgc 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 191 ccatgaagactaccagggtgtgcaatgtcatgtaccacagtcacaaatgtgctgaga 250
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 124 ctatctaatgattgactccctgactgactgctgctgctgacacgacacaaactgctccgta 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 251 caaatgtgtccccaggaactcagctcagaagattatgtgagctcaagtcaactcac 310
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 184 ccaactgggtgacccgggagagcgagccgacatcttattgagctcaagttcacaccgtgc 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 311 ggaactgcaatagcattcattgttttaggaacttgcaagagacattcaacctgtac 370
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 244 gagactgcaatgcttttcgggtggcgacagctcctgcgaagagaccttcaacctctact 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 371 acatgagctctgatacatatgggtgtgaaatttcagagagcatcattcaaaagattg 430
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 304 atgcagacatgacagctgactgactgacacacttccaaagagccagttcaccaagatgc 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 431 aacacatggcagctgataaagttcactcaaatgagctcgtggagacctattctgaagc 490
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 364 acacactgcccctgacgagatcacggtcagcagtgacttggagccttgcaatgtcaagc 423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 491 tcaacactgagattagagaagtaggttcctgttcaacaagaaggaatttca 539
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 424 tgaatgtgagagagcagcatgtggggcccttaccggaaagggcttcta 472
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 5
AI011632      473 bp      mRNA      EST      31-JAN-1999
LOCUS      EST206083 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
DEFINITION ROVA56 3' end, mRNA sequence.
ACCESSION  AI011632
VERSION     AI011632.1 GI:3225464

```


KEYWORDS	EST.	Source
ORGANISM	Rattus sp. Rattus sp. Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 473)	
REFERENCE	Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D. Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat Gene Index Unpublished (1998)	
TITLE	On Jan 19, 1998 this sequence version replaced g1.215374. Contact: Lee, NH	
JOURNAL	ATCC	
COMMENT	The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@igf.org Seq primer: M13-21.	
FEATURES	Location/Qualifiers	
source	1..473 /organism="Rattus sp." /db_xref="ATCC (inhost):2021828" /db_xref="taxon:10118" /clone="ROVA36" /clone_id="Normalized rat ovary, Bento Soares" /note="Organ: ovary; Vector: pUT3pac; Site_1: EcorI; Site_2: NotI"	
BASE COUNT	116 a 127 c 136 g 93 t	1 others
ORIGIN		
Query Match	17.8%; Score 145; DB 41; Length 473;	
Best Local Similarity	57.3%; Pred. No. 1.5e-33;	
Matches	262; Conservative 0; Mismatches 195; Indels 0; Gaps 0;	
QY	82 aatgaagtcacatctctcgtgatccaataaacaattcaaggagctggctgtatctctat	141
Db	17 AAGAGAGTGTCTTCTGCTGACTCCAGCAATGAAGGGGAACTCGCTGCACACAC	76
QY	142 ccatcacatcgtgtggaagagatcgtgtgtgtgatgaacattacacaccatcaggact	201
Db	77 CCTACGGAGAAAGGTGGACCTGATGCAGCAATCATGAAATGACATGCTCTATCATG	136
QY	202 taccaagtggtgcaatgctcatgagcaccagtcacaacaattgctgtagaacaactggtc	261
Db	137 TACTCCGTGTGAATGT	196
QY	262 cccagaaactcagctcagaagaattatgtgtgagctcaagttcaacttaccagactgcaat	321
Db	197 TACCGGAGAGAGCGCGAGCGCATCTTATTATGAGCTCAAGTTCACCGTGGAGAGCTGACAT	256
QY	322 agcatccatcgtgttttggaaactgtcgaaggagacatcaccctgtactacatggtct	381
Db	257 AGCTTCCGGGTGGCGCAGCTCTGCAAGAGAGACCTTCAACCTCTACTATCAGAGTCA	316
QY	382 gatgatgcatcagtggtgaatttcgagagacatcagtttaccagaagtatcacacattga	441
Db	317 GACGTGACATATGGACCAACTTCCAGAGAGCCCGAGTTACCAAGATGCACACCATCGCC	376
QY	442 gctgatgaagtttcaactcaaatgtagctcttggagacgcttatcttgaaagtcacactg	501
Db	377 CCTGACGATGATCAGCGTGAAGTGAATCTGAGGCTCGGCAATGTCAATGTGAATGTGAG	436
QY	502 attagagaagtatgctcctgttcaacaagaagatttt	538
Db	437 GAGCGCATGTGTGGGCCCTTACCGGAGAGGCTTCT	473
RESULT	6	
LOCUS	B36983	424 bp DNN GSS 17-Oct-1997

[illegible]

clone IMAGE:459170 5' similar to gb:U07634 Mus musculus
receptor-protein tyrosine kinase (MOUSE);, mRNA sequence.
ACCESSION AI325344
VERSION AI325344.1 GI:4059773
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 405)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
On Jan 19, 1998 this sequence version replaced gi:2152238.
JOURNAL Contact: Marra M/Mouse EST Project
COMMENT WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:276058
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: 40RP from Gibco.

FEATURES
source
1.406
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:459170"
/clone_lib="Soares mouse placenta 4NBP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: placenta; Vector: p7773D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTCACATCTGAAGTGGAGCGCGCGGAATTTTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 79 a 117 c 109 g 100 t 1 others
ORIGIN

Query Match 15.6%; Score 126.8; DB 44; Length 406;
Best Local Similarity 58.9%; Pred. No. 5.2e-28;
Matches 218; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
QY 82 aatgaagtcactctactgtgtcaaaaacaattcaaggaggatggtgcatctctat 141
DB 393 AAGGAAGTGTGTTGTGTGCTTCGCGACGATGAGGAGAGCTCGCTGCTACGAC 334
QY 142 ccatcacaatggtggaagatcagtggtggtgatgaattacacacccatcaggact 201
DB 333 CCTTATGCGCAAGGCTGGGACCTGATGCAACAATCATGACACATGCTTATCTACATG 274
QY 202 taccaggtgtgtcaatgtcatgagcacaagtcacaacattggtgagacaactgtgtc 261
DB 273 TACTCGGTGTGCAACGTGATCCGGGACACAGACACATGCGTCCGCACTGAGTGGT 214

QY 262 ccaggaactcagctcagaagattatgtgagctcaagtcactctacagactgcaat 321
DB 213 TACCGGAGAGAGCCGACGACATCTTATTGAGCTCAAGTCCAGGTGCAACTGTAAAC 154
QY 322 agcatccatggttttagtaacttcagagagacatcactctacacatgtagtct 381
DB 153 AGCTTCCCGGTGGCGCCGACCTCANTCANAAGACCTTCAACCTTACTATCCAGATGA 94
QY 382 gatgatcatcagtggtggaatttcgagagacatcagttacaaagattacacattga 441
DB 93 GATGTGATGATGAGCAACAACTTCCAGAGCGCCAGATTACCAAGATTGACACATCGCC 34
QY 442 gctgatgaana 451
DB 33 CCGACGAGA 24

RESULT 8
LOCUS R15219
DEFINITION R15219 402 bp mRNA EST 13-APR-1995
y188e12.r1 Soares infant brain INTB Homo sapiens cDNA clone
IMAGE:29543 5' similar to gb:M83941 TYROSINE-PROTEIN KINASE
RECEPTOR HEK PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION R15219
VERSION R15219.1 GI:769492
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 402)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
On Sep 21, 1992 this sequence version replaced gi:276397.
JOURNAL Contact: Wilson RK
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1695
High quality sequence stops: 337
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1695 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 337.

FEATURES
source
1.402
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:401890"
/db_xref="taxon:9606"
/clone_image="IMAGE:29543"
/clone_lib="Soares infant brain INTB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: latmid BA; Site_1: Not
I; Site_2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5',
AAGTGAAGATTCGCGCGCGGACGAGATTTTCTTTTCTTTTCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the latmid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 108 a 75 c 110 g 108 t 1 others
ORIGIN

```
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: EcoRI"
```


DB	ACC	CHROM	START	END	ORIENTATION	FEATURES
262	cccaaggaactcagcgcacaaagattatctgagagcccaagttacactcaggaacgcgat	321				
201	TACCGGAGAGAGCCGAGCGCATCTTTATTGTAGCTCAAGTTACGCTGCGAGACTGTAC	260				
322	agcatccatggtgttagaagacttcgaagaggaacttaacactctacta	371				
261	AGCTTCGCGGGTGGGCGCAGCTCAATGACNAGAGACCTTCAACCTCTACTA	310				
14	AI967980	418 bp	mRNA	EST	25-AUG-1999	
LOCUS	AI967980/c					
DEFINITION	swulf04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516671 3', similar to SW:EP8_MOUSE 009127 EPHRIN TYPE-A RECEPTOR 8 PRECURSOR ; , mRNA sequence.					
ACCESSION	AI967980					
VERSION	AI967980.1					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgp.					
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index					
JOURNAL	Unpublished (1997)					
COMMENT	On Jun 5, 1998 this sequence version replaced gi:3189146. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbcp/image/image.html					
FEATURES	Seq primer: -40UP from G1bco.					
SOURCE	Location/Qualifiers					
	1. 418					
	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
	/clone="IMAGE:2516671"					
	/clone_lib="NCI-CGAP_GC6"					
	/tissue_type="Pooled germ cell tumors"					
	/lab_host="DH10B"					
	/note="Vector: pRT73D-Pac (pharmacia) with a modified polylinker. Plasmid DNA from the normalized library NCI-CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1257096-1258631, 1469664-1470983, and 1475597-1476743)." Subtraction by Bento Soares and M. Fatima Bonaldo.					
BASE COUNT	73 a 152 c 116 g 77 t					
ORIGIN						

	Query Match	Similarity	10.8%	Score 88.2	DB 63	Length 418:
Best Local	Similarity	62.9%	Pred. No. 3	3e-16:		
Matches 154:	Conservative	0:	Mismatches 88:	Indels 3:	Gaps 1	
QY	553	gattgtggtgctcttgctgcttggtgctggtctctgagaggtatacttcaaaagtgccattt	612			
DB	417	gacattgagctcctgctgctgacatctctctctctcgcattcatatgaaagttgctcctgcc	358			
QY	613	acagtgaaagatctggtctatgttttccagaacacgtatccatgagctccagctc---ctg	669			

Db	357	ATGGAGCCATCTGCGTTCCTCTCGGAGCAGTGAGAGGGGCCCACTGTCTCTACTG	298
Oy	670	gtggaagtttagaggcttctgtgtcaacaatcttaagagaagatcctccaagtattac	729
Db	297	GTTGGAGTGAAGGGCCCATGCTGCCTCGGCACACAGAGGCGGACACACCACAATGTAC	238
Oy	730	tgcacataagaagcgaaatggcttgtaaccattggcaagtcttcctgcaatgcctgat	789
Db	237	TGCACCGCGGAGGGCGAATGCTGTGCTGCCCATCGGCAAAATGCTGTGACATGTCGGCTAC	178
Oy	790	gaaga 794	
Db	177	GAGGA 173	
RESULT	15		
LOCUS	AM366937/c		
DEFINITION	344 bp mRNA	EST	04-FEB-2000
ACCESSION	IL0-HR0156-251099-132-e12 HR0156 Homo sapiens CDNA, mRNA sequence.		
VERSION	AM366937.1 GI:6871587		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	HGP http://www.ludwig.org.br/ORESTES.		
COMMENT	The FAPESP/LICR Human Cancer Genome Project Unpublished (1999) On Mar 16, 1998 this sequence version replaced g1:2961824. Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL0&t2=IL0-HR0156- 251099-132-a12&t3=1999-10-25&t4=1) Seq primer: puc 18 forward High quality sequence start: 30 High quality sequence stop: 343. Location/Qualifiers 1..344 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="HR0156" /dev_stage="Adult" /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. letters patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
BASE COUNT	73 a	98 c	95 g
ORIGIN	78 t		

	Query Match	Similarity	10.6%	Score 86	DB 80	Length 344	
Best Local	Similarity	60.1%	Pred	1.4e-15			
Matches	143	Conservative	0	Mismatches	35	Indels	0
						Gaps	0
QY	182	attacacacccatcagagactaccaggtgtgtcaatgtcatgtgagacacagttcaaacatc	241				
DB	268	ATGACATGCGCGATACACTGTACTCGTGTGTCAACGTATGTCGTCGACACCGAGGCACT	209				
QY	242	gacttgagacaaactggatccccaggaactccgctcccaagaattatgttgaggtccaagt	301				

```
db 208 GCGCGCGCACCACTGGGTGTACCGAGAGAGGCTGACGTATCTTCATTGAGCTCAAGT 149
QY 302 TCACTCTAGAGACTGCAATAGCATTCATTGTTAGGAATCTGCAAGGAGACATTCa 361
Db 148 TTTACTGTACGTGACTGCAACAGCTTCCCTGTTGGCGCCAGCTCTCTCAAGAGACTTTCA 89
QY 362 accgttactacatggagtcctgatgatcatcgtgggtgaatttcgagagcatcagtt 419
Db 88 ACCTATACTATGCGGAGTCAAGGACCTGAGACTAGGCTCCCAATTCCAGAAAGCGCTGT 31
```

Search completed: May 15, 2000, 11:20:11
Job time: 19134 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 10:51:21 ; Search time 102.62 Seconds
(without alignments)
1005.931 Million cell updates/sec

Title: US-09-104-340-5
Perfect score: 813
Sequence: 1 atgattgtcagctccat.....aaagaggtttatgtgcaa 813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 226296 seqs, 63486255 residues

Total number of hits satisfying chosen parameters: 452592

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/lna/5C.COMB.seq:*
4: /cgn2_6/ptodata/2/lna/5D.COMB.seq:*
5: /cgn2_6/ptodata/2/lna/6.COMB.seq:*
6: /cgn2_6/ptodata/2/lna/PTUS.COMB.seq:*
7: /cgn2_6/ptodata/2/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813	100.0	3132	1 US-08-167-919A-9	Sequence 9, Appl1
2	813	100.0	3132	5 US-08-715-106-9	Sequence 9, Appl1
3	545	67.0	3254	1 US-08-162-809-15	Sequence 15, Appl1
4	351.4	43.2	3906	3 US-08-469-537A-102	Sequence 102, App
5	351.4	43.2	4165	2 US-08-442-248-1	Sequence 1, Appl1
6	351.4	43.2	4165	2 US-08-440-815-1	Sequence 1, Appl1
7	349.8	43.0	4222	2 US-08-673-789-1	Sequence 1, Appl1
8	348.2	42.8	3592	3 US-08-469-537A-100	Sequence 100, App
9	344.4	42.4	3116	4 US-08-449-645A-14	Sequence 14, Appl1
10	344.4	42.4	3116	4 US-08-702-367A-10	Sequence 14, Appl1
11	344.4	42.4	3116	6 PCT-US95-04681-14	Sequence 14, Appl1
12	344.4	42.4	3348	1 US-08-222-616-34	Sequence 34, Appl1
13	344.4	42.4	3348	6 PCT-US95-04228-34	Sequence 34, Appl1
14	344.4	42.4	4529	4 US-08-449-645A-16	Sequence 16, Appl1
15	344.4	42.4	4529	4 US-08-702-367A-16	Sequence 16, Appl1
16	344.4	42.4	4529	6 PCT-US95-04681-16	Sequence 16, Appl1
17	343.4	42.2	3162	4 US-08-449-645A-12	Sequence 12, Appl1
18	343.4	42.2	3162	4 US-08-702-367A-12	Sequence 12, Appl1
19	343.4	42.2	3262	6 PCT-US95-04681-12	Sequence 12, Appl1
20	334.8	41.2	2323	6 PCT-US96-00419-6	Sequence 6, Appl1
21	334.8	41.2	2901	6 PCT-US96-00419-1	Sequence 4, Appl1
22	334.8	41.2	4304	6 PCT-US96-00419-1	Sequence 1, Appl1
23	245.2	30.2	3059	1 US-08-162-809-21	Sequence 21, Appl1
24	245.2	30.2	3059	1 US-08-162-809-3	Sequence 3, Appl1
25	245.2	30.2	3125	1 US-08-162-809-19	Sequence 19, Appl1
26	219.6	27.0	2820	1 US-08-162-809-5	Sequence 5, Appl1
27	213.4	26.2	4049	1 US-08-162-809-17	Sequence 17, Appl1

28	213.4	26.2	4097	1 US-08-162-809-11	Sequence 11, Appl1
29	194.4	23.9	2962	4 US-08-449-645A-10	Sequence 10, Appl1
30	194.4	23.9	2962	4 US-08-702-367A-10	Sequence 10, Appl1
31	194.4	23.9	2962	6 PCT-US95-04681-10	Sequence 10, Appl1
32	150	18.5	3546	1 US-08-162-809-9	Sequence 9, Appl1
33	150	18.5	3591	1 US-08-162-809-13	Sequence 13, Appl1
34	141.4	17.4	3776	1 US-08-162-809-7	Sequence 7, Appl1
35	136	16.7	2982	1 US-08-348-143-2	Sequence 2, Appl1
36	136	16.7	2982	2 US-08-571-785-2	Sequence 2, Appl1
37	136	16.7	4027	1 US-08-348-143-3	Sequence 3, Appl1
38	136	16.7	4027	1 US-08-348-143-4	Sequence 3, Appl1
39	136	16.7	4027	2 US-08-571-785-3	Sequence 3, Appl1
40	136	16.7	4027	2 US-08-571-785-4	Sequence 4, Appl1
41	115.4	14.2	3133	1 US-08-162-809-1	Sequence 1, Appl1
42	80.8	9.9	3969	1 US-08-436-044-5	Sequence 5, Appl1
43	80.8	9.9	3969	1 US-08-222-616-23	Sequence 23, Appl1
44	80.8	9.9	3969	3 US-08-436-054-5	Sequence 5, Appl1
45	80.8	9.9	3969	6 PCT-US95-04228-23	Sequence 23, Appl1

ALIGNMENTS

RESULT 1
US-08-167-919A-9
; Sequence 9, Application US/08167919A
; Patent No. 5674691
; GENERAL INFORMATION:
; APPLICANT: Boyd, Andrew W.
; APPLICANT: Simpson, Richard J.
; APPLICANT: Wicks, Ian
; APPLICANT: Ward, Larry D.
; APPLICANT: Wilkinson, David
; TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
; NUMBER OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,919A
; FILING DATE: 18-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK6841 (AU)
; FILING DATE: 21-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK9992 (AU)
; FILING DATE: 12-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU92/00294
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3132 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..3048
US-08-167-919A-9

Query Match 100.0%; Score 813; DB 1; Length 3132;
Best Local Similarity 100.0%; Pred. No. 2.9e-253;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgagatgtaagctctccatccctccctccctccagctgctctgttctcgacagcttcg 60
DB 100 ATGAGATGTAGCTCTCCATCTCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTG 159
QY 61 gaactgaattccgagcgccttccaatgaatcaatcactgattccaataaacaattcaagg 120
DB 160 GAACGTGATTCGGACGCTTCCATGAAGTCAATCTACTGATTCMAAAACAATTCAGGG 219
QY 121 gagctggcgtgagatctcttaccatcagtggtggaagaagatcagtggtgagtgaa 180
DB 220 GAGCTGGGCTGGATCTCTTATCCATCATGGGCGGAAGATCAGTGGTGGATGAA 279
QY 181 cattacaaccccatcaggactaccagggtgcaatgtcatgtgacacacagtcacaaacat 240
DB 280 CATTACACACCCCATCAGAGACTTACAGAGTGCMAATGTCAAGACACAGTCAAAACAT 339
QY 241 tggctggaacaaactggtgccccgaagaactcagctcagaagaattttgtggagctcaag 300
DB 340 TGGCTGGAACAAACTGGTCCCGGAGACTCAGACTGAGAAATTTGTTGGAGCTTCAG 399
QY 301 ttcaactcagagagctgcaatcagctccatttggtttaggaacttgcaggagagacatc 360
DB 400 TTCACTCTAGAGAGCTCATAGCATTCATGTTTATAGAACTTCAAGAGACATTC 459
QY 361 aacctgtactacatgagcgtctgatatgatacagtgagtggaatttcgagagcactc 420
DB 460 AACCTGTACTACATGAGAGTGTGATGATGATCATGGGTGAAATTTCCAGAGCATCAT 519
QY 421 acaaaagttagaccatctgagctgagtgaaagtctcactcaaatgagctcttggagagcgt 480
DB 520 ACAAAAGATTGACCATTCAGAGTGTGATGAAATTTCACTCAAAATGATCTTGGGGACGT 579
QY 481 attctgagctcacaactgagatgagaaagtaagtccttccacaagaagagatttat 540
DB 580 ATTCTGAAGCTCAACACTGAGATTAGAGAAAGTAGAGTCTCTGCAACAAGAAAGGATTTAT 639
QY 541 ttggcattcaagaatgttggctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
DB 640 TTGGCATTTCAGATGT 699
QY 601 aagtgcccatcttaccagtggaagaatctgctatgtttccagaacaagtgtaaccatgactcc 660
DB 700 AAGTGCCCATTTTACAGTGAAGAAATCTGGCTATGTTTCCAGACAGGTAACCATGAGTCC 759
QY 661 cagtcacctggtgagagtgtaagaggtctgtgtcaacaatttaaggaagaagatcccca 720
DB 760 CAGTCCCTGGTGGAGGTATTAGAGGCTTGTGTCAACAATTCTAAGGAGAAAGATCTCCCA 819
QY 721 aggaatgactgagtgatcagaagaagcgaaatggtgtacccattggcagaatgttccctgaat 780
DB 820 AGGATGACTGACATGACAGAAAGCGAATGGCTTATACCACATGGCAAGTGTCTGCAAT 879
QY 781 gctggcattagaagaagaaggttttatgtgcaa 813
DB 880 GCTGGCTATGAAGAAAGGTTTATGTGCCAA 912

RESULT 2
US-08-715-106-9
; Sequence 9, Application US/08715106

Patent No. 6020306
GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGILIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SAMS UR
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..3048
US-08-715-106-9

Query Match 100.0%; Score 813; DB 5; Length 3132;
Best Local Similarity 100.0%; Pred. No. 2.9e-253;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgagatgtaagctctccatccctccctccctccagctgctctgttctcgacagcttcg 60
DB 100 ATGAGATGTAGCTCTCCATCTCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTG 159
QY 61 gaactgaattccgagcgccttccaatgaatcaatcactgattccaataaacaattcaagg 120
DB 160 GAACGTGATTCGGACGCTTCCATGAAGTCAATCTACTGATTCMAAAACAATTCAGGG 219
QY 121 gagctggcgtgagatctcttaccatcagtggtggaagaagatcagtggtgagtgaa 180
DB 220 GAGCTGGGCTGGATCTCTTATCCATCATGGGCGGAAGATCAGTGGTGGATGAA 279

```

Qy 181 cttacacacccatcaggacttaccagctgtcgaatgtcatgtgacacagtcacacat 240
Db 280 CATTCACACCCATCAGGACTTACAGAGGTGTCATGTATGACACAGTAAACAT 339
Qy 241 tggctgagaacaactggtccccaagaactagctcagaagaattatgtgagctcaag 300
Db 340 TGGCTGAGAAACAACTGGGTCCCGAGAACTCAGACTCAGAAATTTATGTGAGCTCAAG 399
Qy 301 ttccctcaggagactgtaataagctcattcattgttttaggagacttgaagaagcattc 360
Db 400 TTCCTCAGAGACTGCAATAGCAATTCATTCATGTTTGAAGACTTCAGAGACATTC 459
Qy 361 aacctgtactacatgagctctgatgatcatcagtggtggaatttcagagacatgatt 420
Db 460 AACCTGACTACATGAGATCTGATGATCATGTGGGTGAATTTCCAGAGCATAGTTT 519
Qy 421 acaagaattgacacacattgacgtgaaagtctcactcaaaatgattcttggggacct 480
Db 520 ACAAGATTGACACCATTCAGCTGATGAAAGTTTCACCAAAATGATCTTGGGACCGT 579
Qy 481 attctgaagctcaacactgagattgagaagaagtagtccctgttaacaagaagatttat 540
Db 580 ATTCTGAAGCTCAACACTGAGATTAGAGAAAGTCTCTGTCACCAAGAGGATTTAT 639
Qy 541 ttggaattcaagaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
Db 640 TTGGCATTTCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 699
Qy 601 aagtcaccattacagtgaaagaatcgtgtatgtttcagacacagtgtaaccatgactcc 660
Db 700 AAGTCCCATTTACAGTAAGAAATCTGGCTATGTTCCAGACAGGTACCCATGAGATCC 759
Qy 661 cagtcctcgtggtgaggttagaggtctgtgtcaacaattcgaaggaagaattcccca 720
Db 760 CAGTCCCTGgtgaggttagaggtctgtgtcaacaattcgaaggaagaattcccca 819
Qy 721 agagtgactcgaagtgacgaaggaagcgaatggtctgttaccattggaagtggtccctgca 780
Db 820 AGGATGACTCGAGTACAGAAAGCGAATGGCTGTATGCCATTGGCAAGTGTCTTCGANT 879
Qy 781 gctgctatgaagaagaaggtttatgtgccaa 813
Db 880 GCTGCTATGAAGAAGAGGTTTATGTGCCAA 912

```

RESULT 3
US-08-162-809-15
Sequence 15, Application US/08162809
Patent No. 5457048

GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

```

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3254 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 32..2980
US-08-162-809-15

Query Match 67.0%; Score 545; DB 1; Length 3254;
Best Local Similarity 80.0%; Pred. No. 1.4e-166;
Matches 641; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

Qy 13 ctctccatcctcctcctcctcctcagctgtctgtctcgcacagcttcggggaactgattccg 72
Db 41 CGCCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 100
Qy 73 cagcttccaatgaatgaatctactgtgatacacaacaattcaaggagagctggtctg 132
Db 101 CGCCCGGCAACGAAATGATCTGCTGATTCMAAAACAAATTCAGGGAGCTGGCTGG 160
Qy 133 attcttcatcacaatcaggtgtggaagaatcaggtgtgtgtgtgtgtgtgtgtgtgtgtgt 192
Db 161 ATCTCTCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 220
Qy 193 atcaggaattacagagtgatgacatgtgacacagacagtcacaacaattgtgtgaaaca 252
Db 221 ATCAGAACTTACCAAGAGAGCAATGTATGTATGATCACTCAAAACAAATGTGCTGGAACA 280
Qy 253 aactggtccccaaggaactcagctcagaagaattatgtgagctcaagttcaactctaca 312
Db 281 AACTGGATTCCACGCAATTCAGCGCAGAAATATGTGAGAGCTTCMACTTACCTTGAGG 340
Qy 313 gactcgaatcagatccatcagtggttttaggaacttgcaaggaagaattcaactgactac 372
Db 341 GACTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 400
Qy 373 atgagctcgaatgacatcaggtgtgaaattcgaagacacagtcagttacaagaattgac 432
Db 401 ATGGAATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 460
Qy 433 accattcagctgatatgaagaattcactcaaatgtgacttggggagaccttcgaagctc 492
Db 461 AOCATGGGGGCTGATGAGAGAGCTTACCAGATGATGATGATGATGATGATGATGATGATG 520
Qy 493 aacattgagattgaagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 552
Db 521 AATACCGAATGCTCGGAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 580
Qy 553 gatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 612
Db 581 GATGTAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 640
Qy 613 acaatgaagaatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 672
Db 641 ACTGTCAAGAACTCGCCATGTTTCCAGATACAGTTCCTATGAGACTCCCACTCCGTGGTG 700
Qy 673 gaggttagaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 732
Db 701 GAGGTGCGGGTCTTGTGTATTCATTCACAGAGGAGAGCCACCAAAATGATGATGATG 760
Qy 733 agtacaagaagggaatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 792
Db 761 AGCAGGAAGAGAAATGCTAGTGTGCTATGAGGAAGTCTGTGTAACTGTGCTATGAA 820

```

[illegible]

```

Dh 750 ATGAAACTATGCCCCCATCATCACCACTATCAAGTGTGCAAAATTATGAAACAGATTCAGA 809
Oy 236 acaatttcctgagaaacaaacttggctcccaagaacctcagctcaagaagtttctatgagac 295
Dh 810 ATAAATGGCTGTGGACCAAGTTGGATGTTCTTACCAAGAGTCTCTCCAGAAATTTTATTTAGAC 869
Oy 296 tcaagttcctactcctcgaagactcgaatagaagcatccatctggtctttaagaacctgcaagagaa 355
Dh 870 TCAAGTTTACTGTGAGGGAGATTCGAACAGCGCTTCTGTGAGAGACTGGGGACTTGCAAGAGA 929
Oy 356 catcaaccctgtactacaatgagctcgtatgataatcatgagtgagtgaggttgaatttcgagacatc 415
Dh 930 CTTTAAACATGATTTATTTTGGAGTCCGATGTAGATGAGATGGGAAATATTCAAAGGAACCC 989
Oy 416 agttacaaagatgacacacccattgcaagctcgaatgaagtttcaactcaaatgagatcttggag 475
Dh 990 AGTACATCAAGATCGAATACCATTTGCTGCTGATGAGAGCTTCAACCGAATCTTGACCTTGGAG 1049
Oy 476 acagatctcgaagctcaacactcgaatagaatagaagtaagttcctgttcaacaaagaagagat 535
Dh 1050 ACCGGGTCATGAAAGCTGAATACCGAGAGTCAAGATGTAGAGACTCTGAGCAAAAAGGAGAT 1109
Oy 536 ttatttggagatttcaagaatggttggctgtgtgttgcccttggtctgttgagagatcact 595
Dh 1110 TTTATCTTGCTTTCCAAAGATGTGGTGCTTGACATGCTGTGTTCTGTGTCGTGTCTACT 1169
Oy 596 tcaaaagatgccatttaccagtgtaagaagaatctgctatgttctcagaacacggttaccacatg 655
Dh 1170 ATAAAAATGTCCTTGATGTAGATGAGATTTGGCTGTTTCCCTGACACGATCACTGAG 1229
Oy 656 actccacgtccc---tggatgaggttaagagggtctctgtgtcaacaatctctaagaagaag 712
Dh 1230 CAGATTTCTCCCAAGTGTCTGAGAGTGTCAAGGCTCCCTGACCAACTTCTGTGACAGACG 1289
Oy 713 atctccaaagatgactagtcagtcagacagaagaagcgaatgagctgtaccacattgccaagtgtt 772
Dh 1280 ATCTCCCAAAATGCAATGCAATGCAAGTCTGAAAGGGAGTGGCTGTTCTCCATCGGGAATGCA 1349
Oy 773 cctgcaatgctggcctatgaaagaagaaggttttatgtgcctaa 813
Dh 1350 TGTCAAGCCCGGATATGAAAGAAAAATGATGCTGTCAA 1390

RESULT 5
US-08-442-248-1
: Sequence 1, Application US/08442248
: Patent No. 5759863
: GENERAL INFORMATION:
: APPLICANT: Caras, Igorid W.
: APPLICANT: Winslow, John W.
: TITLE OF INVENTION: AL-1 Neurotrophic Factor
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patln (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/442,248
: FILING DATE: 15-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/330128
: FILING DATE: 27-OCT-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Torchia, Timothy E.

```

REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: 920C4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8674
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4165 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-442-248-1

Query Match 43.2%; Score 351.4; DB 2; Length 4165;
 Best Local Similarity 67.3%; Pred. No. 6.9e-104;
 Matches 512; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

```

QY 56 tcggggaactgattccgagccttcccaatgagatcattctgattcacaacaattc 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 695 TCCGGACCCCTTTGGCCAGCCCAAGTACGAAGTATTTATGATTCGCGCACTGTC 754

QY 116 aagggaagctgggctgagctctctatccacatgagtgaggagaagatcagtggtg 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 755 TGGGAGACCTTGATGATGATGCTTTCCAAAGAAATGGGTGGGAAGATGGTGAAGTTG 814

QY 176 atgaacattacacccatcaggacttccaggtgtgcaatgtcatgtgacacagtc 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 815 ATGAAATATACCCCCCAACACCTATCAAGTGTCAAGTATGCAAGATGAGATGAGA 874

QY 236 acaattgctgtagaacaactgggtcccccaggaaactcagctcagagaaattatg 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 875 ATATTTGGCTTTTGACCGTGTGATCTTAACGAAGGTGCTTCCAGATTTTATTTGAC 934

QY 296 tcaagttcaactcagagactgcaatagcattccattgttttaagaaactgcaagaga 355
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 935 TCAAGTTACTCTGAGGATGCAACACCTCTCGAGAGACTGGGAGACTTGCAAGAGA 994

QY 356 catcaacctgtactacatgagtgatgtatgatacagtgagggtgaaattcgaagatc 415
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 995 CCTTAACTATATTTATTTAGTGTGATGATGAGATGGGAGAAATATCAAGAGAAC 1054

QY 416 agttcaaaagattgacacactgctgagtgatgaaagttcactcaaatgagatcctg 475
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1055 AGTACATCAATGATGATACATGCTGCTGATGAGAGCTTCAACGAACTTGACCTTGAG 1114

QY 476 accglatctgagctcaacactgagattagaaagtagtgcctgtgtcacaagaagagat 535
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1115 ACCGGTCAATGAGCTGAATACGAGGTGACAGATGTAGAACCTCTGAGCAAAAGGAT 1174

QY 536 ttatttggacttccaagaattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 595
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1175 TTTATCTGCTTTCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234

QY 596 tcaaaaagtgccatttcaagtgaaagatctggtctatgttccagacaggttaccatag 655
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1235 ATAAAATATGCTCTTCTTACTAGTACATTTGGCTGTTTCCCTTACACGATCAGTGA 1294

QY 656 actcccaagtc---tggtagagtgtagaggtgtgtgtgtgtgtgtgtgtgtgtgtgt 712
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1295 CAGATTTCTCCAGTGTGCTAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAG 1354

QY 713 atcttccaagatgtactgagcagtagaagaagcgaatggtgtgtgtgtgtgtgtgtgtgt 772
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1355 ATCCCTCCAAATGATGATGAGTGTGAGAGGAGATGGCTGCTGCTGCTGCTGCTGCTGCA 1414

QY 773 cctgcaatgctgctatgaaagaaggtttatgtgcaa 813
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1415 TGTGAGAGCCGGATATGAAGAGAAATGATCTGTCA 1455
  
```

RESULT 6

US-08-440-815-1
 Sequence 1, Application US/08440815
 Patent No. 5798448
 GENERAL INFORMATION:
 APPLICANT: Caras, Ingrid W.
 APPLICANT: Winslow, John W.
 TITLE OF INVENTION: AL-1 Neurotrophic Factor
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/440,815
 FILING DATE: 15-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/330128
 FILING DATE: 27-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: 920C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8674
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4165 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-440-815-1

Query Match 43.2%; Score 351.4; DB 2; Length 4165;
 Best Local Similarity 67.3%; Pred. No. 6.9e-104;
 Matches 512; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

```

QY 56 tcggggaactgattccgagccttcccaatgagatcattctgattcacaacaattc 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 695 TCCGGACCCCTTTGGCCAGCCCAAGTACGAAGTATTTATGATTCGCGCACTGTC 754

QY 116 aagggaagctgggctgagctctctatccacatgagtgaggagaagatcagtggtg 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 755 TGGGAGACCTTGATGATGATGCTTTCCAAAGAAATGGGTGGGAAGATGGTGAAGTTG 814

QY 176 atgaacattacacccatcaggacttccaggtgtgcaatgtcatgtgacacagtc 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 815 ATGAAATATACCCCCCAACACCTATCAAGTGTCAAGTATGCAAGATGAGATGAGA 874

QY 236 acaattgctgtagaacaactgggtcccccaggaaactcagctcagagaaattatg 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 875 ATATTTGGCTTTTGACCGTGTGATCTTAACGAAGGTGCTTCCAGATTTTATTTGAC 934

QY 296 tcaagttcaactcagagactgcaatagcattccattgttttaagaaactgcaagaga 355
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 935 TCAAGTTACTCTGAGGATGCAACACCTCTCTGAGAGACTGGGAGACTTGCAAGAGA 994

QY 356 catcaacctgtactacatgagtgatgtatgatacagtgagggtgaaattcgaagatc 415
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 995 CCTTAACTATATTTATTTAGTGTGATGATGAGATGGGAGAAATATCAAGAGAAC 1054

QY 416 agttcaaaagattgacacactgctgagtgatgaaagttcactcaaatgagatcctg 475
  
```

Db 1055 AGTACATCAGATCATACCATTCCTGCTGATGAGAGCTTCAACCGAACTTGAGAG 1114
Qy 476 accgatctcgaagctcaaacactgagattagaagaagtagtctcgtcaacaagaaggat 535
Db 1115 ACCGGGTGATGAGATGATAGAGAGTACAGATGTAGACTCTGACCAAAAAGGAT 1174
Qy 536 ttatttgcatctcaagatgtgtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 595
Db 1175 TTTATCTGCTTCCAAAGATGTGGGCTGCTGATCGCTGCTGCTGCTGCTGCTGCTGCT 1234
Qy 596 tcaaaagagccatttaacagtagaagaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 655
Db 1235 ATAAAAATGTCTCTGTGATGATGACATTTGGCTGTTTCCCTGACACGATCAGTGAG 1294
Qy 656 actccagctccc---tggtgagagttagaaggctgtgtgtgtgtgtgtgtgtgtgtgtgt 712
Db 1295 CAGATTCCTCCAGTTGCTGAGAGGTGTGAGGCTCCTGCTCAACCTTTGTGTGACAGAG 1354
Qy 713 atctccaaagatgtactgacgtacagaagagcgaatgtgtgtgtgtgtgtgtgtgtgtgt 772
Db 1355 ATCCCTCCCAAAATGATTCAGTGTGAGAGGGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1414
Qy 773 cctgcaatgt 813
Db 1415 TGTGCAAGCGGATGATGAGAAAAATGTACTGTCAA 1455

RESULT 7
US-08-673-789-1
; Sequence 1, Application US/08673789
; Patent No. 5814479
; GENERAL INFORMATION:
; APPLICANT: ZHOU, RENSING; SCHULZ, NICHOLAS,
; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
; APPLICANT: GEORGE, F.
; TITLE OF INVENTION: BSK RECEPTOR LIKE
; TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
; TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,789
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/177,812
; FILING DATE: 04-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GROPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4322
; TYPE: NUCLEOTIDE
; STRANDEDNESS: DOUBLE

; TOPOLOGY: UNKNOWN
US-08-673-789-1
Query Match 43.0%; Score 349 8; DB 2; Length 4322;
Best Local Similarity 67.1%; Pred. No. 2.3e-103;
Matches 511; Conservative 0; Mismatches 247; Indels 3; Gaps 1;
Qy 56 tcggggaactgtatccgaagccttcacatgaagtcacatcctgtgtatccaanaacattc 115
Db 572 TCCGAGACCTTTGGCCACAGCCGCCACAGAAAGTAATTTGTGTGATTCGGGCATGTCA 631
Qy 116 aagggaagctgggt 175
Db 632 TGGGGACCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
Qy 176 atgaacattacacacccatccgaagcttccgaagctgtgtgtgtgtgtgtgtgtgtgtgtgt 235
Db 692 ATGAGAACTATGCCCCCATCCACATACCAAGTGTGAAATTTGTGACAGAAATCAGA 751
Qy 236 acaatgt 295
Db 752 ATAAATGGCTGTGACAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 811
Qy 296 tcaagttcaactcagagactgtcaatagcatcattgtgtgtgtgtgtgtgtgtgtgtgtgt 355
Db 812 TCAAGTTTACTTTTAAAGGCTGCAACAGCTCTGAGAGACTGGGAGCTGTGAGAGA 871
Qy 356 catcaacctgtactcaatagtggt 415
Db 872 CATTTAACTGTATTATTATTGATGATGATGATGATGATGATGATGATGATGATGATGATG 931
Qy 416 agttcaaaagatgtac 475
Db 932 AATACATCAAGTTTATACATCAGCTGCAAGATGAGAGCTTCAAGAAATTTGATCTGTGTG 991
Qy 476 accgatctcgaagctcaaacactgagattagaagaagtagtctgtgtgtgtgtgtgtgtgt 535
Db 992 ACCGTGTCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1051
Qy 536 ttatttgcatctcaagatgt 595
Db 1052 TTTATCTGCTTCCAAAGATGTGGGCTGCTGATGCTGTGTGTGTGTGTGTGTGTGTGT 1111
Qy 596 tcaaaagatgtcccatctcaagtagaagaatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 652
Db 1112 ATAAAAAGTGTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1171
Qy 653 tggactccagctccgt 712
Db 1172 CAGATTCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1231
Qy 713 atctccaaagatgt 772
Db 1232 ATCTCTCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1291
Qy 773 cctgcaatgt 813
Db 1292 TGTGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1352

RESULT 8
US-08-469-537A-100
; Sequence 100, Application US/08469537A
; Patent No. 5843749
; GENERAL INFORMATION:
; APPLICANT: Maisongier, et al.
; TITLE OF INVENTION: EHR AND ROR TYROSINE
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road

```

1 CITY: Tarrytown
2 STATE: NY
3 COUNTRY: U.S.A.
4 ZIP: 10591
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Diskette
7 COMPUTER: IBM Compatible
8 OPERATING SYSTEM: DOS
9 SOFTWARE: FastSeq version 2.0
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/469,537A
12 FILING DATE: 06-JUN-1995
13 CLASSIFICATION: 435
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: USSN 08/406,247
16 FILING DATE: 17-MAR-1995
17 APPLICATION NUMBER: USSN 08/144,992
18 FILING DATE: 28-OCT-1993
19 APPLICATION NUMBER: USSN 07/736,559
20 FILING DATE: 26-JUL-1991
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Kempner, Ph.D., Gail M
23 REGISTRATION NUMBER: 32,143
24 REFERENCE/DOCKET NUMBER: REG 070C
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 914-345-7400
27 TELEFAX: 914-345-7721
28 TELEX:
29 INFORMATION FOR SEQ ID NO: 100:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 3592 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: unknown
34 TOPOLOGY: unknown
35 MOLECULE TYPE: DNA
36 FEATURE:
37 NAME/KEY: CDS
38 LOCATION: 598..3444
39 FEATURE:
40 NAME/KEY: modified_base
41 LOCATION: 56
42 OTHER INFORMATION: /mod_base- OTHER
43 OTHER INFORMATION: /label- N
44 OTHER INFORMATION: /note- "Where N = G, A, C or T"
45 FEATURE:
46 NAME/KEY: modified_base
47 LOCATION: 3538
48 OTHER INFORMATION: /mod_base- OTHER
49 OTHER INFORMATION: /label- N
50 OTHER INFORMATION: /note- "Where N = G, A, C or T"
51
52 JS-08-469-537A-100

```

OY	319	atagcattccatggttlltaggaacttgcagaaggaacattcaacctgacctagag	378
Db	928	AACGACATCCCATGGGCTTTGGGAAGCTGTAAGAAACAATTTACGTGATTAATTTATA	987
OY	379	tcctatgatcatcagtgaggaaattctcgagcatcagttctacaagaattgacacatt	438
Db	988	TCTAGCGAATCCACGGAACTAAATTCAGCCAGCCAAATATATAGATTGACCAATT	1047
OY	439	gcagctgaagaagtttcaactcaatgatactctgaggaccgattctgaagctcaact	498
Db	1048	GCTGGGATGAGAACTTTTACTGATGATGATTTGGGATCGCATCCTTAACTCAACT	1107
OY	499	gagattgagaagtaagtcctctgcaacaagaaggaatttatttggcatttcaagaatc	558
Db	1108	GAAATTGCTGAGGTGGGGCCAAATGAAAGGAAGATTTCTATTGGCTTTCAAAATAT	1167
OY	559	ggtctctgttgccttgggtgctctgtagagataacttcaaaaagtgccattacatg	618
Db	1168	GGACCATGCAATGCTCTGGGCTCAGTCCGGTCTTTTACAAAAAATGCCCTTCAC	1227
OY	619	aagactctggctatgtttccagaacagatgacca---tggactccaaagtcctgttggag	675
Db	1228	CGGAATCTGGCTAGTCTTCCGGATACCAATCCCAAGGCTGACTCTTCTTGGTCAA	1287
OY	676	gttagaaggtctctgtgcaacaattctaaaggagaagaatcctccaagaagtactgcagt	735
Db	1288	GTGGGGGGCTCATCCGTGAAGAGTGTGAAGACGAGAAATCTCTAAACTCATCTGATGA	1347
OY	736	acagaagagcgaatggtctgtaccattgycgaagtgttctctgcaatgcttgcataaaga	795
Db	1348	GCTATGAGACATGGCTGCTCCCTTGGAGAGTGTATCTGCACATACAGGATATAGAA	1407
OY	796	agaagtttattgtgcga	812
Db	1408	ATCGAAGGATCTTGCCA	1424

Query Match	42.8%	Score 348.2	DB 3	Length 3592
Best Local Similarity	68.0%	Pred. Nm. 7e-103		
Matches 501	Conservative 0	Mismatches 233	Indels 3	Gaps 1
QY	79	lccaatgaagtaactctactgattcgaacaaacaattccaagggagctggtcgatctct	138	
Db	688	TCCAACCAAGTTGCTTCTGCTATACATCTACAGTCATGGGAACTAGAGTAAACA	747	
QY	139	tatcatcacatgggtgaggaaagatcagttgtgtgaaatcacaccatcagg	198	
Db	748	TATCACCAGTAATGGCTGGGATGCCATTACTGAAATGGATGAACACACAGGCCCATCAT	807	
QY	159	acttcacagggtgtgaaagtcatatgaccacagttcaaaaataattgctgtgagcaaatcgt	258	
Db	808	ACATACCCAGTGTGAATGCAATGCATGGACCAACCGAAMAACTGGTTGTACTAATCG	867	
QY	259	gtccccaagaaactcagctcagaagaatttatgtggaagctcaagttcactctaaagaagctgc	318	
Db	868	ATCTCTCGTGAATGCTGCTCAGAAATCTATGTGGAAATGAAGTTCCATTGAGAGATTTCT	927	

```

1      RESULT      9
2      US-08-449-645A-14
3      ; Sequence 14, Application US/08449645A
4      ; Patent No. 5981245
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Fox, Gary M.
7      ; TITLE OF INVENTION: Eph-like Receptor Protein Tyrosine
8      ; TITLE OF INVENTION: Kinases
9      ; NUMBER OF SEQUENCES: 43
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESSEE: Amgen Patent Operations/RBW
12     ; STREET: 1840 Dehavilland Drive
13     ; CITY: Thousand Oaks
14     ; STATE: California
15     ; COUNTRY: USA
16     ; ZIP: 91320
17     ; COMPUTER READABLE FORM:
18     ; MEDIUM TYPE: Floppy disk
19     ; COMPUTER: IBM PC compatible
20     ; OPERATING SYSTEM: PC-DOS/MS-DOS
21     ; SOFTWARE: Patentin Release #1.0, Version #1.30
22     ; CURRENT APPLICATION DATA:
23     ; APPLICATION NUMBER: US/08/449,645A
24     ; FILING DATE:
25     ; CLASSIFICATION: 435
26     ; ATTORNEY/AGENT INFORMATION:
27     ; NAME: Winter, Robert B.
28     ; REFERENCE/DOCKET NUMBER: A-287
29     ; INFORMATION FOR SEQ ID NO: 14:
30     ; SEQUENCE CHARACTERISTICS:
31     ; LENGTH: 316 base pairs
32     ; TYPE: nucleic acid
33     ; STRANDEDNESS: single
34     ; TOPOLOGY: linear
35     ; MOLECULE TYPE: cDNA
36     ; FEATURE:

```

NAME/KEY: CDS
LOCATION: 34...2994
US-08-449-645A-14

Query Match 42.4%; Score 344.4; DB 4; Length 3116;
Best Local Similarity 68.2%; Pred. No. 1.1e-101;
Matches 509; Conservative 0; Mismatches 231; Indels 6; Gaps 2;

```
OY 74 agcctccatgaatgaatcactcactcagatcctcaaaaacatcaaggagagcctggcctga 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 110 ACCCGCGAATGAATACCTTATTGATTCAGATCTTTGAGGAGAACTGGGTGA 169
OY 134 tctc---ttatccatcacatgggtgggaagatacagtgctgtaatacattcacac 190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 170 TAGCAAGCCCTTGAGAGAGAGGGTGAGAGGAGTATGATGATAAATAATACAC 229
OY 191 ccatagaagatcctcagaggtgctcaatgtcatgacacacgtcaaaaacattgctgaga 250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 230 CAATCGAAGCTTACCAAGTGTGCAATGTATGAAACCCGCAAGATAACTGGCTACGA 289
OY 251 caaactgggtcccccaggaactcagctcagaagaattatgtgagctcaagctcacttac 310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 290 CTGATTGGATCACCGAGAGAGGGGCTCAGAGGCTGATATTGAGATTAAATTCACCTTA 349
OY 311 gagactgcataatgacatcccatggttttagaacttgcaggagagacatcaacctgtact 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 350 GGGACTGCAATAGTCTTCCGGGCGTCATGGGACTTGCAGAGAGACGTTTAACCTGTACT 409
OY 371 acatgagatcgtatgatatactatgggtgaaatttcgagaacatcaatgttaacaaagatg 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 410 ACTATGAATCAGACAAACGCAAGAGCGTTTCATCAGAGAGAACCACTTGTCTAAATTG 469
OY 431 acaccatgcagctgactgaagaattcactcaaatgactctgggagacgtatcttgaaagc 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 470 ACACATTTGCTCTATGAGAGCTTACCCAGTGAACCTTGTGTGACAGAAATCATGAAAC 529
OY 491 tcaacactgagattagagaagtagtccctgtcaacaagaagaagatttatttggcatttc 550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 530 TGAACACCGAGATCCGGGATGTAGGGGCCATTAAGCAAAAAGGGTTTACTGGCTTTTC 589
OY 551 aagatggtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 610
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 590 AGGATGTGGGGCTGTGATCGCCCTGTGTATCACTGCTGTCTATTAATAAAGTGTCCAC 649
OY 611 ttacagtgagaagatcgtgctatgttccacagacaggtacccatg---gactccacgtccc 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 650 TCACAGTCCGCAATCTGGGCCAGTTTCCGTGACACCATCAAGGGCTGTATAGCTTCCC 709
OY 668 tgggtgaggttagaggtgtctgtgtcaacaattcctaaggagaaagatcctccaagatgt 727
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 710 TGGTGGAAATTCGAGGCTCTCTGTCAACACTCAGAAAGAAAGATGTGCCAAAAATGT 769
OY 728 actgtagtacaagaagaggtgtgtgtacatgtggcaaggtgtccctcaatgtcgtgt 787
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 770 ACTGTGGGCAATGTGTATGAGTGTGTATCCCATTTGGCACTGCTATGCAAGCTGGGC 829
OY 788 atgaagaagaaggtttattgtgtccaa 813
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 830 ATGAGAGAGCGGAGCGGAATGCCAA 855
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 10
US-08-702-367A-14
Sequence 14, Application US/08702367A
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 34...2994
US-08-702-367A-14

Query Match 42.4%; Score 344.4; DB 4; Length 3116;
Best Local Similarity 68.2%; Pred. No. 1.1e-101;
Matches 509; Conservative 0; Mismatches 231; Indels 6; Gaps 2;

```
OY 74 agcctccatgaatgaatcactcactcagatcctcaaaaacatcaaggagagcctggcctga 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 110 ACCCGCGAATGAATACCTTATTGATTCAGATCTTTGAGGAGAACTGGGTGA 169
OY 134 tctc---ttatccatcacatgggtgggaagatcagtgctgtaatacattcacac 190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 170 TAGCAAGCCCTTGAGAGAGAGGGTGAGAGGAGTATGATGATAAATAATACAC 229
OY 191 ccatagaagatcctcagaggtgctcaatgtcatgacacacgtcaaaaacattgctgaga 250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 230 CAATCGAAGCTTACCAAGTGTGCAATGTATGAAACCCGCAAGATAACTGGCTACGA 289
OY 251 caaactgggtcccccaggaactcagctcagaagaattatgtgagctcaagctcacttac 310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 290 CTGATTGGATCACCGAGAGAGGGGCTCAGAGGCTGATATTGAGATTAAATTCACCTTGA 349
OY 311 gagactgcataatgacatcccatggttttagaacttgcaggagagacatcaacctgtact 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 350 GGGACTGCAATAGTCTTCCGGGCGTCATGGGACTTGCAGAGAGACGTTTAACCTGTACT 409
OY 371 acatgagatcgtatgatatactatgggtgaaatttcgagaacatcaatgttaacaaagatg 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 410 ACTATGAATCAGACAAACGCAAGAGCGTTTCATCAGAGAGAACCACTTGTCTAAATTG 469
OY 431 acaccatgcagctgactgaagaattcactcaaatgactctgggagacgtatcttgaaagc 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 470 ACACATTTGCTCTATGAGAGCTTACCCAGTGTGAAAGTGTGACAGAAATCATGAAGC 529
OY 491 tcaacactgagattagagaagtagtccctgtcaacaagaagaagatttatttggcatttc 550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 530 TGAACACCGAGATCCGGGATGTAGGGCCATTAAGCAAAAAGGGTTTAACTGGCTTTTC 589
OY 551 aagatggtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 610
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 590 AGGATGTGGGGCTGTGATCGCCCTGTGTATCACTGCTGTCTATTAATAAAGTGTCCAC 649
OY 611 ttacagtgagaagatcgtgctatgttccacagacaggtacccatg---gactccacgtccc 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 650 TCACAGTCCGCAATCTGGGCCAGTTTCCGTGACACCATCAAGGGCTGTATAGCTTCCC 709
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```



```

Oy 668 tggttgaggttggagggcttctgtgcacaatcttaaggaggaagtctctccaagatgt 727
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 710 tggttgaggttggagggcttctgtgtcacaactcagacaagaaagatgtgccaaaaatgt 769
Oy 728 actgcagtcacaagaagcgaatgtgcttgtaaccatgtgcgaagtgcttcctgcaatgcctgct 787
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 770 actgtggcgacagatggtgaatgctgctgtaaccatttgcgaactgcgaactgcaatgcacgctggac 829
Oy 768 atgaagaagaagtgcttattatgtgccaa 813
      ||||| ||||| ||||| |||||
Db 830 atgagagagcgagcgagagaatgccaa 855

RESULT 11
PCT-US95-04681-14
; Sequence 14, Application PC/TUS9504681
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04681
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 34..2994
; PCT-US95-04681-14

Query Match 42.4%; Score 344.4; DB 6; Length 316;
Best Local Similarity 68.2%; Pred. No. 1,1e-101;
Matches 509; Conservative 0; Mismatches 231; Indels 6; Gaps 2

Oy 74 aggcctccaatgaatcatcatctactcgtgattccaacaaacattcaaggggagctgggctgga 133
Db 110 accccggcaattgaattgaccttatttggaattccagatctgttcagaggagaaacttggtggatga 169
Oy 134 tctc---ttatccatcacatcagtggtggaagagatcagtggtgtgtgtagaacattacacac 190
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 tagcaagacccttggaaagagaggggtggaggaagtagtcatgtgagtgaaaaaaatcac 229
Oy 191 ccatacgaacttaaccaggtgtgcaatgtcatcgtgaccacagatcaaaaacaatgtgctgaga 250
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 230 caatccgaaccttaccgaagtgcatagtgatggaacccagcagaaataactggcttcgaa 289
Oy 251 caaatgggtgcccaaggaactcagctcagaagaattatgtgtagctcgaatgtcactctac 310
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 290 ctgatttgatcaccggagagagggcttcagaggggtgataatttgagatttaaatccaccttga 349

```

QY	311	gagactgcgaataacgcatlccattcgtgtlltlaagaaactgcgaagagacatcaacctgact	370
Db	350	GGGACTGCAAAATAGTCTTCCTCCGGCGCTCATGGGGACTTCGACAGAACGTTTAACCTGACT	409
QY	371	acatggaatcgcgatgatcatcgtatcgtgggtlgaaaattcggagagcatcagtttacaagaattg	430
Db	410	ACTATGAATCTGACACACACAAAGAGGCTTTCATCTCAGAGAAACCAAGTTTGTCAAAATTG	469
QY	431	acaccattgcagcctgcgatbaaagtttcaactcaaatggaatcttgaggaccgtatcttcgaagc	490
Db	470	ACACATATTGCTGCTGATAGAGCTTCACCCAGAGGGACATTGGAGACAGATATATGAAC	529
QY	491	tcaacactgaaattagaaagtagtccctgcgaacaaagaaaggaatttatttgcgcatlc	550
Db	530	TGAACACCGAGATCCGGGATGTAGGGCCATTAAACCAAAAGGGGTTTACTCGGCTTTC	589
QY	551	aagatggttggtgctctgtgtgtccttggtgtgtctgtgagagatatacttcaaaaagtgccat	610
Db	590	AGGAGTGTGGGGCCCTGCATCCCTCCGTGATCAGTCCGTGTCTTATAAAAAGTGTCAC	649
QY	611	ttacagtgaaagaactctggtctatggtttccagacaagagaccag --- gactccagagccc	667
Db	650	TCACAGTCCGCAATCTGGCCCGAGTTTCTTGACACATCTACAGGGGGCTGATACGCTTTCCC	709
QY	668	tggtgaggtttagaaggtgtctgtgttcaacaaattcctaagaggaagatccccaaggaagt	727
Db	710	TGTGTGAGTTCGAGGGCTCCCTGTCTCAACAACTAGAAAGGAAAGATGTGCCCCAAAATGT	765
QY	728	actgcagtacagaagagcgaaatgctgttaccacatttggcgaagtgtcttcctgcaatgct	787
Db	770	ACTGTGGGGCAGATGATGTAATGCGCTGTGATCCATTGGCACTGCTATGCAACGCTGGGC	829
QY	788	atgaagaagaaggtttattatggtccaa	813
Db	830	ATGAGAGCGGAGCGGAGAAATGCCAA	855

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

```

? FILING DATE: 22-JAN-1992
? ATTORNEY/AGENT INFORMATION:
?
? NAME: Lee, Wendy M.
? REGISTRATION NUMBER:
? REFERENCE/DOCKET NUMBER: 821P22
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/225-1994
? TELEFAX: 415/952-9881
?
? TELER: 910/371-7168
? INFORMATION FOR SEQ ID NO: 34:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 3348 bases
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
US-08-222-616-34

```

Query Match	42.4%	Score 344.4	DB 1	Length 3348
Best Local Similarity	68.2%	Pred. No. 1.1e-101		
Matches 509; Conservative	0	Mismatches 231;	Indels 6;	Gaps 2

QY	74	agctctccaagaaagtcacatctactctggtatccaataaacatccaaggggagcttggctggga	133
Db	77	ACCCCGGAATGAAGTTAACTTATTGGATTCTCGAGATCTGTTCAGGGAGAACTTGGGTGGa	136
QY	134	tctc---tlatcacaatggttgggaagagatcaagtgggtgttggatgaaatatacacac	190
Db	137	TAGCAAGCCCTCTGGAAGAGGGGTGGGAGGAAGAGTATCATGTGATGAAGAAAAATACAC	196
QY	191	ccatcaggaacttaccaggtgtgcaatgtcatatgagcccaagtcataaacaaatctgctgaaga	250
Db	197	CAATCCGAACCTTACCAAGTGTGCATGTGATGAAGGAACCCACCAGAAATACGTGCTACGAa	256
QY	251	caaaacttgggtcccccaggaactccaactcagaagaatttatgtggagctcaagttaactctac	310
Db	257	CTGATTGGATTACCCCGAAGAGGGGCTCAGAGGGTGTTATTAGATTAATTAATCACTTGA	316
QY	311	gagactgcgaatagcatctccatttggtttttaggaacttgcagaagagacatacactgtact	370
Db	317	GGGACTGCAATAAGTCTTCGCCGGGCTCATGGGGACTTCCAAAGAGAGCTTAACCTGACT	376
QY	371	acatgtagtctcgtatgatagtatcatgtgggttgaaattctgagagcatcagtttaacaagattg	430
Db	377	ACTATGATCTGAGAACAGACAAAGAGCGTTTCATCAAGAGAGAACCACTTTGTCAAAATTG	436
QY	431	acacacattgcagctgcatgaaagtttcaactcaaatgagatctttgggagccgattctgaagc	490
Db	437	ACACCAATTGCTGCTGATGAGAGCTTCAACCAAGTGGACATTGGTGACAGATATATGAAGC	496
QY	491	tcaaacactgagattatgaaagaagtaagtcctgtccaacaagaagaggaatttatatttggcatctc	550
Db	497	TGAACACCGAATCCGGGAGTGTAGGGCATTAACCAAAAAGGGGTTTAACTTGCTTTTC	556
QY	551	aagatgttgtgtgtcttgtgtgcttgggtgtctgttggagatatacttcaaaaglygccat	610
Db	557	AGGATGTGGGGGCGCTGTGATCGCCCTGGTATCAGTCCGTGTCTATPAAAAATGTTCAC	616
QY	611	ttacagatgaagaatcttggctatgttttttcagacaagagtaaccatg---gactccagttccc	667
Db	617	TCAACAGTCCGCCAATCTGGGCCCAAGTTTCTGTGACACATCAACAGGGGGGTGAATAGCTTTCC	676
QY	668	tgtgtcgaaggttttagaggggtcctgtgttccaacaatcttaaggggaagaatccctccaagatgt	727
Db	677	TGGTGGGAAGTTTCGAGGGCTCCTGTGTCCAACAATCAGAAAGAAAAGATGTCCAAAAATGT	736
QY	728	actgtcagttacagaagagcgaaatgtgctgttaccacatttggcagaagtgttctctgaatgtgact	787
Db	737	ACTGTGGGGCGAGATGGTGAATAGCTGTGTACCACTTGGCACTGCGCATTGCAAGCGTGGGC	796
QY	788	atgagaagaagaggtttcatatggtccaa	813
Db	797	ATGAGAGAGCGGAGCGGAATGTCCAA	822

RESULT 13
PCT-US95-04228-34

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:

CITY: South San Francisco
STATE: California
COUNTRY: USA

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 KB f1d
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US5/042228

```

CLASSIFICATION:
PRIOR APPLICATION DATE: 08/22/22
APPLICATION NUMBER: 04-APR-1994
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 8
TELECOMMUNICATION INFORMATION
TELEPHONE: 415/225-1994
TELEFAX: 415/955-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 34:

Query Match	42.48;	Score 344.4;	DB 6;	Length 3348;
Best Local Similarity	68.28;	Pred. No. 1.1e-101;		
Matches 509; Conservative	0;	Mismatches 231;	Indels 6;	Gaps 2

QY	74	agcttcgaatgaagtcacatctatggaattcaaaaacaaatcaaggagctggctggga	133
Db	77	ACCCCGGAGTGAAGTACTTATGATTCAGATTTGTTCCAGGGGAACCTTGGGTGGA	136
QY	134	tctc---ttatcacaatgatgggtgggaagagatcagtggtggtgatgaacataacacac	190
Db	137	TAGCAAGCCCTCTGGAAGGAGGGTGGAGAGAGTATCATGAGGAGAAAAATTTAC	196
QY	191	ccatcgaagacttacagctgtgcacgttcaatggacacagtcacaacaaatctggtcgaa	250
Db	197	CAATCGAACCTTACCAGTGTGCAATGTATGAAACCCACGAAATTAATGGCTACGAA	256
QY	251	caaaacttggtccccaagaactcagctcagaagatctatgtggagctcaagttcaacttac	310
Db	257	CTGATTGGATCACCCGGAAGGGGCTCAGAGGGGTGTTATTGAGATTAAATTCACCTTGA	316
QY	311	gagactcgaatgacattccatttggtttcttaagaacttgcaggagacattcaactctact	370

Db 317 GGGAGTCAATAGTCTTCGGGGCTCATGGGACTTGGAGAGACGTTTAACCTGTACT 376
Qy 371 acatgagctcgtatgatcatcatggtggaatttcgagagcatcagtttcaaaagtatg 430
Db 377 ACTATGATTCAGACACACAAAGAGCTTTCATCAGAGAGAACCAAGTTTGTCAAAATG 436
Qy 431 acacccatcgcagctgatatgaatttcaactcaaatgacatcttgaggacgtatctgaagc 490
Db 437 ACACATGCTGCTGATGATGAGAGCTTCACCCAAAGTGCATTTGGTACAGAAATCATGAAGC 496
Qy 491 tcaacagcagaattagagaagtagtctctgtcacaagaagaaggtatttatttgcatctc 550
Db 497 TGAACACCGAATCCGGGATGTAGGGCATTAAAGCAAAAGGGGTTTACCTGCGTTTTC 556
Qy 551 aagatgttggtcgtctgtgttccttgctgtctgtgagagatcttcaaaaagtcgcat 610
Db 557 AGGATGTGGGGGCTGCATCCGCTCGTATCATGCTCGTGTCTATATAAAGTGTCCAC 616
Qy 611 ttacagtgaagaatctgtgtatgtttccagacacggtacccatg---gactccagatccc 667
Db 617 TCACAGTCCGCAATCTGCGCCAGTTTCTGACACCATCATCAGGGGCTGATAGCTTCC 676
Qy 668 tgggtggaggttagagggctgtgtcacaacattcagaagagaagatctcccaagatgt 727
Db 677 TGGTGGAGGTTCGAGGCTCTGTGCAACACTCAGAAAGAAAGATGTGCCAAATGT 736
Qy 728 actgcagtagaagaagcgaatgagctgtgaccattggaaggtgtcttcgaatgtgct 787
Db 737 ACTGTGGGGCAGATGTGTAAATGCGTGTGTAACCATTTGGCACTGCTATGCAACGCTGGC 796
Qy 788 atgaagaagaaggtttatgtccaa 813
Db 797 ATGAGAGCGGAGCGAGATGCCAA 822

RESULT 14
US-08-449-645A-16
Sequence 16, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBM
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 186..3182

US-08-449-645A-16

Query Match 42.48; Score 344.4; DB 4; Length 4529;
Best Local Similarity 68.18; Pred. No. 1.3e-101;
Matches 512; Conservative 0; Mismatches 231; Indels 9; Gaps 2;

Qy 71 cgaagccttccatgaatgatactactgatttcaaaacattccaagggagtgct 130
Db 265 CGCAGGCTCGAGAGGAACTACTGCTGATTTTAAAGCAACAAACAGAGTTGGAGT 324
Qy 131 ggaactctatccatccatgagtggtggaagaagatcagtggtgatatgaatcaccac 190
Db 325 GGATTTCTCTCCACCAACCAATGGTGGGAGAAATTAGTGCTTTGATGAGAACTATACC 384
Qy 191 ccatcagaactaccaggtgtgtcaatgtcatalgagccacagtcacaacaaatgtgtgaa 250
Db 385 CGATACGAACATACCAAGTGTGCCAAGTCATGAGCCCAACCAAAACAACTGCGCGGA 444
Qy 251 caaactggtccccaaggaactcaagctcagaagaattatgtgagctcaagtcactac 310
Db 445 CTAACTGGATTTCCAAAGCGCAATGCACAAAGATTTTGTGAATTAATTCACCTGGA 504
Qy 311 ggaactgcaatagatctccatgttttaagaacttgaagagacattcaactgact 370
Db 505 GGGATTTGTAAACAGTCTTCTGAGATGACTGGAACCTTGCAGAGAAACATTTATTTGTA 564
Qy 371 acatgagctcgtatgatatcattgagtggaatttcgagagacatcagttcaagaattg 430
Db 565 ATATGAACACAGACTATGACACTGCGAGAAATATAGAAACCTGTATGTAAATAG 624
Qy 431 acacattgcagctgatatgaagtttcaactcaatgagatcttgaggacgtatctgaagc 490
Db 625 ACACCATTTGCTGCAGATGAAGTTTACCCAGGTGACTGTGTAAGAAAGATGAAGC 684
Qy 491 tcaacactgagattaggaagtagtctgtcacaagaagaagattatatttgcatctc 550
Db 685 TTAACACTGAGGTGAGAGAGATTTGACCTTTGTCCAAAGAGATTTCTATTTCTCTTC 744
Qy 551 aagatgtgtgtctgt 610
Db 745 AGGATGTAGGGGCTGTGATGACTTGTGTTCTGTCAAAAGTGTACTACAAAGAGTGTGT 804
Qy 611 ttacaggaagaatctgt 667
Db 805 CCATTTATGAGAACTTGAATCTTCTCCAGATTAAGTGTGTTCAAAATTTCTCTT 864
Qy 668 tgggtggaggttagagggctgtgtcacaacattcagaaga-----ggaagatctccaa 721
Db 865 TAGTCGAGGTTTCGAGGAGCATGTCTCAGCAGTGCAGAGAGAAAGCGGAAAGCCGCCCA 924
Qy 722 ggaatcctgcagtcagagaagcgaatgagctgtgaccattggaaggtgtctcagatg 781
Db 925 GGATGCACTGCAGTGCAGAGAGAAATGTTAGTGTGCCATTTGGAATAATGTATCTGCAAG 984
Qy 782 ctggtctagaagaaggttttattgtccaa 813
Db 985 CAGGCTACGACGCAAAAGAGACACTTGTGAA 1016

RESULT 15
US-08-702-367A-16
Sequence 16, Application US/08702367A
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBM
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks

STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 186..3182
US-08-702-367A-16

Query Match 42.4%; Score 344.4; DB 4; Length 4529;
Best Local Similarity 68.1%; Pred. No. 1.3e-101;

Matches 512; Conservative 0; Mismatches 231; Indels 9; Gaps 2;

QY 71 cgcagccttcacatgaatcactatcgtatcgaataaacaattcaaggagctggct 130
DB 265 cccagccttcacatgaatcactatcgtatcgaataaacaattcaaggagctggct 324
QY 131 ggaatccttaccatcactatggtggagagagtcagtggtgagtggaattacacac 190
DB 325 ggaattccctccaccac 384
QY 191 ccacagagactacagagtggtgcaatgcatgagaccacagtcacacacacacacacac 250
DB 385 cgaatgagac 444
QY 251 caaactgggtcccccaggaactcagtcagagagattatgtygagctcaagttcactac 310
DB 445 cttaactggaattccaaagcacaatgcacaaagacattttgagaaattgaaattcaccctga 504
QY 311 ggaactgcacatgacatcattcattggttttaggaactgcagagagacatcacaactgact 370
DB 505 ggaattgtaacagctcttctggaactggaactggaactggaactggaactggaact 564
QY 371 acatgagagctgagatgagatgagatgagatgagatgagatgagatgagatgagatg 430
DB 565 attatgaaacagacatgacatgacatgacatgacatgacatgacatgacatgacatg 624
QY 431 acacacatgcagctgagatgagatgagatgagatgagatgagatgagatgagatg 490
DB 625 acacacatgctgagatgagatgagatgagatgagatgagatgagatgagatgagatg 684
QY 491 tcaacacatgagatgagatgagatgagatgagatgagatgagatgagatgagatg 550
DB 685 ttaacacatgagatgagatgagatgagatgagatgagatgagatgagatgagatg 744
QY 551 aagatgttggtgctgt 610
DB 745 aggatgttggtgctgt 804
QY 611 ttaacagtgagatgagatgagatgagatgagatgagatgagatgagatgagatg 667
DB 805 ccattattgagacatgacatgacatgacatgacatgacatgacatgacatgacatg 864
QY 668 tgggtgaggttgagaggtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 721

DB 865 tagtcgaggttcgagagacatgctgacagagacagagacagagacagagacagagac 924
QY 722 ggaatgactgagatgagatgagatgagatgagatgagatgagatgagatgagatg 781
DB 925 ggaatgactgagatgagatgagatgagatgagatgagatgagatgagatgagatg 984
QY 782 ctggtatgag 843
DB 985 cagcctaccagcag 1016

Search completed: May 15, 2000, 12:05:01
Job time: 4420 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 10:52:01 ; Search time 111.14 Seconds
(without alignments)
1830.180 Million cell updates/sec

Title: US-09-104-340-5

Perfect score: 813
Sequence: 1 atgagatgcagctccatcaat.....aaagagtttatgtgcca 813

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813	100.0	3132	1	HEK coding sequenc
2	545	67.0	3254	1	Eph-related PTK Ce
3	351.4	43.2	3906	1	Rat receptor tyros
4	351.4	43.0	4165	1	Rat RSK7 CDNA. AL-
5	349.8	43.0	4322	1	Mouse Bsk receptor
6	348.2	42.8	3592	1	Rat receptor tyros
7	344.4	42.4	3115	1	EPH-like receptor
8	344.4	42.4	3348	1	Protein tyrosine-k
9	344.4	42.4	4529	1	EPH-like receptor
10	343.4	41.2	3162	1	EPH-like receptor
11	334.8	41.2	2323	1	Mouse developmenta
12	334.8	41.2	2901	1	Mouse developmenta
13	334.8	41.2	4304	1	Mouse developmenta
14	245.2	30.2	3056	1	EPH-related PTK Ce
15	245.2	30.2	3059	1	EPH-related PTK Ce
16	245.2	30.2	3125	1	EPH-related PTK Ce
17	219.6	27.0	2820	1	EPH-related PTK Ce
18	218.8	26.9	4281	1	elk cDNA. Expressi
19	218	26.8	3105	1	Receptor tyrosine
20	218	26.8	3105	1	Mouse Nuk tyrosine
21	213.4	26.2	4049	1	EPH-related PTK Ce
22	213.4	26.2	4097	1	EPH-related PTK Ce
23	194.4	23.9	2962	1	EPH-like receptor
24	150	18.5	3546	1	EPH-related PTK Ce
25	150	18.5	3591	1	EPH-related PTK Ce
26	143.4	17.6	3751	1	Human embryonal ki
27	141.4	17.4	3776	1	EPH-related PTK Ce
28	136	16.7	2982	1	EPH-related PTK Ce
29	136	16.7	4027	1	Protein p140 CDNA
30	136	16.7	4027	1	Protein p140 CDNA
31	129.6	15.9	3663	1	Embryonic stem cel
32	115.4	14.2	3133	1	EPH-related tyrosi
33	81.6	10.0	3969	1	PTK gene HPTK5. Ne
34	80.8	9.9	3969	1	Protein tyrosine-k

35	80.8	9.9	4290	1	092641	Human non-differen
36	80.8	9.9	4290	1	T18394	Receptor type tyro
37	80.8	9.9	4290	1	T42593	Coding sequence fo
38	80.8	9.9	4290	1	T51235	Receptor-type tyro
39	64	7.9	450	1	V90061	EST clone CW960. N
40	64	7.9	3673	1	V33697	Human thymus recep
41	64	7.9	4022	1	V62177	Human receptor typ
42	37.4	4.6	324	1	O61342	Human brain Expres
43	32.8	4.0	9927	1	X12997	Enterococcus faeca
44	32	3.9	1893	1	095110	Human thyroid horm
45	31.4	3.9	4822	1	V04445	Sequence used in d

ALIGNMENTS

RESULT 1	
Q34513	Q34513 standard; DNA; 3132 BP.
ID	Q34513:
AC	24-MAY-1993 (first entry)
DE	HEK coding sequence.
KW	primer: expression vector; extracellular domain; human; HEK;
KW	eph/elk-like; kinase; pre-B; cell; T; tumour; lymphoid; LK63;
KW	Lila-1; JM; epithelial; Hela; receptor-type; thymidine kinase;
KW	TK; ligand; B; cellular response; growth; differentiation; ss.
OS	Synthetic.
FS	Key
FT	Location/Qualifiers
FT	5'utr
FT	1..99
FT	/*tag= a
FT	100..3051
FT	/*tag= b
FT	3052..3132
FT	/*tag= c
FT	signal_peptide 100..159
FT	/*tag= d
FT	1723..1795
FT	/*tag= e
FT	/*note= "Potential transmembrane region"
FT	160..216
FT	/*tag= f
FT	/*note= "Purified HEK protein #1"
FT	2617..2679
FT	/*tag= g
FT	/*note= "Purified HEK protein #2"
FT	W09300425-A.
FT	PD 07-JAN-1993.
FT	PF 19-JUN-1992; AU0294.
FT	PR 21-JUN-1991; AU-006841.
FT	PR 12-DEC-1991; AU-009992.
FT	PA (HALL-) HALT INST MEDICAL RES WALTER & ELITA.
FT	PI Boyd AD, Simpson R, Ward LD, Wicks I, Wilkinson D;
FT	DR WPI; 93-036373/04.
FT	P-PSDB; R31466.
FT	PT Receptor-type tyrosine kinase reactive with monoclonal antibody
FT	PT IIT-14 - is EPH-ELK-like kinase, useful for phosphorylating
FT	PT proteins in modulating pre-B, B and T cell function, in cancer
FT	PT therapy etc.
FT	PS Claim 6; Fig 1; 58pp; English.
FT	CC This sequence encodes human eph/elk-like kinase (HEK). HEK is
FT	CC expressed in both pre-B cells and T cell lines and in a number of
FT	CC tumours of human origin, eg. lymphoid tumours LK63, Lila-1 and JM,
FT	CC and the epithelial tumour Hela. This receptor-type thymidine kinase
FT	CC (TK) and/or its ligands are useful as agents in modulation of the
FT	CC production and/or function of pre-B, B and T cells. The TK and its
FT	CC analogues have activity in transducing signals or in stimulating
FT	CC cellular responses such as growth and/or differentiation.
FT	CC Sequence 3132 BP; 888 A; 711 C; 759 G; 774 T;
FT	SO

Query Match 100.0%; Score 813; DB 1; Length 3132;
Best Local Similarity 100.0%; Pred. No. 6.9e-259;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

Db      821 GAGAGAGCGCTTGCCTGCCAA 841
      || ||||| ||| |||||
RESULT 3
ID      V70207 standard; DNA: 3906 BP.
AC      V70207;
DE      11-FEB-1999 (first entry)
KW      Rat receptor tyrosine kinase Etk-1 encoding DNA
KW      Receptor tyrosine kinase; Ror-1; Ror-2; Etk-1; Etk-2; detection;
KW      neurotrophin activity; LTKs; proto-oncogene; tyrosine kinase receptor;
KW      binding protein; BDNF; Nr-3; diagnosis; ss.
OS      Rattus sp.
FH      Key
FH      CDS
      Location/Qualifiers
      476..3493
      /*tag= a
PN      US5843749-A.
PD      01-DEC-1998.
PE      06-JUN-1995; 469537.
PR      17-MAR-1995; US-406247.
PR      26-JUL-1991; US-736559.
PR      28-OCT-1993; US-144892.
PR      06-JUN-1995; US-469537.
PA      (REG- ) REGENERON PHARM INC.
PI      Malsompierre PC, Maslakowski P, Yancopoulos GD;
DR      P-PSDB; W83147.
PT      DNA encoding receptor tyrosine kinase proteins - and corresponding
PT      proteins
PS      Claim 5; Fig 22; 194pp; English.
CC      The present invention describes nucleic acid molecules for ror-1,
CC      ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins:
CC      Ror-1; Ror-2; Etk-1; and Etk-2. The proteins are orphan receptor
CC      tyrosine kinases. The present sequence encodes rat Etk-1.
SQ      Sequence 3906 BP; 1097 A; 876 C; 990 G; 943 T;

Query Match      43.2%; Score 351.4; DB 1; Length 3906;
Best Local Similarity 67.3%; Pred. No. 4.5e-106;
Matches 512; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

OY      56 tcgggaactgattccgcagccttccaaatgaagtcactgagtcacaaacaaatc 115
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      630 TCCGAGACCTTTGGCCAGCCCAAGAGAGAGTGAATTATTTGATTTGCCACATGTC 689
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      116 aaggagagctggctggatcttattcaatcaatgagtgaggagaagatcagtggtg 175
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      690 TGGGAGACCTTGGATGGATTGCTTTCCAAAGATGGGTGGAGAGATTGGTGAAGTTG 749
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      176 atgaacattacacaccatcagagcttaccagtggtgcaatgtctatgtgaccagtcacaa 235
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      750 ATGAATACTATCCCCCATCCACACCTATCAAGTGGCAAAATTATNGAACAAGAAATCAGA 809
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      236 acaattgctggaacaaactggtgtcccaagaactcagctcagaagaattatgtgagac 295
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      810 ATAATTGGCTGTGACAGAGTTGATCTCTAAGAGAGTCTCTCCAGAAATTTTATTTGAAAC 869
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      296 tcaattcacttaagagagatcaatagatcattcattggtttaggaacttgcagaaggaga 355
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      870 TCMAATTACTTGGAGGGATTGCAACAGCCTTCCTGGAGAGACTGGGGAGATTCACAGGANA 929
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      356 catcaacctgactacatgagatgctgatatgcatcatgagtgagtggaatttcagaagcacc 415
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      930 CCTTAAACATGTATTTATTTGATGGATGAGATGAGATGGGAAATATCAAAAGAAAC 989
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      416 agttacaagaattgacacattgacgtgatatgaagtttccatcaaatgagtccttggg 475
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      990 AGTACATCAAGATCATACCATTTGCTGTGATGAGAGCTTCAACCGAAGCTTGACCTTGGAG 1049
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      476 accgatattcgaagctcaaacactgagatagaagaatgagtcctgtcacaagaaggagat 535
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1050 ACCGGGTATGAAGCTGAATAGAGAGTGAAGATGTAGAGCTCTGAGCAAAAAGGGAT 1109
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

OY      536 ttatttgcaattcaagaatggtgtgctgtgttgccttgggtgtcgtgagagatcact 595
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1110 TTATCTTGCTCTTCCAAAGATGCGGTGCTTCATGCTGTGTTCTGTCTGCTTACT 1169
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      596 tcaaaaagtgcacatttaccagtaagaatctgctatgtttccacagacaggtaccatg 655
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1170 ATAAAAAATGCTCTCTGTAGTACATTTGGCTGTTTCCCTCAGACGATCATCTGGAG 1229
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      656 actcccaagtc---tggtgaggttaagaggtcttgtgtcaaatcctaaggaggaag 712
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1230 CAGATTCTTCCAGTGTGATGAGGTGTCAAGGCTCCTGGGTCAACCATCTGTGACAGAGC 1289
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      713 atccccaagagatgactacagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 772
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1290 ATCTCTCCCAAAATGCATTTGCATGCTGANAAGGAGATGGCTGCTTCCATCGGAAATGCA 1349
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      773 cctgcaatgctgctatgaagaagaaggttttatgtccaa 813
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1350 TGTGCAAGCGCGGATATGAGAGAAAATGTAACCTGTCA 1390
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
ID      T18893 standard; cDNA: 4165 BP.
AC      T18893;
DE      05-JAN-1997 (first entry)
DE      Rat REK7 cDNA.
KW      REK7; eph-related tyrosine kinase receptor; AL-1; ligand;
KW      neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis;
KW      ss.
OS      Rattus sp.
FH      Key
FH      CDS
      Location/Qualifiers
      541..3327
      /*tag= a
FT      signal_peptide 541..711
FT      /*tag= b
FT      mat_peptide 712..3324
FT      /*tag= c
PN      WO9613518-A1.
PD      09-MAY-1996.
PE      26-OCT-1995; U14016.
PR      27-OCT-1994; US-330128.
PR      07-JUN-1995; US-486449.
PA      (GERH ) GENENTECH INC.
PI      Caras JW, Winslow JW;
DR      WPI; 96-239448/24.
DR      P-PSDB; R97853.
PT      AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in
PT      treatment and diagnosis of neuronal disorders and
PT      angiogenesis-related conditions.
PS      Example 1; Page 47-49; 75pp; English.
CC      A cDNA clone (T18893) codes for rat REK7 (R97853), an eph-related
CC      tyrosine kinase receptor, for which AL-1 (see also W97854) is a
CC      ligand. It was isolated using degenerate receptor tyrosine kinase
CC      primers (T18894-96) to amplify cDNAs of an adult mouse hippocampal
CC      cDNA library. A PCR fragment was used as a probe to isolate the
CC      full-length REK7 cDNA from a rat hippocampal cDNA library. An
CC      REK7-1g fusion was used to screen cultured cell lines for surface
CC      expression of REK7-binding activity. Primers based on isolated
CC      ligands were used to amplify human breast carcinoma BT20 cell
CC      cDNA, and an amplified fragment was used to screen a human foetal
CC      brain cDNA library, leading to the isolation of AL-1 cDNA (T18897).
SQ      Sequence 4165 BP; 1157 A; 907 C; 1035 G; 1066 T;

Query Match      43.2%; Score 351.4; DB 1; Length 4165;
Best Local Similarity 67.3%; Pred. No. 4.7e-106;
Matches 512; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

OY      56 tcgggaactgattccgcagccttccaaatgaagtcactgagtcacaaacaaatc 115
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      695 TCCGAGACCTTTGGCCAGCCCAAGAGAGTGAATTATTTGATTTGCCACATGTC 754
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

QY 116 aaggagagctggcgtgagctcttaccatcacatggtggaagaagatcagtggtg 175
DB 755 TGGGAGACCTTGATGATGATGCTTTTCCAAAGATGGTGGGAGAGATGGAGTGG 814
QY 176 atgaacattacacaccatcagagcttaccaggtgtgcaatgtcagagaccagcaaa 235
DB 815 ATGAAATCATTCCTCCCTCCACCTATCACTATGCAAGTAAAGAAACAAATCA 874
QY 236 acaattgtctgaagaacaactggtccccaagaccagctcagaagattatgtgagc 295
DB 875 ATAAATGGCTGTGACACTGTGATCTTAACAAAGTGTGCTTCCAAATTTTATTAAC 934
QY 296 tcaagtctcctcagagagctcgaatagatccatgtgttttaggaacttgcaagaa 355
DB 935 TCAAGTTTACTCTGAGGAGATTGCAACAGCTTCTGAGAGACTGGGAGACTTGAAGA 994
QY 356 catttaactgtactcagaggtctgagatgatactatgaggtggaatttcgagacac 415
DB 995 CCTTTACATGATTTATTTTGAAGTCCGATGATGAGAAATGGAATATCAAGAAAC 1054
QY 416 agttacaagaattgacacacatgctcagctgagtaagaatttcaactcaatgagatc 475
DB 1055 AGTACATCAAGATCGATACCATTCGCTGATGAGAGCTTCAACGAACTTGACCTTGAG 1114
QY 476 accgatctctgaagctcaaacctgagattagagaagtaggtcctgtcaacaagaaggat 535
DB 1115 ACCGGGTCAATGAAGCTGAATACGAGAGTCAAGATGATAGACCTTGAGCAAAAGGAT 1174
QY 536 ttatttgcatctcagagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 595
DB 1175 TTTATTTCTTTCCAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234
QY 596 tcaaaagtgccatttacaagatgtaagaatcgtgtgtgtgtgtgtgtgtgtgtgtgt 655
DB 1235 ATAAAAAATGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 1294
QY 656 actccagctccc--tggtggaaggttagaggtctgtgtgtgtgtgtgtgtgtgtgt 712
DB 1295 CAGATTCTTCCGAGTGTGATGAGAGTGTGAGGCTCCTGCGCAACATTCGTGACAGAG 1354
QY 713 atcctcagaagatgtaactcagatcagatcagagagagagagagagagagagagag 772
DB 1355 ATCTCTCCAAATGCTATGCAAGTGTGAGAGGAGAGTGGCTGCTGCTGCTGCTGCT 1414
QY 773 cctgcaatgt 813
DB 1415 TGTGCAAGGCCGATATGAAGAAATGATGATGATGATGATGATGATGATGATGATG 1455

RESULT 5
V58192
ID V58192 standard: cDNA: 4322 BP.
AC V58192:
DT 25-NOV-1998 (first entry)
DE Mouse Bsk receptor-like tyrosine kinase cDNA clone.
KW Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neoplasm;
KW neurodegenerative disease; limbic system neuron regeneration;
KW chromosomal abnormality; degenerative growth; development disorder;
KW viral infection; bacterial infection; Alzheimer's disease; epilepsy;
KW schizophrenia; stroke; cerebral ischaemia; ds.
OS Mus sp.
FH Key
FT Location/Qualifiers
FT 418..3051
FT CDS
FT /tag= "a"
FT /product= "Bsk"
FT /note= "receptor-like tyrosine kinase"
FN US5814479-A.
PD 29-SEP-1998.
PF 11-JUN-1996: 673789.
PR 04-JAN-1994: US-177812.
PR 11-JUN-1996: US-673789.
PA (KROMER) KROMER L F.

PA (SCHU/) SCHULZ N T.
PA (WOOD/) WOUDE G F V.
PA (ZHOU/) ZHOU R.
PI Kromer LE, Schulz NT, Woude GFV, Zhou R;
DR MPI: 98-541751/46.
DR P-PSDB: W11628.
PT Isolated nucleic acid sequence encoding protein - used in Bsk
PT nucleic acid probes, used in detecting alterations in level of Bsk
PT messenger-RNA in biological samples isolated from mammal afflicted
PT with disease
PS Claim 2: Fig 2: 72pp: English.
CC The present sequence encodes mouse Bsk, which is a receptor-like
CC tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in
CC Bsk nucleic acid probes, which can be used in detecting alterations in
CC the level of Bsk messenger-RNA (mRNA) in biological samples isolated
CC from a mammal afflicted with a disease, such as neurodegenerative
CC diseases or disorders and neoplasms. The nucleic acid sequence can also
CC be delivered into the limbic system of patients with limbic system
CC neurodegenerative disease, disorder or injury, to promote or enhance
CC limbic system neuron regeneration or growth. Such neurodegenerative
CC diseases include, chromosomal abnormalities, degenerative growth and
CC development disorders, viral infections, bacterial infections, brain
CC injuries, neoplastic conditions, Alzheimer's disease, epilepsy,
CC schizophrenia, or stroke and cerebral ischaemia.
SQ Sequence 4322 BP; 1260 A; 887 C; 1055 G; 1120 T;

Query Match 43.0%; Score 349.8; DB 1; Length 4322;
Best Local Similarity 67.1%; Pred. No. 1,66-105;
Matches 511; Conservative 0; Mismatches 247; Indels 3; Gaps 1;

QY 56 tcggggaactgtatccgcagcttccaaatgaagtaacttactgattcaaaaacatlc 115
DB 572 TCCGGACCTTTTGGCCACCCAGAGAGATGATGATGATGATGATGATGATGATGATGATG 631
QY 116 aaggagagctggcgtgagctcttaccatcacatggtggaagaagatcagtggtg 175
DB 632 TGGGGGACCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
QY 176 atgaacattacacaccatcagagcttaccaggtgtgcaatgtcagagcagagcaaa 235
DB 692 ATGAGACATCATGCCCTCCATCCACATCAACATGATGCAAACTTATGCAAGATTCGA 751
QY 236 acaattgtctgaagaacaactgtgtccccaagaaactcagatcagaagattttagtggagc 295
DB 752 ATAAATGGCTGTGACCACTGATGATGATGATGATGATGATGATGATGATGATGATG 811
QY 296 tcaagtctcctcagagagctcgaatagatccatgtgttttaggaacttgcaagaa 355
DB 812 TCAAGTTTACTTTAAGGAGCTCAACAGCTTCTGAGAGACTGGGAGACTTGTAGAGAGA 871
QY 356 cattcaactgtactcagagagctgagatgatactatgaggtggaatttcgagagctc 415
DB 872 CATTTACATGATTTATTTTGAATCAGATGATGATGATGATGATGATGATGATGATGATG 931
QY 416 agttacaagaattgacacacatgctcagctgagtaagaatttcaactcaatgagatc 475
DB 932 AATACATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 991
QY 476 accgatctctgaagctcaaacctgagattagagaagtaggtcctgtgtcaacaagaaggat 535
DB 992 ACCGGTCAATGAAGCTGAATACAGAGCTCAGAGATGCTGAGACTTGAAGAAAGGAT 1051
QY 536 ttatttgcatctcagagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 595
DB 1052 TTTATCTTCTTTCCAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1111
QY 596 tcaaaagtgccatttacaagatgtaagaatcgtgtgtgtgtgtgtgtgtgtgtgtgt 652
DB 1112 ATAAAAAATGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1171
QY 653 tggactccagctccctgtgtggaaggtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 712

DB 110 ACCCCGCGATGAGTTACCTATTGGATTCCAGATCTGTTACGGAGAACTTGGGTGGA 169
QY 134 tctc---ttatccatcacatcagtggtggaagagatcagtgctgtgtgatacattacacac 190
DB 170 TTAGCAAGCCCTCGAAGAGAGAGGTGGAGAGTAGTATCATAGATGAAAAAATACAC 229
QY 191 ccatcagaacttaccaggtgtgtcaatgtcatgtgacacagtcacaaatcttgctgagaa 250
DB 230 CATTCGGAACCTACCAAGTGTGCAATGTATGAGAACCCAGCCAGATACTGCTACGAA 289
QY 251 caaacctgggtcccccagaagaactcagctcagaagaattatgtgtgagcccaagttcacctac 310
DB 290 CTGATTGGATCACCCAGAGAGGGGCTCAGAGGGGTGATATGTGATTAATTAATTCCTTGA 349
QY 311 gagactgcatacagatccatccatctggttttaggaactctgcagaagagacatccaactgtact 370
DB 350 GGGACTGCAATAGTCTTCGGGGGCTCATGGGAGCTTGCAAGAGAGAGCTTAACTTACT 409
QY 371 acatgagtcctgatagtatcatatggtgtgaaatttcgagaagcatcagtttacaagaattg 430
DB 410 ACTATGAATCAGACAAAGCAAGAACGCTTTCATCAGAGAGAACAGTTTGTCAAAATTG 469
QY 431 acacactgcagctgatagtgaagtcttcaactcaaatgtgatacttgtaggcgtatctgaagc 490
DB 470 ACACCATTTGCTGCTGATGAGAGCTTACCCAACTGATGATGATTAATTAATTCATAGC 529
QY 491 tcaacactgagattagaagtagtgcctgtcacaagaagaagatttatttgcatctc 550
DB 530 TGAACACCCAGATCCGGGATGTAGGGCCATTAGCAAAAAGGGGTTTACCTGGCTTTC 589
QY 551 aagatgtgtgtctgt 610
DB 590 AGAGTGTGGGGGCTCATCGCCCTGTGTATCATCTCGTGTGTATTAATAAGTGTCCAC 649
QY 611 tcaactgagaagaactcgtcgtatgttccagagacagttacccatg---gactccagttccc 667
DB 650 TCACAGATCCGCAATCTGCGCCCACTTCTGACACCATTCACAGGGGCTGATACCTTCCC 709
QY 668 tggtagaggttagagaggtctgtgtcacaacatctcaagaagagatccctccaagatgt 727
DB 710 TGGTGAAGATTGAGAGCTCTCTGTGTCAACACTCAGAAAGAAAGTAGTGCCAAAATGT 769
QY 728 actgcagtcagaagaagcgaatgtgttaccatcttgcaatgtgtgtgtgtgtgtgtgtgt 787
DB 770 ACTGTGGGCGAGATGCTGTGATGCTGTGATGCCATTCGCAATGCGCAAGCTGGGC 829
QY 788 atgaagaagaaggtttatgtgtccaa 813
DB 830 ATGAGAGCGGAGCGAGAGATGCCAA 855

RESULT 8
ID T03100 standard; DNA: 3348 BP.
AC T03100.
DT 14-FEB-1996 (first entry)
DE Protein tyrosine-kinase bptk7 gene.
KW Protein tyrosine-kinase; ptk; bptk7; agonist; cell growth;
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..2961
FT signal_peptide 1..57
FT mat_peptide 58..2958
FT W09527061-A1.
PD 12-OCT-1995.
PR 04-APR-1995; 004228.
PR 04-APR-1994; US-222616.
PA (GENE) GENENTECH INC.
PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;

PI Wood WI;
DR WPI: 95-366160/47.
DR P-PSDB: R85936.
PT Agonist antibodies which activate specific protein tyrosine
PT kinase(s) - also activate chimeric proteins of kinase extracellular
PT domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation
PS Disclosure: Page 88-92; 125pp; English.
CC DNA probes based on protein tyrosine-kinase (ptk) sequences were used
CC to screen cDNA libraries to identify novel ptk genes. The bptks,
CC bptk1, bptk2, bptk3, bptk4, bptk5 and bptk7 (R85924-28 and R85935,
CC respectively) are expressed in human brain tissue and show homology
CC to known ptk. A full-length sequence for the bptk7 gene (703100)
CC was obtd. This gene may be used to design new drugs, peptides and
CC antisense constructs that modulate ptk activity.
SQ Sequence 3348 BP; 924 A; 769 C; 855 G; 800 T;

Query Match 42.4%; Score 344.4; DB 1: Length 3348;
Best Local Similarity 68.2%; Pred. No. 8.6e-104;
Matches 509; Conservative 0; Mismatches 231; Indels 6; Gaps 2;

QY 74 agccttccatgaatgaatcactctactggtatcaaaacattcaagggagctggctgga 133
DB 77 ACCCGCGAGATGAGTTACCTTATTGGATTCCAGATCTGTTAGGAGAGAACTTGGGTGGA 136
QY 134 tctc---ttatccatcacatcagtggtggaagagatcagtgctgtgtgatacattacacac 190
DB 137 TTAGCAAGCCCTCGAAGAGAGAGGTGGAGAGTAGTATCATAGATGAAAAAATACAC 196
QY 191 ccatcagaacttaccaggtgtgtcaatgtcatgtgacacagtcacaaatcttgctgagaa 250
DB 197 CATTCGGAACCTACCAAGTGTGCAATGTATGAGAACCCAGCCAGATACTGCTACGAA 256
QY 251 caaacctgggtcccccagaagaactcagctcagaagaattatgtgtgagctcagttcacctac 310
DB 257 CTGATTGGATCACCCGAGAGAGGGGCTCAGAGGGTGTATATTAATTAATTCACCTTGA 316
QY 311 gagactgcatacagatccatccatctggttttaggaactctgcagaagacatccaactgtact 370
DB 317 GGGACTGCAATAGTCTTCGGGGCTCATGGGAGCTTGCAAGAGACGTTTAACTGTTACT 376
QY 371 acatgagtcgatagtatgtatcattgtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 430
DB 377 ACTATGAATCAGACAAAGCAAGAACGCTTTCATCAGAGAGAACCAAGTTTGCABAATTG 436
QY 431 acacactgcagctgatagtgaagtcttaccctcaaatgtgtcttggagacagttatctgaagc 490
DB 437 ACACCATTTGCTGCTGATGAGAGCTTTCACCCAGTGTGACATTGTGACAGAAATCATGAAGC 496
QY 491 tcaacactgagaattagaagtagtgcctgtcacaagaagaagagatttatttgagcttc 550
DB 497 TGAACACCCAGATCCGGGATGTAGGGCCATTAGCAAAAAGGGGTTTAACTTGGCTTTC 556
QY 551 aagatgtgtgtctgt 610
DB 557 AGAGTGTGGGCGCGACATCGCCCGGTGATCAGTCCGTGTGTATTAATAAGTGTCCAC 616
QY 611 tcaactgagaagaatctgtgtatgtttccagaacagtgtaaccatg---gactccagttccc 667
DB 617 TCACAGTCCGCAATCTGCGCCCACTTCTGACACCATTCACAGGGGCTGATAGTCTTCCC 676
QY 668 tggtagaggttagagaggtctgtgtcacaacatctcaagaagaagatccctccaagatgt 727
DB 677 TGGTGAAGATTGAGAGCTCTCTGTGTCAACACTCAGAAAGAAAGATGTGCGAAAATGT 736
QY 728 actgcagtcagaagaagcgaatgtgttaccatcttgcaatgtgtgtgtgtgtgtgtgtgt 787
DB 737 ACTGTGGGCGAGATGCTGTGATGCTGTGATGCCATTCGCAATGCGCAAGCTTATGCAAGCTGGGC 796
QY 788 atgaagaagaaggtttatgtgtccaa 813
DB 797 ATGAGAGCGGAGCGAGAGATGCCAA 822

QY	176	atgacatctaacacacccctcaaggaccttcacaggtgctgcaatgctatgaccacagttcaaa	235
Db	197	ATGAATAATTATGCCCCCTTCCACACATCTCAAGATATGCAAAAGTATGTAACACAGATTCAGA	256
QY	236	acaattgctcgaaacacaacttgggtcccccaggaacctcagctcagaagaattatgtgagc	295
Db	257	ATTAACCTGGCTTTTGACCGAGTTGGATCTCCATATGAAGAGTGTCTTCAGAAATCTTATAGAAC	316
QY	296	tcaagttcactctaaagaaactgcgaatgcatccatctggttttagagacttgcagagaga	355
Db	317	TCAAAATTATACCTCGGGGAGCTGCAACACACCTTCTCGAGAGACTGGGGACCTGTAAAGGAAA	376
QY	356	catcaaaccttgactacatactgagctctgtatgtatgcattgggggtgaaatttcagagcacc	415
Db	377	CCTTTAATATGATGATTACTCTTGAGTCAGATGATGCAATGGAGAGAAATCATAGGAAAC	436
QY	416	agttacacaagaattgacaccatctgcagctgtatgaagtttcaactcaaatgtaattcttg99	475
Db	437	AATACATCAAAATTATGATACCATTCCTGCCGATGAAGACTTTACAGAACTTGATCTTG9TG	496
QY	476	accgatactcgaagctcaacactgagatataagaagtaagtccctgtcaacaagaagagat	535
Db	497	ACCGGTTATGAAATGTGATACAGAGGGTCAAGATGTAGGACCTCTTAGGAAAAAGGAT	556
QY	536	tttatcttgcaattcacaagtctgtgtctgttgcttcctgtgtctgtatagaatcact	595
Db	557	TTTATCTGCTTTTCAABATGTGGTCTTCATTCCTCTGCTGTCTGTGCTGTATACT	616
QY	596	tcaaaaagtcgccattcacaagtgaaagaactgtgctatgattccagacaggtaccatg9	655
Db	617	ATMAAAATATGCCCTTCTCTGTGTACAGACACTTGGCTGTCTTCCCTGACACCATCATCTGAG	676
QY	656	actcccaagtc---tggtgaggttagaggtctctgtgcacaattctcaagagagag	712
Db	677	CTGATCTTCCCAATTGCTCGAAGTCTGGGCTCTCTGTCAACCATCTGTGTACCAGATG	736
QY	713	atccctcacaagatgtactctgcagtcacagaagcgaatgtgctgtacccattgcaagtgt	772
Db	737	AACCTCCCAAAATGCACTGCAAGCGCGCAAGGGAGATGGCTGTGTGCCATGGGAAATGCA	796
QY	773	cctgcaatgctggtcctatgaaagaagagtttattgtgtccaa	813
Db	797	TGTGCAAGGCAAGATGTGAAGAAAAATGGCACCTGTCAA	837
RESULT 11			
T32962			
ID	T32962 standard; cDNA; 2323 BP.		
AC	T32962;		
DT	11-NOV-1996 (first entry)		
DE	Mouse developmental kinase 1 MDK1 T2 clone.		
KW	Mouse developmental kinase 1; MDK1 T2; receptor tyrosine kinase;		
KW	RTK; signal transduction; probe; diagnosis; gene therapy;		
KW	neurodegeneration; neuroproliferation; cancer; ss.		
OS	Mus sp.		
FH	Key		
FT	cds		
FT	233..2113		
FT	Location/Qualifiers		
FT	/*tag= a		
FT	signal_peptide		
FT	233..316		
FT	/*tag= b		
FT	mat_peptide		
FT	317..2110		
FT	/*tag= c		
FT	misc_feature		
FT	2017..2113		
FT	/*tag= d		
FT	/note= "divergent sequence due to alternative		
FT	splicing"		
PN	W09621013-A1.		
PD	11-JUL-1996.		
PF	03-JAN-1996; U00419.		
PA	03-JAN-1995; US-368776.		
(PLAC)) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.		
(PA	(SUG-) SUGEN INC.		

PI Closesek T., Millauner B., Ullrich A;
DR MPI: 96-333988/33.
DR P-PSDs: W03423.
PT New mouse development kinase 1 gene - used for developing prods. for
PT diagnosis and treatment of abnormalities in signal transduction
PT pathways
PS Example 1: Page 115-116; 128pp; English.
CC cDNA cloning using adult mouse brains and Northern blotting
CC identified 2 clones, MDK1 T1 (T32961) and MDK1 T2 (T32962), that
CC coded for truncated versions (W03442 and W03423, respectively) of
CC the novel mouse developmental kinase 1 (MDK1) (see also T32960), a
CC new member of the eck/eph family of receptor tyrosine kinases.
CC MDK1 T1 and T2 each possess the entire ectodomain, the transmembrane
CC domain and part of the juxtamembrane region of MDK1 (see also W03421)
CC but lack the catalytic tyrosine kinase domain. They may have a
CC modulatory function. The cDNA clones can be used to produce MDK1
CC T1 and T2, which are useful for screening potential agents for
CC treatment of diseases characterized by abnormal signal transduction.
S0 Sequence 2223 bp; 680 A; 497 C; 609 G; 537 T;

Query Match	41.28;	Score 334.8;	DB 1;	Length 2323;
Best Local Similarity	67.38;	Pred. NO. 1,1e-100;		
Matches 506;	Conservative 0;	Mismatches 237;	Indels 9;	Gaps 21

Oy	71	CGAGCCTCCGAAGATGCAATCCTACTCTGATTCACAAACAATTCGAAGGAGCGTCGGCT	130
Db	312	CGCAGGCTGCCAGAGANGACTTATTACTGTGACTCGAAGACACACAAACAGATTGGAAAT	371
Oy	131	ggatctcttaccacacacatggtgtgggaagagatcagttggtgtggtatgacaattacac	190
Db	372	GGATTTCCTCCACCACAGTGGGGGGAAGAAATTAGTGGTTGGATGAGACTACACTC	431
Oy	191	ccatcaggaacttaccaggtgttgcattgtcaatgtgacacagtcacaaacaattgctgaga	250
Db	432	CGAATAGAACATATTACAGAGTGTCGACAGTCTATGAGCCCAACAGAAACAATCGCTGCGGA	491
Oy	251	caaatggtgtccccaagaaactcagctccagaaagttaattatgttggagctccaaagtctactac	310
Db	492	CTAACTGGATTCTTAAAGGCAACGACGACAAAGGATTTTGTATGAAATGGAATTCACCTTGA	551
Oy	311	gagactcgaatagatcatcctatggtttttaagaacttgcagaagagacatcacaactcgtact	370
Db	552	GGGATTGTGAATAGCTTCCCGGAGTCTCTGGGAATCTGCAGGAAGAGTTTAATTGTACT	611
Oy	371	acatgagctctgatatgatacatatggtgtggaatttcgaaagatcagtttacaagaattg	430
Db	612	ATTATGAACAGACTAGCAGACCCGGCAGGAATATACGAGAAACCTTTATGTATAAATAG	671
Oy	431	acaccattgcagctgatatgaaagatttcaactcaaatgtaacttgygagcgtaattcgaagc	490
Db	672	ACACCATTTGTCGCGAATGAAGAAATTTTACACAAAGCTACCTTGGTGAAMAAAGATGAAGC	731
Oy	491	tcaacactgagatataggaagtagtgcgtgtcaacaagaaggaatttttggcaattc	550
Db	732	TGAACACTGAGGTTAGAGAAATTGGACCTTTGTCCAAAAGGAAATCTATCTTGCCTTTC	791
Oy	551	aagaattgtggtctgtgttgccttgggtctgtgtctgagagtatacttcaaaagtcccat	610
Db	792	AGGATGTAGGGGCTTGATAGCAATTGGTTTCTGTCAAAATGTACTCAAGAAAGTGTGGA	851
Oy	611	ttacagtgaaagaaatctggtctatgtttccagacacggttacc--catggaactccagatccc	667
Db	852	CCATTGTTGGAAGACTTAGCTGTCTTTCCAGATACAGTCACTGGTTCGGAATTTTCTCTCT	911
Oy	668	ttgtgtgaggttaagaggggtcttgtgtcaacaattctaaga-----ggaagatcctcaaa	721
Db	912	TAGTCGAGGCTCCGCGGACATGTGTACGCACTGCCAGAGAAAGAGCGAGAAATTTCCCCA	971
Oy	722	ggatgtactgcaagtaagaagagcgcaatggtcttaccatttggaaggttttcttgcattg	781
Db	972	GAATGTCAATTGCAGTCGACGAAGAGAGTGGCTTACTACCCATTGGAAATATCATCTCTCAAG	1031

[illegible]

DR W24, 30 000000/00.
P-PSDB; W03421.

DR WPI; 96-333988/33.

PI Closssek T, Millauner B, Ullrich A;
0000-0000-0000-0000

PT New mouse development kinase 1 gene - used for developing prods. for
 PT diagnosis and treatment of abnormalities in signal transduction
 PT pathways
 PS Example 1: Page 103-105: 128pp: English.
 CC A cDNA clone (T32860) codes for mouse developmental kinase 1 (MDK1)
 CC (W03421), a new member of the eck/eph family of receptor tyrosine
 CC kinases (RTKs). To isolate the clone, cDNA from mouse embryos was
 CC subjected to PCR amplification with primers based on conserved
 CC motifs (see also W03426-27) of RTKs. An amplified fragment was used
 CC to screen an 11.5-day-old mouse embryo and an adult mouse brain cDNA
 CC library to obtain the MDK1 clone. 4 Sequence variants (see also
 CC T32861-62 and W03422-25) of MDK1 were also identified. MDK1 nucleic
 CC acids can be used for the recombinant prodn. of MDK1, as probes to
 CC detect MDK1, and for the gene therapy of diseases involving
 CC abnormalities in signal transduction, such as neurodegenerative and
 CC neoproliferative disorders and cancer.
 SO Sequence 4304 BP; 1297 A; 875 C; 1043 G; 1089 T;

Query Match 41.2%; Score 334.8; DB 1; Length 4304;
 Best Local Similarity 67.3%; Pred. No. 1.5e-100;
 Matches 506; Conservative 0; Mismatches 237; Indels 9; Gaps 2;

QY 71 cgcagcctcccaatgaatcaatctactgatacaaaacaattcaaggagcctggct 130
 DB 312 CGAGGCTCGAAGAGATCTACTGACCTCGAAGCACAACAGATTGGAAAT 371
 QY 131 ggaatcctatcatcatcagtggtggaagaagatcagtggtggaatgaatcagac 190
 DB 372 GGAATTCCTCTCCACCACGAGGGGTGGGAAGAAATTAGTGTTGGATGAGACTACAC 431
 QY 191 ccatcagaactcagcagtggtgcaatgctcagcagcagcagcagcagcagcagcagc 250
 DB 432 CGATAGAACATCATCAGAGTGTCAGAGTCAATGAGCCCAACAGAACTGGCTGGGA 491
 QY 251 caaacctgggtcccaaggaaactcagctcagaagatttatgtggagctcaagttac 310
 DB 492 CTAACTGGATTTCTAAAGCGACACAAAGGATTTTGTAGAAATGAAATTCACCTTGA 551
 QY 311 ggaactgcataatagcattccattggttttagaacttgcagaggaactcaaaccttact 370
 DB 552 GGGATGTATATAGTCTTCCGGAGTCTCTGGAACTTGCAAGAAAGCTTAAATTTGTA 611
 QY 371 acatgagctcagatgcatgcatgagtggaatttcagagagcagcagttaccagaatg 430
 DB 612 ATTATGAACAGACATCGACACCGCAGAGATATACGAGAAACCTTATGTTAAATAG 671
 QY 431 acacccctgagctgagtggaagttcactcaaatgatacttgggagccgtatctcgaagc 490
 DB 672 ACACATGCTGCAGATGAAGATTTCACACAAAGGTGACCTGGTGAAGAAAGATGAA 731
 QY 491 tcaaacctgagatgaagaatgagtcctgccaacaagaagaatttatgtgcatct 550
 DB 732 TGAACACTGAGGTGAGAGATGAGACTTGTCCAAAAGGATTTCTATCTGCTTTC 791
 QY 551 aagaatgttgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 610
 DB 792 AGGATGTAGGGCTTGATAGCATTTGGTTCTCTCAAGGTACTACAAAGATGCTGGA 851
 QY 611 ttcagtgagaatctggcagtgcttccagacacggtac---cagygactcccaagtc 667
 DB 852 CCAATTGTGGAACCTTAGCTGCTTCCAGATACAGTGAAGTGGTGGAAATTTTCCCTCT 911
 QY 668 tggtagaggttagaaggtctctgtcacaacattcaaga-----ggaagatccctca 721
 DB 912 TAGTCAGAGTCCTGGACATGTGTACAGAGTCCGAGAGAGAGGAGGAGAAATTTCC 971
 QY 722 ggaatgactcagtaacagaagcgaatgctgtacccattggcgaagtgttccctgca 791
 DB 972 GAATGATTCAGTCAAG 1031
 QY 782 ctggctatgagaagaaggttttatgtgcca 813

DB 1032 CAGGCTATCAGCAAAAAGGGGACACTTGGCA 1063

RESULT 14

ID Q90662 standard; cDNA; 3056 BP.
 AC Q90662;
 DT 11-NOV-1995 (first entry)
 DE Eph-related PK Cdk7' cDNA.
 KW Cdk7'; Eph: protein tyrosine-kinase; PTK; cancer; diagnosis;
 KW prognosis; ss.
 OS Gallus sp.
 FH Key
 FT Location/Qualifiers
 FT cds 2..2134
 FT /*tag= a
 PN W09515375-A.
 PD 08-JUN-1995.
 PE 07-SEP-1994; U10140.
 PR 03-DEC-1993; US-162809.
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 PI Pasquale EB, Sajjadi FG;
 DR WPI: 95-215256/28.
 DR P-PSDB: R75714.
 PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
 PT cancer.
 PS Claim 2: Page 106-109; 129pp: English.
 CC Novel EPH-related PTK cDNA clone Cdk7 (given in Q90663) and its
 CC variant Cdk7+ (Q90661) were isolated from a chick embryo library in
 CC lambda gt11, and another variant, Cdk7' (Q90662), from a chick
 CC embryonic brain cDNA library in lambda gt11. The variants may originate
 CC via alternative splicing of the same gene. Cdk7 had the lowest level
 CC of expression of 7 novel Eph-related kinases examined and was barely
 CC detectable in adult tissues.
 SO Sequence 3056 BP; 871 A; 661 C; 762 G; 762 T;

Query Match 30.2%; Score 245.2; DB 1; Length 3056;
 Best Local Similarity 68.2%; Pred. No. 5.5e-71;
 Matches 356; Conservative 0; Mismatches 163; Indels 3; Gaps 1;

QY 295 ctcaagttactctcagaagatgcaatgaatccattcgttttagaacttgcagaag 354
 DB 2 CTCMAATTCACCTTGAGGAGCTGTACACCTTCCAGAGACTTGGCAAGAG 61
 QY 355 acattcaacctgacacatgagctgagtgatgatcagtgagtgagtgagtgagtgagtgag 414
 DB 62 ACTTTTAACTATGATCTTCTTGGTCAATGATGAGAGATGGAGAACTCAGAGAAAT 121
 QY 415 cagttacaagaatgacacacattcagctgagtgagtgagtgagtgagtgagtgagtgag 474
 DB 122 CAGTACATCAAGATACATACATGCTGCTGATGAGAGAGCTTCACGAGTTGGACTCG 181
 QY 475 gaccgcatctgagatgcaacctgagatgagtgagtgagtgagtgagtgagtgagtgagtgag 534
 DB 182 GACAGAGTTATGAAGTTAAACACAGAGAGTGAAGAGTGGGCTCTTCAAAAAAGGA 241
 QY 535 ttattatggtcattcaagaatggttggttggttggttggttggttggttggttggttggt 594
 DB 242 TTTTACCTTGCTTCCAGATGATGGGCGCTCGATTGCCCTGCTGCTGCTGCTGCTGCTG 301
 QY 595 ttcaaaagtgccatttcaagtgagaatctggtcattgtttccagacacggtaccatg 654
 DB 302 TACAAAGAAATGCCCATCAGATGCCCAACCTGCGACGCTTTCACATACATCACAGGA 361
 QY 655 ---gactccagtccttggtgagtggttagaggtctctgttcaacaatctcaagtgaga 711
 DB 362 GCAGATTCTCGCAGCTGCTAGAGGTGTCAGGCGTCTGTCTCAACACCTCAGTACTGAT 421
 QY 712 gatccccaaggaatgctcagtaacagaagcgaatggctcttaccattgcaagtgat 771
 DB 422 GAGGCAACAAAGATGCATCTGCACTTCAAGAGGAGAAATGGCTGCTCCATTGGGAAGT 481
 QY 772 tcttgcaatgctgctatgagaagaaggttttatgtgcca 813

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 06:32:53 ; Search time 1225.64 seconds
(without alignments)
-645.279 Million cell updates/sec

Title: US-09-104-340-5
Perfect score: 813
Sequence: 1 atgattgtcagctctccat.....aaagaggtttatgtgccaa 813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sts:*
14: gb_sy:*
15: gb_un:*
16: gb_vl:*
17: em_fun:*
18: em_hum1:*
19: em_hum2:*
20: em_in:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_sy:*
30: em_un:*
31: em_vl:*
32: gb_htg1:*
33: gb_htg2:*
34: gb_in1:*
35: gb_in2:*
36: em_ba1:*
37: em_ba2:*
38: em_hum3:*
39: em_hum4:*
40: gb_pr4:*
41: gb_htg3:*
42: gb_htg4:*
43: gb_htg5:*
44: gb_htg6:*

45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum3:*
50: gb_pl3:*
51: gb_pr5:*
52: gb_htg8:*
53: gb_htg9:*
54: gb_htg10:*
55: gb_htg11:*
56: gb_htg12:*
57: gb_htg13:*
58: gb_htg14:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	813	100.0	3132	5	A28003	A28003 H.sapiens H
2	813	100.0	3132	5	I68018	I68018 Sequence 9
3	813	100.0	3149	9	HUMHEK	M83941 Human recep
4	678.6	89.5	3077	12	RNU69278	U69278 Rattus norv
5	661	81.3	2032	12	MUSMER4SE	M68515 Mouse eph-r
6	661	81.3	3197	12	MUSMER4	M68514 Chicken eph
7	546.6	67.2	3241	4	CHCKER4	I15007 Sequence 15
8	545	67.0	3254	5	I15007	D38174 Gallus gall
9	362.8	44.6	3600	4	CHCKER8	U58332 Mus musculu
10	359.4	44.2	3943	12	MMU58332	X78689 R.norvegicu
11	351.4	43.2	3531	12	RNEHR1	AR062744 Sequence
12	351.4	43.2	3906	5	AR062744	AR025488 Sequence
13	351.4	43.2	4165	5	AR025488	X65138 M.musculus
14	351.2	43.2	4242	12	MMSEK	S57168
15	351.2	43.2	4242	12	S57168	AR043381 Sequence
16	349.8	43.0	4322	5	AR043381	U07357 Mus musculu
17	349.8	43.0	4322	12	MMU07357	AR062743 Sequence
18	348.2	42.8	3592	5	AR062743	X05425 H.sapiens m
19	345	42.4	3162	10	HUMRPTKB	I36645 Homo sapien
20	345	42.4	3903	10	HSEHR1	I44522 Sequence 34
21	344.4	42.4	3107	10	HUMRPTKC	L36642 Homo sapien
22	344.4	42.4	3348	5	I44522	X91191 X.laeyls mr
23	344.4	42.4	4523	10	HUMRPTK	L26099 Xenopus lae
24	341.4	42.0	3042	4	XELSEK1	X79084 M.musculus
25	341.4	42.0	3193	4	XELPAGAAA	X79083 M.musculus
26	341.4	42.0	3042	4	XELPAGAAA	X79082 M.musculus
27	334.8	41.2	2901	12	MMKINIT2	U21954 Rattus norv
28	334.8	41.2	2901	12	MMKINIT1	Y14271 Gallus gall
29	331.6	40.8	2006	12	RNU21955	U980093 Human Chit
30	331.6	40.8	3208	12	RNU21954	U03910 Gallus gall
31	331.6	40.8	3943	4	GGY14371	AC021499 Homo sapi
32	330.6	40.7	77197	11	U980093	U72207 Mus musculu
33	329	40.5	4124	4	GGCEK7B	AC009425 Homo sapi
34	321.2	39.5	76022	45	AC021499	AL121966 Homo sapi
35	316.2	38.9	4737	12	MMU72207	U89295 Danto rerio
36	307.4	37.8	132805	41	AC009425	AJ005030 Danto fer
37	305.8	37.6	116490	32	HS1189K14	AL035703 Human DNA
38	305	37.5	44577	4	DRU89295	I15001 Sequence 21
39	297.2	36.6	2640	4	DRU89295	I15001 Sequence 3
40	276.6	34.0	160703	10	HS61A9	I15009 Sequence 19
41	245.2	30.2	3056	5	I15010	AJ002493 Xenopus l
42	245.2	30.2	3059	5	I15001	AC023783 Homo sapi
43	245.2	30.2	3125	5	I15009	
44	233.6	28.7	4664	4	XLAJ2493	
45	230.2	28.3	63166	55	AC023783	

ALIGNMENTS

[illegible][illegible]

Db 220 GAGCTGGCTGATCTCTTATCCATCATGAGGTGGAGAGATCACTGGTGGATGAA 279
Qy 181 cattacacaccatcaggaactaccaggtgtgcaatgtcatgtgagaccagtcacaacat 240
Db 280 CATTACACACCACCATCAGGATTTACAGAGTGTGCAATCTATGACCACTCAAAACAT 339
Qy 241 tggcttgaagaacaaactgggtccccaaggaactcagctcagaagaatttatgtgagctcaag 300
Db 340 TGCGTGAAGAACAACTGGGTCGCCAGAGACTCAGCTCAGAAATTTATGTGGAGCTCAAG 399
Qy 301 ttactctacagagacgcgaatacattccattgtgtttttaggaacttgcaagagacatcc 360
Db 400 TTACTCTACAGAGACTGCAATACATTCATGTGTTTAAAGAACTTGCAAGGAGACATTC 459
Qy 361 aaccttactacatgtgagctgtagatcatcaggggtgagaatttcgagagacatcaatt 420
Db 460 AACCTGTACTACATGAGATGTGATGATGATCAGGGGTGAAATTTTCAGAGCATCATTT 519
Qy 421 acaaaattgacacacattgagctgtagaagtttccactcaaatggaattcttgaggacct 480
Db 520 ACAAGATTGACACCAATTCGACGTGATGAAAGTTTCACTCAATGATCTTGGGGACCT 579
Qy 481 attctgaagctcaacactgagatagagaagtagtgcctgttcaacaagaaggatcttat 540
Db 580 ATTCTGAAGCTCAACACTGAGATTGAGAGTAGTGTCTCTCAACAAGAGGATTTTAT 639
Qy 541 ttggcattcaagaattgt 600
Db 640 TTGGCATTTCAAGATGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 699
Qy 601 aagtgccatttcaagtgaaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
Db 700 AAGTGCCCATTTACAGTAGAAGATCTGGCTATGTTTCCACACACAGGATGACCATGCTCC 759
Qy 661 cagtcctcgtgtgaggttagaaggtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
Db 760 CAATCCCTGTGTGAGGTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 819
Qy 721 agagtgtactgacagtagaagagcgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 780
Db 820 AGGATGTACTGCGATGACAGAGCGGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 879
Qy 781 gctgtgctatgaaagaagaggttttatgtgtcaa 813
Db 880 GCTGCTATGAGAGAGAGGTTTATGTGCCAA 912

RESULT 3
HUMHEK 3149 bp mRNA PRI 31-DEC-1994
LOCUS Human receptor tyrosine kinase (HEK) mRNA, complete cds.
DEFINITION M83941.1 GI:183931
ACCESSION M83941.1
KEYWORDS receptor protein-tyrosine kinase.
SOURCE Homo sapiens lymphoid tumor cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 3149)
AUTHORS Wicks, I.P., Wilkinson, D., Salvaris, E. and Boyd, A.W.
TITLE Molecular cloning of HEK, the gene encoding a receptor tyrosine
JOURNAL kinase expressed by human lymphoid tumor cell lines
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 89 (5), 1611-1615 (1992)
FEATURES
source location/Qualifiers
1..3149
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="LK63"
/tissue_type="lymphoid tumor"
101..3052
/gene="HEK"
101..3052
CDS

/gene="HEK"
/codon_start=1
/product="receptor protein kinase"
/protein_id="AA58633.1"
/db_xref="GI:183931"
/translation="MDQQLSILLILSCVSLDSFGLIPDPSENVNLDLSTKIIOGELGM
ISPSHGEWEISGVDEHYPIPTIYOVNMDSONMWTNTNYPNRSACKIYELKET
LSDNSIPLVLTGCKETENLYYMESDDHGVFRHOFKIDITLDAESFTMDLGDRL
ILKUNFEIRVGNPKKGYLAFQVYGCALVALSVRYFKKPFYKINLAMPDTPYPM
DSQSLVEYRSCVNNKSEDPFRMTCSIEGELVFIGKSCNAGIEERFQACRPG
FKRALDGNKCKPPHSTQDGSNRCENNYRADKPSMACTRPPSPRNVIS
NINETSVLIDMSPLDTGGRKDVETNIICKKGAMIKOCEPCSPNRYELPRQGLNT
IVTVYDLAHTNPTFEIDAENVSELSPPROFAVSIITNQAASPVYTIKQRTSR
NSISLMQEPHEPNCIILDYEVKYEKEOQETSYILRARGNTVYISLKPDTIVFO
IARIRACGCTSKRFPETSPDSISSESSQVYMIASAVAILILVTVYVLFQ
FCGYTSKHGADERKLHFGNGHLKPLGLTVDVPHYTEQVAFHEFALDNTNISID
KVYVAGEEVEVCSGRKLKPSKEISVALIKLVGYTERQRPDLBASIMGQFDHPI
IRLEGVYKSKPVMIVTEYMENGLSDSEFLRKDAQFTVQLVGMIRGLASGKYSDM
GYVHDLAARNILINSILCYKSDSEGLSVLEDDPEAAVTTGGRKIPRMTSPALAY
RKFTSADPWSYGIYLMYMSYGERPYEMMSMODYIKAVDEGRLLPMPDCPALAYOL
MUDCKQKRNPNKPEQIYSLIDKILRNPGSKITISAARPSNLLDQSNVDTFR
TTGDMUNGRIAHCKEILFTGVYSSCDITAKISTUDMKKVGTVVGPORKIISIKAL
ETQSKRNPVPV"

BASE COUNT 891 a 711 c 768 g 779 t
ORIGIN

Query Match 100.0%; Score 813; DB 9; Length 3149;
Best Local Similarity 100.0%; Pred. No. 4.3e-241;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atgattgtcagctctccatccctcccttctcagctgtctgttctcgacagcttcgg 60
Db 101 ATGATTGTCAAGCTCTCCATCCCTCCTTCAGTGTCTGTTCGACACCTTCGG 160
Qy 61 gaactgttcgcagccttccaaatgaatcctcctgattcacaacaacatcagaag 120
Db 161 GAAGTATTCGCGACGCTTCATGAGTCAATCTGATTCAAAACATTCAGAGG 220
Qy 121 gagctggcgtgactctctatccatcacatggtgtggaagagatcagtggtgtgaa 180
Db 221 GAGCTGGCTGATCTCTTATCCATCAGATGAGGTGGAGAGATCAGTGTGTGATGAA 280
Qy 181 cattacacaccatcaggaactaccaggtgtgcaatgtcatgtgagaccagtcacaacat 240
Db 281 CATTACACACCACCATCAGGATTTACAGAGTGTGCAATCTATGACCACTCAAAACAT 340
Qy 241 tggcttgaagaacaaactgggtccccaaggaactcagctcagaagaatttatgtgagctcaag 300
Db 341 TGCGTGAAGAACAACTGGGTCGCCAGAGACTCAGCTCAGAAATTTATGTGGAGCTCAAG 400
Qy 301 ttactctacagagacgcgaatacattccattgtgtttttaggaacttgcaagagacatcc 360
Db 401 TTACTCTACAGAGACTGCAATACATTCATGTGTTTAAAGAACTTGCAAGGAGACATTC 460
Qy 361 aaccttactacatgtgagctgtagatcatcaggggtgagaatttcgagagacatcaatt 420
Db 461 AACCTGTACTACATGAGATGTGATGATGATCAGGGGTGAAATTTTCAGAGCATCATTT 520
Qy 421 acaaaattgacacacattgagctgtagaagtttccactcaaatggaattcttgaggacct 480
Db 521 ACAAGATTGACACCAATTCGACGTGATGAAAGTTTCACTCAATGATCTTGGGGACCT 580
Qy 481 attctgaagctcaacactgagatagagaagtagtgcctgttcaacaagaaggatcttat 540
Db 581 ATTCTGAAGCTCAACACTGAGATTGAGAGTAGTGTCTCTCAACAAGAGGATTTTAT 640
Qy 541 ttggcattcaagaattgt 600
Db 641 TTGGCATTTCAAGATGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 700
Qy 601 aagtgccatttcaagtgaaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660

Db	701	AAGTGGCCATTACAGTGAAGATCTGGCTATGTTTCCAGACACAGGTAACCCAGGACTCC	760
Qy	661	cagtccctggctgaggttaagagggctctgtgtcacacaattcaagaggaagatcccca	720
Db	761	CAGTCCCTGGTGGAGGTTAGAGGCTCTGTGTCAACAATTCTAGAGGAAGATCCCA	820
Qy	721	aggatgtactgcagttacagaagcgaaatgctgttaccattggcaagtcttcgcaat	780
Db	821	AGGATGTACTGCAGTACAGAGGGAATGGCTTGTACCCATTGGCAAGTGTCTCGCAAT	880
Qy	781	gctggcattgaagaagaggtttattgtgccaa	813
Db	881	GCTGGCTATGAGAAAGGTTTTATGTGCCAA	913
RESULT	4		
LOCUS	RNU69278	3077 bp	RNA
DEFINITION	Rattus norvegicus eph-related receptor tyrosine kinase homolog		23-MAR-1998
ACCESSION	U69278		
VERSION	U69278.1	GI:1943913	
KEYWORDS			
SOURCE	Norway rat.		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
AUTHORS	Li, Y. Y., McTierman, C. F. and Feldman, A. M.		
TITLE	Il-1 beta alters the expression of the receptor tyrosine kinase gene r-EphA3 in neonatal rat cardiomyocytes		
JOURNAL	Am. J. Physiol.	274 (1), H331-H341	(1998)
MEDLINE	98120505		
REFERENCE	2 (bases 1 to 3077)		
AUTHORS	Li, Y. Y., McTierman, C. F. and Feldman, A. M.		
JOURNAL	Submitted (01-SEP-1996) Cardiology, University of Pittsburgh, 200 Lothrop Street, Pittsburgh, PA 15213, USA		
COMMENT	On Apr 18, 1997 this sequence version replaced gi:1698721.		
FEATURES	Location/Qualifiers		
source	1..3077		
organism	"Rattus norvegicus"		
strain	"Sprague-Dawley"		
db_xref	"taxon:10116"		
dev_stage	"neonatal"		
cell_type	"cardiomyocytes"		
gene	1..3077		
gene	/gene="Rex4"		
cds	35..2989		
cds	/codon_start=1		
product	"eph-related receptor tyrosine kinase homolog"		
protein_id	"AAC06273.1"		
db_xref	"GI:1698722"		
translation	"MDCHLSILILFGCCVSCSRELSPOPSNVEVNLIDSKTIGELGM ISTPSHMEISGVDEHYPIRTYQVCNVSDHSONMMLRTNWPNSAQIYELKFT LRDNCNIPVLGCKEFTNLVYMSDDHCVKLEHQTIDIDIADESTQMDLGR ILKLNTEIREVGVNKKGFYLAQDCAVALSVRYEFKCEFTVNLNMFPTVYV DSQSLVNRGSCVNSKEEDPRMYCTSEEMLVPIGKCTPCMGACRGPTICACRG FYKALDGVAKCTCPHSSQEDGSMNRCENNYFPAKEXPMSACRPRPSARNTIS NINETSIIIDMSPLDGGKDDITFNICKCKMNRQCEPCSPNRFRLRDLNLT TVVTDILAHNTTFETDAINGVSELSPPRAVSIITNQAAPSVMTIKDRISR NSISLQEPERNGIILDEYVYKEQEBETSYTILRAGTNTTSSLDPTTYVQ IRARTAGYGTNSRKFEFNSPDSFSGISGNSHVMIAISAVALIYLAVTVLVQR FCGYHKSHSDEKRLHFNGHLRLPELRTYVDPHYEDPTQAVHEFAKELDATNTAI DKVYAGGERGVCSGRKLPSKKEISVAITTLVGYTEKRRPFLGASIMQFDPBN IIRLEGVYTSKVMYITTEYMENGLSDFLRKHDQFTVQLVGMKLSGKYLSD MGVYHRDLARNILINSNLVCKVSDFLSKDDPEAAVTTGGKLPVMTSPKATSD YRKETSADVMSYGIYLVEMVSYGERPYMSQDVKAVEDEGRPLPLMCPALAYO LMDQKDRNNRPKEOIVSILDKLRNGSKLITISAARSNLLIDSNVDIATF HTTGDMNGMRTAKHCKEITFGVEVSSCDTIAKISTDMMKVTVVVGPOKIIISIKI LEFOSKNGRPV"		
BASE COUNT	877 a 714 c 758 g 728 t		

ORIGIN																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
--------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

ORGANISM CDNA to mRNA.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2032)
AUTHORS Sajjadi, F.G., Pasquale, E.B. and Subramani, S.
TITLE Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor
JOURNAL New Biol. 3, 769-778 (1991)
MEDLINE 92031278
COMMENT On Feb 16, 1994 this sequence version replaced gi:199121.
FEATURES
Location/Qualifiers
1..2032
/organism="Mus musculus"
/strain="IRC x Swiss Webster"
/db_xref="taxon:10090"
/dev_stage="11.5 day embryo"
/tissue_type="embryo"
89..1702
/codon_start=1
/product="Mek4 secreted"
/protein_id="AAA39522.1"
/db_xref="GI:454829"
/translation="MDCHLSILVLGCVLSCSGELSPQSPNEVNLDSKTIOGELG
ISPSHGWEISGVDEHYTPIRTYOVCMVMDHSONMTLRNVPNSOKIYELKFT
LRDNSILVLGTCKEFENLYMESDGHVFRHFOPIKIDTIADESFTQMDGDR
LKINTEIREVGPVNRKGFYLAFOYGAVALYSVYVFRKCPYKINLAMPDTPMD
SOSLVEVSGCVNNSKEDPPRMTCSTEGELVPIGKTCNAGIEBERFICQACRPG
IKASDGAARKCAKCPHSSTOEDGSNCCENNYFAERDPSMACARPPSAPRVNIS
INENSVIIDMSWPLDGTGRKIDITENIICKKGMVROCEPCSPNVRFLPRLGLNTT
VTVIDLAHNTYFEIDAIVNGVSELSPPROYAASITNOAAPSVAWT IKDRISRN
SISLSMOEPHNGLIIDYEVKYYOKOQOETSYTILRAGTNVITSSLPKPTTYVFOI
RARTAGYGTNSRNFEPETSPDCMYRFSF"

CDS

polya_signal
polya_site
BASE COWNT 578 a 473 c 460 g 521 t
ORIGIN

Query Match 81.3%; Score 661; DB 12; Length 2032;
Best Local Similarity 89.2%; Pred. No. 5.5e-194;
Matches 725; Conservative 0; Mismatches 85; Indels 3; Gaps 1;
QY 1 atggatgttcagctcttcacatccctcccttcacagctgctctggttcgacagcttcgg 60
DB 89 ATGGATGTTCAGCTCTTCACATCCCTCGTCTGCTGCTGCTGCTGCTGCTGCTGCGA 148
QY 61 gaactgattccgcagccttcacatgaagtcacatctactgattcaaaaacaattcaagg 120
DB 149 GAACGAGGCCACAGCCTTCCAAAGCAAGTTAATCTAGATTGCAAAAACAATTCAAGGA 208
QY 121 gagctggagctgatactctatcatcacaatgagtgaggagagatcagtggtgtgata 180
DB 209 GAGCTGGCTGATCTCCATCCATCCATGGGTGGGAAGAGATCAGTGTGTGATGAA 268
QY 181 catiaacaccatcagagctaccagagtgtgcaatgcatgagcaagtcagaacat 240
DB 269 CATTCACACCCATTCAGGACTTACCAAGTGTGCAATGATGATACAGCCAAAATAAT 328
QY 241 tggcttgaagaacaaactgggtcccccagaactcagctccagaagaattatgtgagccaa 300
DB 329 TGGCTGAGACAAACTGGGTACCCGAAACTCAGCTCAGAGAATCTATGTGAGCTAAAG 388
QY 301 ttcactctcagagactgcaatgcaatcattggttttaggaacttgcaagagagacatc 360
DB 389 TTCACACTCGGGACTGTAAACGACATTCCATTGGTTTGGGGACTTGCAAGAGACCTTT 448
QY 361 aaccttactacatgagactgtagttagttagtgagggtgaaatttgagagatcagctt 420
DB 449 AACCTTACTACTATGGAAGTC--TGATGATCAAGGGGTCAAAATTCGGAAGGACTCAGTTC 505
QY 421 acaaaagattgacaaccattgcagctgtagaaagttcactcaaatgatatcttgggacgct 480

DB 506 ACCAAGATGACACCATTCGCCCTGATGAAAGTTTCACATCAGATGGATCGGGGATCGC 565
QY 481 attctgaagctaaacacgtagatgagagaagtagctgctgttcaacaagaaggatttat 540
DB 566 ATTCGAAACTCAACACTGAGATTAGAGAAAGGGGACCGTAGTCAACAAAAGGGGTTTAT 625
QY 541 ttggcatccaagatgttgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
DB 626 TTGGCTTTCAAGATGTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 685
QY 601 aagttcccatcttaccagtgtagaagatctggtatgtttccagacaagctacacatgactcc 660
DB 686 AAGTGCCCGTTTACAGTGAAGATCGGCTATGTTTCCAGACACAGTGCCCATGAGCTCC 745
QY 661 cagtcctcctgtgtaggtagtagaggtctctgtgttcaacaattcctaaggaagaatccca 720
DB 746 CAGTCTTGTGTGAGATTAGGGGCTCTTGTGTCAATTAATCCAAAGAGAGAGACCTCC 805
QY 721 aggatgtactgagtagaagaagcgaaatgctgtaccacattggcagaagtgtccgtgcaat 780
DB 806 AGGATGTACTGACGACACAGAGGAGATGCTGTGCCCATTTGGCAAAATGCACCTTCAAT 865
QY 781 gctgcatgtagaagaagaagtttatgtgccaa 813
DB 866 GCTGGTATGAGAGACAGACGAGCTTCATATGCCAA 898

RESULT 6
MUSMEK4
LOCUS
DEFINITION Mus eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.
ACCESSION M68513
VERSION M68513.1
KEYWORDS receptor tyrosine kinase.
SOURCE Mus musculus (strain IRC x Swiss Webster) 11.5 day embryo
ORGANISM CDNA to mRNA.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3197)
AUTHORS Sajjadi, F.G., Pasquale, E.B. and Subramani, S.
TITLE Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor
JOURNAL New Biol. 3, 769-778 (1991)
MEDLINE 92031278
FEATURES
Location/Qualifiers
1..3197
/organism="Mus musculus"
/strain="IRC x Swiss Webster"
/db_xref="taxon:10090"
/dev_stage="11.5 day embryo"
/tissue_type="embryo"
89..3040
/gene="Mek4"
/gene="Mek4"
/gene="Mek4"
/codon_start=1
/product="receptor tyrosine kinase"
/protein_id="AAA39521.1"
/db_xref="GI:199120"
/translation="MDCHLSILVLGCVLSCSGELSPQSPNEVNLDSKTIOGELG
ISPSHGWEISGVDEHYTPIRTYOVCMVMDHSONMTLRNVPNSOKIYELKFT
LRDNSILVLGTCKEFENLYMESDGHVFRHFOPIKIDTIADESFTQMDGDR
LKINTEIREVGPVNRKGFYLAFOYGAVALYSVYVFRKCPYKINLAMPDTPMD
SOSLVEVSGCVNNSKEDPPRMTCSTEGELVPIGKTCNAGIEBERFICQACRPG
IKASDGAARKCAKCPHSSTOEDGSNCCENNYFAERDPSMACARPPSAPRVNIS
INENSVIIDMSWPLDGTGRKIDITENIICKKGMVROCEPCSPNVRFLPRLGLNTT
VTVIDLAHNTYFEIDAIVNGVSELSPPROYAASITNOAAPSVAWT IKDRISRN
SISLSMOEPHNGLIIDYEVKYYOKOQOETSYTILRAGTNVITSSLPKPTTYVFOI
RARTAGYGTNSRNFEPETSPDSSISENSHYVMIAISAVALIIVLTIVTYLVGR

QY	193	aagaagattaccaggtgtgtaaatgtcaatgtgacacagtcacaaacaaatgtgcggaagaa	252
Db	221	ATCACAACCTTACCAAGAGCAATGTTAGATACAGTCAACAAAATTTGGTCGGCAACA	280
QY	253	aacttggtcccccagaagaaactcagctccacagaagaattatgtgagctccaagttactactcaga	312
Db	281	AACCTGGATTCCACCGAATTCAGCCGACAGAGATATATGTGGAGCTCAAGTTTACTCTTGAGG	340
QY	313	gactgcaatagcatctcatgtgttttaggaacattgcagaagagacatcaacctgtactac	372
Db	341	GACTGCATTAATATCCCTCTAGTTCTGTGGGCTCTGCAAAAGAGACTTTCATCTGTAATTAC	400
QY	373	atggagcttgatgtatgatacatgagggtgaatttcagagatcataagttataaagaattggac	432
Db	401	ATGGAAATCCGATGATGATACCAATTGCGCAAAAGTTCAAGAGACACCAATTTACGAAGATTGAC	460
QY	433	accattgcagctgataagaaagtttactcaataatgatcatcttgaggacglatctgaaagctc	492
Db	461	ACCATTGCGCGGTGATGATGAGAGCTTCAACCAAGATGATCTTGGGAGCCGGATTTCCAGCTG	520
QY	493	aacactgagattagaagaagtagtgcctgtccaacaagaaggatttattttgtgcaatttcaa	552
Db	521	AATACCGAAGTCCCGGAGAGTGGGACCTGTTAGTAAGAAAGGCGCTTTTACTGTGCTTCCAA	580
QY	553	gatgtgtgtgtttgtgttgcccttggtgtgtgtgtgagatataactcaaaaagtgtccattt	612
Db	581	GATGTAGTGTGATGATGTTGTGCTTATGTTCTCGGTGCGAGTGTACTTCAAGAAAGTCCCTTTC	640
QY	613	acagtgaaagaaatctgagctatgtttccacagacaggtaccatgtgactccagctccctgtg	672
Db	641	ACTGTCAGAAACCTCGGCATGTTTCCAGATTCATTTCTTATGGAGCTCCAGTCCCTGGTG	700
QY	673	gaaggttagaagggtcttgtgttcaacaattctaagagaagaagatccctccaagatgtactgc	732
Db	701	GAGGTGCGGGGTTCCTTGTGTCAATCATTTCCAAAGAGAGAAAGCCACCACCAAGATGTACTGC	760
QY	733	agtacagaagccagatgctgtgtatcccatgtgacagtgcttcctgcagatgtgtgtatgaa	792
Db	761	AGCAGCGAAGAGAAATGCTTAGTGTCCCATATGGAAAGTGTGTGTATAGTGTGCTATGAA	820
QY	793	gaagaaggtttatagtgcca	813
Db	821	GAGAGAGGCTTGTGCGTCCAA	841
RESULT	8		
LOCUS	115007	3254 bp	DNA
DEFINITION	Sequence	15	from patent US 5457048.
ACCESSION	115007		
VERSION	115007.1	GI:124915	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE	1	(bases 1 to 3254)	
AUTHORS	Pasquale,E.B. and Sajjadi,F.G.		
TITLE	Epi-related tyrosine kinases, nucleotide sequences and methods of use		
JOURNAL	Patent: US 5457048-A	15	10-OCT-1995;
FEATURES	Location/Qualifiers		
source	1..3254		
BASE COUNT	926 a	737 c	796 g 795 t
ORIGIN			

	Query Match	67.0%	Score 545;	DB 5;	Length 3254;	
	Best Local Similarity	80.0%;	Pred. No. 5.4e-158;			
	Matches 641; Conservative	0;	Mismatches 160;	Indels	0;	Gaps 0;
0y	13 cctccatcctcctccttcagcgcgttctgrrtcgcacagtctggggaaactgatccg	72				

Db	41	CGCGCCGTCGCGCTGCTGCTTGTGGCGTCCCTCGGCTCCGCGCGGCGCTTGACGCC	100
Oy	73	cagccttccaatgtaagtoaatctactgattgattccaaaacaattcaagggagctggtgctg	132
Db	101	CGCCCCGGCAACGAAGTTAACTCTCTGTGATTCCAAAACATTCAAGGGAGCTGGGCTTG	160
Oy	133	attctctatccatcatggtgtgggaagagatcaatgtygtgtgatacaattacacacc	192
Db	161	ATCTCTACCATCATCATAGGTGGGAGAGATTAGTGTGTGATGACATTATACTCCA	220
Oy	193	atcaggaattaccaggtgtgtgcaatgtaatgtagccacagtcataaacaattgcttgagaa	252
Db	221	ATCAAACTTTCACAAAGAGAGCAATGTTATGATGATCAGTCAACATTAATGGCTCGGACA	280
Oy	253	aacttggtccccagaactcagctcagaaagattatgtgtgagtcgaattcactcaga	312
Db	281	AACTGGATTCCACCAATTCAGGCCCAABAATATGTGGAGTTCAGATTACCTTGAGG	340
Oy	313	gactcgaatagcatctccattggtttttaggaacttgcagaagagacatccaacctgtatcc	372
Db	341	GACTGCATATATATCCCTCTGTGTTCTGTGGCACTTGCAAAGAGCTTTCATCTGTATTAC	400
Oy	373	atggaatctgatagtatcatcagtggtgtgaaatttcgagagcatcagtttcaaaagattgac	432
Db	401	ATGGAAATCCGATGATGAACCAATTGGCAAAAGTTCAGAGACCAATTTACGAAGATTGAC	460
Oy	433	accatttcagctgtatgaaagtttcaactcaaaatggatcttggggacggtattctgaagctc	492
Db	461	ACCAATGGCGCTGATGAGAGCTTACCCCAATGGAATCTTTGGGAGCCGATTTCAAGCTG	520
Oy	493	aaactgtgattaaagaagtagtgccttcgtacaacaagaaggaatttatttggcattcca	552
Db	521	AATACCGAAAGTCCCGAGAGTGGACCTGTATGTAAGAAGGGCTTTTACTTGGCTTCCAA	580
Oy	553	gatgttggtgtgtgtatgcacctgtgtgtcgtgtagatctactcaaaaagtcccat	612
Db	581	GATGTAGGTGCATGTGTGCTTATGTGTGCTGTGGAGTGTACTTTCAAGAGTCCCTTTC	640
Oy	613	acagtgaagaatctcgtctatgtttccagaacaaggttaccctcagtcacccagtcctcgtgtg	672
Db	641	ACTGTCAAGAACCTGTGGCAGTCTTCCAGATNACAGTTCTATGACATCCAGTCCCGTG	700
Oy	673	gaggttagaaggctctgtgtcaacaaltctaaggaggaagatctctcaagaagtacgtcgo	732
Db	701	GAGGTGCGGGCTTCTTGTGTCAATCATTTCCAAAGAGGAGAGCCACCAAGATGTACTGC	760
Oy	733	agtacagaagcgaatggtctgtatcccatctggcgaagtgttccctgcaatctgtctatgaa	792
Db	761	AGCAAGGAAGAGATGGCTATGTCCCATAGGGAAGAGCTTGTGTATGCTGGCTATGAA	820
Oy	793	gaagaggttttatgtgtccaa	813
Db	821	GAGAGAGGCTTTGGCTGCCAA	841

RESULT	9				
CHECKER8					
LOCUS					
DEFINITION	CHKR8	3600 bp	mRNA	VRT	01-FEB-2000
ACCESSION					
VERSION	D88174				
KEYWORDS	D88174.1	GI:1236732			
SOURCE	receptor tyrosine kinase; Cck8.				
ORGANISM	Gallus gallus spinal cord cDNA to mRNA.				
	Gallus gallus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;				
	Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus				
	1 (sites)				
AUTHORS	Ohta, K., Nakanura, M., Hirokawa, K., Tanaka, S., Iwama, A., Suda, T.,				
TITLE	Ando, M. and Tanaka, H.				
JOURNAL	The receptor tyrosine kinase, Cck8, is transiently expressed on				
MEDLINE	subtypes of motoneurons in the spinal cord during development				
	Mech. Dev. 54 (1), 59-69 (1996)				
	96404128				

REFERENCE 2 (bases 1 to 3600)
AUTHORS Ohta, K.
JOURNAL Unpublished (1996)
REFERENCE 3 (bases 1 to 3600)
AUTHORS Ohta, K.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1994) to the DBJ/EMBL/GenBank databases.
Kunimasa Ohta, Kumamoto University Graduate School of Medical
Sciences, Dept. of Neuroscience and Immunology, 4-24-1 Kohonji1,
Kumamoto, Kumamoto 862, Japan
(E-mail: ohta9203@pro.kumamoto-u.ac.jp, Tel: 096-344-2111 (ex. 6754),
Fax: 096-364-3554)

FEATURES
source
1. .3600
/organism="Gallus gallus"
/db_xref="taxon:9031"
/tissue_type="spinal cord"
3. .47
3. .2963
/codon_start=1
/product="Cek8"
/protein_id="BAA07373.1"
/db_xref="GI:1236733"
/translation="MACVPGALLPLLYGCGAVYGSRYPANETVLLDSRSVSGEL
MIASPLEGMEBVSIMDEKNPTIRTYQCVNWEPSQNMFLRDMIPREGADRVYIEIK
ETLRQNSLPGVMGICKETFNLYIESNNDEKRFRESQFAIDTIDADESTOYDIG
DRIMKLNTEVRDVGPLSKSGFYLAQDYGACIALVSIVFYKCPILVYNLAQFPDI
TGADTSLVEYVSGSVNSEEKVDKMGADGEWLVPGNCLNAGYEERNGEAC
KIGYKALSTDVACAKCPHYSISWEGSTSCDGFPRANDASMECTRPSPAPN
LISNVNTESVNLEWSAPQNGRQDDISYVNRKCGAEPSPHSCRCGSGVHPSPQNG
LKTIVSTIDLAHNTTPEYAVNVSQVANSQVANSVATVTTQQAAPSPALIOAK
ETIRNSVALWLEDPDPNGVILIEYEVKYEKQDNRSYRIYKTAARNMDIGLPLTS
YVFHVRARTAAVGDSPFEFTNTVSPPIIGDINPTVLVSVAAGSVLVAVIIIA
KVIYSRRSKYSKAKOADEBEKLNQVRYVDFEEDNPQVREFAKEIDPSCKIE
KVIYGEVEGSCGRKLVKPGKREICVAIKTKAGYTDORDELSEASIMGOEPHNT
IHLEGVTKCKRPMVITTEYMEGSLDARFKNDGSEFTYQLVGMIRGSGSKYISDA
SYVARDLAARNLIVNSNLVCKYSDKMSRVLDEDEPAVYTHGKIPLRWTRPEAIAY
KRETSASVWSVIGIVMEWESVGERPVWMSQDVYKAIIEEYRLPMPMDCPIALHOL
MLDCWQKRSRDPKFGQIVNMLDKLIRPNNSIKRTGSSSRSTALDPPSSEFEAV
SVSDMLQAIKMERKDNFTAAGYTTLEAVVHMNDOLARIGITATTHQNKILSVQAM
RSOQMOHGRMVPV"

mat_peptide

BASE COUNT 944 a 876 c 935 g 845 t
ORIGIN

Query Match 44.6%; Score 362.8; DB 4; Length 3600;
Best Local Similarity 67.7%; Pred. No. 1.7e-101;
Matches 540; Conservative 0; Mismatches 252; Indels 6; Gaps 2;

QY 22 ctctctctctcagctgctctgctctcgcagcagctcggggaactgattccgcagcctcc 81
DB 27 ctctctctctcagctgctctgctctcgcagcagctcggggaactgattccgcagcctcc 86
QY 82 aatgaagtcacatctactgattcaaaaacaaatcaagggagctgggctgtagctcttat 141
DB 87 AACGAAGTACACCTCTGAGACTCCCGCTCGGTGACAGGAGAGCTGGGCTGAGTGGAGAC 146
QY 142 ccatcaccat---gggtgggaagagatcagtggtgtagatggaacattacacccatcaag 198
DB 147 CCGCTGGAAGAGAGGGTGGAGGAGAGTACATATGATGAGAAACACTCCGATCCGC 206
QY 199 acttaccaggttgcgaatgctcatagaccacagtcacaaacaaatgctgtagaacaactgg 258
DB 207 ACCTACCAAGTTTGCAATGATGATGAGAGCCACAGTCAAAATATGTGTACGAACTGTTTG 266
QY 259 gtccccaaggaactcagctcagaagatttatctgtgagctcaagttcacctctacgagactgc 318
DB 267 ATTCCCGCGAGAGGGCTCAAGAGGCTATATGAATCAAGTTCACTGAGAGAGACTGC 326
QY 319 aatgattccatggttttaggaacttgcaagggaacattcaactgtactacatcaggag 378

DB 327 AACAGCTGCCAGGTGTCTATGSGAACTTGCAAAAGAACTTTCACCTCTATTATGAA 386
QY 379 tctgatgatcatcagtgaggatgaaattcgaagcactcagtttacaagaattgacacatt 438
DB 387 TCAACACAGAACAGAGAGCGTTTATTGACAGAGACCAGTGTGCCAAGATTGACACATT 446
QY 439 gaagctgatgaaagtttcaactcaaaatggaattcttggagacccgattatcgaagctcaact 498
DB 447 GCTGCTGATGAGAGCTTCCACCAGGTGGACATTTGTTGACAGAGATCATGAACTGAATCA 506
QY 499 ggattatgaagagatggtgtcctgtctcaacaagaagagatttatttgcatcttcaagaattc 558
DB 507 GAGGTCGGGAGAGTGGGGCTCTCAGCAAGAAAGGGTTTACTTGGCTTTCAGAGACATC 566
QY 559 ggtgtctgtgtgctctgtgtgtctgtgagagatacttcaaaaagtgcccatcagtg 618
DB 567 GTTGCTGCTGATTTGCTTTGGTGTCTGTCTGTCTCTATMAGAAATGCCACATGACATT 626
QY 619 aagaatctgtgctatgtttccacagacaggttacccatg---gaatcccaatccctgtgag 675
DB 627 CGAAACCTGGCACAGATTTCACAGACACACATTAATGAGGCTGATACATCCTCTGTGGAG 686
QY 676 gttagaaggtcttctgtgtaacaacattcaagagagagatccccaagatgactgcagct 735
DB 687 GTTGTGCTCTCTGTCTCAACAACTCGAAGAGAGAGACGTGCCAAAAATGTACTGCGGG 746
QY 736 acagaagcgaaatggtctgtaccatctgcaagtgcttccctgcaatgctggtcgtatgaagaa 795
DB 747 GAGAGATGATGATGGCTGTGATACCATTTGACACATCTCTGTGCAATGCTGTGCTATAGAA 806
QY 796 aagagtttattgtgcca 813
DB 807 CCCAATGCTGATGCCAA 824

RESULT 10

MM058332 3943 bp mRNA ROD 08-MAY-1997
LOCUS Mus musculus receptor tyrosine kinase mRNA, complete cds.
DEFINITION U58332
ACCESSION U58332
VERSION U58332.1 GI:1457960

KEYWORDS
SOURCE
ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3943)
AUTHORS Lee, A.M., Navaratan, D., Ichimiya, S., Greene, M.I. and Davis, J.G.
TITLE Cloning of m-ehk2 from the murine inner ear, an eph family receptor
tyrosine kinase expressed in the developing and adult cochlea
JOURNAL DNA Cell Biol. 15 (10), 817-825 (1996)
MEDLINE 97047913
REFERENCE 2 (bases 1 to 3943)
AUTHORS Lee, A.M., Ichimiya, S., Greene, M.I. and Davis, J.G.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-1996) Pathology & Laboratory Medicine, University
of Pennsylvania, 36th and Hamilton Walk, Philadelphia, PA
19104-6082, USA

FEATURES
source
Location/Qualifiers

1. .3943
/organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
285. .3392
/note="eph-related tyrosine kinase: similar to Rattus
norvegicus receptor-like tyrosine kinase Etk-2, SwissProt
Accession Number S51605"

Accession Number S51605
/codon_start=1
/product="receptor tyrosine kinase"
/protein_id="AAB53836.1"
/db_xref="GI:1457961"
/translation="MGCEVEEPLIGFELPLITAVTDCSHVSNQVLLDTTVNG
ELGKTYPLNGMDAITEDEHNRIHYQVNVNPEPQNMNMLRTNWSRDAOKIYVE


```

MKYLSDMGYVHRDLAARNILINSLVCKVSDGSLRVLEDDPEAAVTRGKIPRTMT
AAPEALAFERKTSASDWSYGIYMEVVSXGEPYEMTNODVKAVEGYRLPSPMDC
PALYQALMDCKDRNSRPFKDDIVNNLMDKLIRPSSSLKTLVNASHSVSTLAEHGS
LGSQVRSVGEWLEAIKMGRTYEIMENGYSMDVAQVITL"
424
conflict
/gene="ekh-1"
/citation={3}
/replace="g"
435^436
/gene="ekh-1"
/citation={3}
/replace="g"
458
/gene="ekh-1"
/citation={3}
/replace="g"
462..482
/misc_feature
/gene="ekh-1"
/note="putative alt. splice region (by comparison with
publ. seq. and PCR cDNA fragments)"
934
conflict
/gene="ekh-1"
/citation={3}
/replace="c"
1531
conflict
/gene="ekh-1"
/citation={3}
/replace="g"
1816
conflict
/gene="ekh-1"
/citation={3}
/replace="c"
1821
conflict
/gene="ekh-1"
/citation={3}
/replace="g"
1885..1950
/misc_feature
/gene="ekh-1"
/note="putative alt. splice region (by comparison with
publ. seq. and PCR cDNA fragments)"
2094
conflict
/gene="ekh-1"
/citation={3}
/replace="g"
2211
conflict
/gene="ekh-1"
/citation={3}
/replace="c"
3219^3220
/conflict
/citation={3}
/replace="c"
3308
BASE COUNT 1001 a 772 c 892 g 866 t
ORIGIN
Query Match 43.2%: Score 351.4; DB 12; Length 3531;
Best Local Similarity 67.3%; Pred. No. 5.7e-98;
Matches 512; Conservative 0; Mismatches 246; Indels 3; Gaps 1;
QY 56 tcggggaactgattccgcagccttcacatgaatcaatcactacgattcaaaacaatc 115
DB 579 TCGGGACCCTTTGGCCAGCCAGTAAGAGTGAATTATGATTCGGCCGACGTGTC 638
QY 116 aagggaagctggcgtgattcttaccacacatgggtgggaagagatcagtgtgtg 175
DB 639 TGGGAGACCTTGATGATGCTTTTCCAAAGAATGGGTGGGAAGATGTGTGAAGTTC 698
QY 176 atgaacattacacacacacacacacacacacacacacacacacacacacacacac 235
DB 699 ATGAAACTATGCCCCCATTCCACACCTATCAAGTGTGCAAAAGTTATGGAACAGAAATCAGA 758
```

```

QY 236 acaattgctcagaacaacactggtccccaaggaaactcagctcagaagaatttatgtgagc 295
DB 759 AATAATGGCTGTGACCAAGTTGATGATCTCAACGAAGGCGCTCCAGAAATTTTATGAAC 818
QY 296 tcaagttcaactcacaagacatgcaatagcattccattggttttaagaaactgcaagaga 355
DB 819 TCAAGTTTACTGTGAGGGATTCACACAGCTCTCGAGGAGTGGGAGCTTGCAAGGAGA 878
QY 356 catcacaactgactacacatgagatgagatgagatgagatgagatgagatgagatgagatc 415
DB 879 CTTTACATGATGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 938
QY 416 agttacaagaattgacaacattgagcagctgagatgagatgagatgagatgagatgagatgag 475
DB 939 AGTACATCAAGATCGATACCATGCTGCGATGAGAGGCTTACCGAAGTGTGACCTTGGAG 998
QY 476 accgatctcgaagctcaacactgagatgagatgagatgagatgagatgagatgagatgagat 535
DB 999 ACCGGGTCAATGAGCTGATACGAGGCTCAGAGATGATGAGACCTCTGAGCAAAAAGGAT 1058
QY 536 ttatttgcatcacaagaattggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 595
DB 1059 TTATCTTCTTCCAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1118
QY 596 tcaaaagtgcccaattlaagatgagaaactggtctatgtttccagacacagttaccatg 655
DB 1119 ATMAAAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1178
QY 656 actccagtc---tggtgagagttagaagggtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 712
DB 1179 CAGATTCCTCCAGTGTGCTGAGGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1238
QY 713 atccccaagagtgatcagctcagctcagctcagctcagctcagctcagctcagctcagctcagct 772
DB 1239 ATCTCTCCAAATGCAATTCAGTCTGAGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1298
QY 773 cctgcaatgctgctatgagaagaagagtttatgtgccaa 813
DB 1299 TGTGCAAGCCCGATATGAAAGAAATGATACCTGTGTA 1399
RESULT 12
AR062744 3906 bp DNA PAT 29-SEP-1999
LOCUS AR062744
DEFINITION Sequence 102 from patent US 5843749.
ACCESSION AR062744
VERSION AR062744.1 GI:5990435
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3906)
AUTHORS Maisonneville P.C., Maslakowski P. and Yancopoulos G.D.
TITLE Enh and Koi tyrosine kinases
JOURNAL Patent: US 5843749-A 102 01-DEC-1998;
FEATURES
source 1..3906
BASE COUNT 1097 a 876 c 990 g 943 t
ORIGIN
Query Match 43.2%: Score 351.4; DB 5; Length 3906;
Best Local Similarity 67.3%; Pred. No. 5.8e-98;
Matches 512; Conservative 0; Mismatches 246; Indels 3; Gaps 1;
QY 56 tcggggaactgattccgcagccttcacatgaatcaatcactacgattcaaaacaatc 115
DB 630 TCGGGACCCTTTGGCCAGCCAGTAAGAGTGAATTATGATTCGGCCGACGTGTC 689
QY 116 aagggaagctggcgtgattcttaccacacatgggtgggaagagatcagtgtgtg 175
```

D	b	690	TGGGAGCCTTGATGGATTGCTTTTCCAAAGAAATGGGTGGGAAGAGANTGGTGAAGTC	743
O	y	176	atgaacattacaccccatcagaagctaccaggtgtgcacgtctcatbgaacacagtcacaa	235
D	b	750	ATGAAACTATGCCCCCATCACACCCATCACTCAACTGATGTGCAAAAGTTATGTGAACGAATTCGA	809
O	y	236	acaattgctcgaagacaaactggtgtcccccgaagccacagctcaagaagattctbgaagc	295
D	b	810	ATAATTGGCTGTGACCAAGTTGGATCTCTACGAAAGTGCTTCCAGAAATTTTATTGAAC	869
O	y	296	tcaagttcactctcagaagactcgaataagcattccattggtttttaggaacttcaagaga	355
D	b	870	TCAAGTTTACTCTGAGGGGATTTGCACAGCCTTCTGGAGAGACTGGGGACTTTCAGAGAGA	929
O	y	356	cattcaacactgtaactaactgagatctgatatgatcatcattgggttgtaattcgaagctc	415
D	b	930	CCTTTAACATGATATTATTATTGAGTCGGATGATGAGATGGGAAATATCAAGAAAC	989
O	y	416	agttacaaagatbgaacacattgcagctgatatgaagtttcactcaaatbgaatctctggg	475
D	b	990	AGTACATCAAGATGATGATACCATGCTGTCGTGATGAGAGCTTCACCGAATCTGACCTTGGAG	1049
O	y	476	accgatattcgaagctcaaacactcgagattagagaagtagtgcctgtcacaagaaggat	535
D	b	1050	ACCGGGTCATGAAACCTGAAATACGAGAGTCAGAAATGTAGAGCTCTGACCAAAAAGGAT	1109
O	y	536	tttaattgagcatctcagaagatgttggtgctgtgtgtcctgtgtgtctbgaagatcact	595
D	b	1110	TTTATCTGCTTCCAGATGAGTGTGGTCTTGACATGCCCTGTGTTCTGTCCCTGTCTACT	1169
O	y	596	tcaaaagtcgccattcttaacagtcgaagaatctgtgctatgtttccagaacagytaccact	655
D	b	1170	ATAAAATATGCTCTTCTGTAGTTAGACATTTGGCTGTTTCCCTGCACGATCACTGTAG	1229
O	y	656	atcccaagtcgcc---tggtagaggttagaagggctctgtgttcaacaattctaagsgaag	712
D	b	1230	CAGATTCTTCCCACTTCTTGAAGGTGTCAAGGCTCTCTGCGTCAACATTTGTGACAGCG	1289
O	y	713	atcctcaagaagtgtactgtcagtcagaaagcgaatgctgttaccocatgtgcaagtgt	772
D	b	1290	ATCTCCCAAAATCATTTGCAGTGTGCTGAAGGAGGTGGTGGTCCATCGGAAATCA	1349
O	y	773	ctctgaatgctgctgatgaagaagaggttttatgtgccaa	813
D	b	1350	TGTGTAAAGCCGGATATGAAGAAATATGCTCTGTCA	1390

RESULT	13				
AR025488					
LOCUS	AR025488	4165 bp	DNA	PAT	05-DEC-1998
DEFINITION	Sequence 1 from dataset NC_070046				

REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 4165)
TITLE	Caras, I.W. and Winslow, J.W.
JOURNAL	Al-1 neurotrophic factor antibodies
FEATURES	Patent: US 5798448-A 1 25-NOV-1998;
SOURCE	Location/Qualifiers
	1..4165
BASE COUNT	/organism="unknown"
ORIGIN	1157 a 907 c 1035 g 1066 t

Q7	56	tcggggaactgattccgcagccttccaatgaagtcattactgattcaaaacaattc	115
Query Match	43.28	Score 351.4; DB 5; Length 4165;	
Best Local Similarity	67.3%	Pred. No. 5, 8e-98;	
Matches 512; Conservative	0;	Mismatches 246; Indels 3; Gaps 1;	

Db	695	TCGCGACCCCTTTTGGCCAGGCCCGAGTAAGGAAGTGATTTATTTGGATTTCGCGCACTGTCC	754
Qy	116	aagggaagcctgggctgagctatccttaccatcaacatcggtgggaagaagatacagttggtg	175
Db	755	TGGGAGACCTTGGATGGATGCTTCTTTCCAAAGAAATGGGTGGGAGAGATTTGGTAAATTG	814
Qy	176	atgacattacacaccatcaagacttaagcttaccaggtgtgcacatgtcactgacacagttca	235
Db	815	ATGAAACTATCCCCCATCTCACACCTATTCAGTGTGCAAGTTATGGACAGATACGA	874
Qy	236	acaaatgctgtagaacaacaactgggttcccaagaaactcagctcagaagaattatgttgaac	295
Db	875	ATAATTGGCTGTGACCAAGTTGGATCTCTAACGAAGGTGCTTCCAGATTTTATTGAC	934
Qy	296	tcaagttcatctcaagagagacttgaatgaattacattcatttgtttaggaacttgaagaaga	355
Db	935	TCAAGTTACTCTGAGGGGATTCGACAGGCTTCTCGAGAGACTGGGGCTTCGACAGGGA	994
Qy	356	cattcaaccctgatacacaatgagtcgcatgcatgatacatgagggtgaattctcagaagc	415
Db	995	CCTTTAACATGTATTTATTGAGTCCGATGATGAGAAATGGGAAATTCAAAGGAAAC	1054
Qy	416	agttacaaagattgacacccattgcagctcgtatgaagaatttcaactcaaatgagcttg	475
Db	1055	AGTACATCAGATCGATACATTGCTGCTGATGAGAGCGTTACCGAATTGACCTGTGAG	1114
Qy	476	acggtattctgaagctcacaacatgagataagagaagtagtgcctgttcaacaagaaggat	535
Db	1115	ACCGGTCATCAGAGCTGAAATCGAGAGGTACAGATGTAGAGACCTTGAGCAAAAAGGAT	1174
Qy	536	tttatgttggaattcaagaatggttggtgctgtgttcctgtgtgtgtgtgtgtgtat	595
Db	1175	TTTATCTTGCTTCCAAAGATGGGTGGCTGGATGCTCTGGTTCTCTCCGTGTACT	1234
Qy	596	tcaaaagtcoccatctaacagatgaagaatctgctcatgtttccacagaacggtaccatc	655
Db	1235	ATTAATAATGTCTCTCTGTAGTATGACATTTGGCTGTTTCCCTTACACGATCACTGGAG	1294
Qy	656	actcccaagtc---tggtgaggtttagaagggttctgtgttcaacaattctaaggagaag	712
Db	1295	CAGATCTCTCCAGTTGCTGAGGTGTCAAGGCTCCGCGTCAACATCTGTGACAGACG	1354
Qy	713	atctctcaagaagtactcagtcagtcacagaagcggaatgctgtgtaccatctggcaagt	772
Db	1355	ATCTCCCAAAATGCAATTGCAAGTCTGGAAGGGGAGTGGCTGGTTCCCATCGGGAATGCA	1414
Qy	773	cttgcacatgtgctatagaagaaggttattgtgcaa	813
Db	1415	TGTGCAAAGCGCGGATATGAAAGAAAAAAGTGATCCTGTAA	1455

RESULT	14
MMSEK	
LOCUS	4242 bp
DEFINITION	mRNA
MMSEK	
LOCUS	30-JUN-1993
DEFINITION	ROD

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

1 (bases 1 to 4242)
Charnay, P.
Direct Submission
Submitted (25-MAR-1992) P. Charnay, Ecole Normale Supérieure, Lab
de Génétique Moléculaire, URA 1302, 46 Rue d'Ulm, 75230 Paris Cedex
05, FRANCE
2 (bases 1 to 4242)
Gillardi-Hebenstreit, P., Nieto, M.A., Frahm, M., Mattel, M.G.,
Chestier, A., Wilkinson, D.G., and Charnay, P.
An Eph-related receptor protein tyrosine kinase gene segmentally

JOURNAL expressed in the developing mouse hindbrain
Oncogene 7 (12), 2499-2506 (1992)
MEDLINE 93096484
Erratum: [[published erratum appears in Oncogene 1993
REMARK Apr:8(4):1103]]

FEATURES Location/Qualifiers
source 1..4242

gene /organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/dev_stage="8.5 days"
/map="band C"
58..3018
/gene="Sek"
58..3018
/gene="Sek"
/note="Bph. receptor related"
/codon_start=1
/product="tyrosine kinase"
/protein_id="CAA46268.1"
/db_xref="GI:54084"
/db_xref="MGD:MGI:98277"
/db_xref="SWISS-PROT:003137"
/translation="MAGIFVFLEFSLFCICNAVMSRYPANETTLDSRSVQELG
KIASPLEGMEVYSINDEKNPIRTIOVCNWEASNNMLRTDWITREGAQVYIEIK
FTLRDCNSLPVWGPKETENLYEESDNDKERFKIESQFGKTDIADSEPTVDIG
DRIMKLNTEIRVVGPLSKRGFLAFQDVACIALSVRYFKCPLTVNLNQPDPI
TGADTSILVEKSGCVNNSEKQVDEPKMGAGDEMVPFGNCLCNAGHEONGEOAC
KIGYKALSTDASCANCKPMSYVMGASCTCDGFEFNDADAASMPCTRPSAPLN
LISNVMESVNLNEMSPQMGRODISYVWCKKGAQPSKCRGSGSVHTTPQNG
LKTIVSTIDLAHNTYRTEIWAHNSVSTINSPDSVSIVTTNOAASIALVOAK
EYTRYSVALWLEPRNGVILLEYEVKYEKDNQNSYRIVRTAANDIKGLNPLTS
LYEHRARAAAGYGFSEPLEVTNTVPRIIGDGMSTVLVSVGSVYLVIILIA
EYISRRSKYSKAKOEADEKHLNCGVRYVDFTEJEDNOAAREFAKIDASKIE
KIVGEEGECVSGRLKVPGRKEICVAIKTLKAGYDRDRDFLSPASIMQEDHPI
IHLEGVYTKCKRPMITTEYMENSGIDAPLRKNDGRTYQIYGLMRGISGSKYISDM
SYVHRDLARNTLVNSNLCKYSDREMSVLDDEPAATTTGGKIPIMTAPLEAIAY
RKFISASDVWSTGIVWVEVMSYGERPYWMSNOVDYKAIIEGYRLPPMDCPIALHOL
MLDCWQKERSDGRKGOIVNMDKLIRNPNLSLRKGSSESRNTALLDPSSEFSAYV
SYGDMLOAIKMDRYKDNFTYAGYTTLEAVVHMSQDLARIGITATIHQKILISSVQAM
PTMOOMHGRMPV"

slg_peptide /gene="Sek"
mat_peptide /gene="Sek"
misc_feature /Product="tyrosine kinase"
/gene="Sek"
/note="tyrosine autophosphorylated"
BASE COUNT 1155 a 1034 c 1052 g 1001 t
ORIGIN

Query Match 43 2%; Score 351.2; DB 12; Length 4242;
Best Local Similarity 66.5%; Pred. No. 6.7e-98;
Matches 353; Conservative 0; Mismatches 263; Indels 6; Gaps 2;

Qy 16 tccatccctccctctccagctgctcgtctcgacagctcgaggagacgtatccgcag 75
Db 76 TtCATCTCTTTTCGTTTCTTCTTGAAATTGGACCCCTTACCCGTTTAAAGGATAC 135
Qy 76 ccttcacatgaagtcacatctactgattccaacaaacatcaaggagagctggctgatac 135
Db 136 CCCGCAATGAAGTACTTATTGATTCAGATCTGTTCAGGAGAGCTTGGGTGATA 195
Qy 136 tcttatacat---cacatgggtgggaagagatcagctggtgtgataacattcacaccc 192
Db 196 GCAAGCCCTCTGGAAGAGGGGTGGAGAGTAGCATTTATGATGAGAAATAATACCCG 255
Qy 193 atcaggacttaccaggtgtgtcaatgtcatgtgaccacagtcacaaacatgtgctgagaca 252
Db 256 ATCCGAACCTACCAAGGTGTGCAACGTGATGTGAAGCCACGACAAACAACCTGCTGCGAACT 315

Qy 253 aactggccccgaagaaactcagctcagaaagattatgtgagctcaccattcactcaga 312
Db 316 GACTGGATCACCCGCGAAGGGGGCGAGAGGGGTGTACATGAATTTAACTTACTCTAAG 375
Qy 313 gactgcaatagcatctccatgtgttttagaacttgcaagagaacatcactgtactac 372
Db 376 GACTGCAACAGCTTCTCCGGGCGTCATAGGGGACTTCGMAAGAACGTTTAACTTACTAC 435
Qy 373 atggaactcgtatgatcatcgtgggtgaaatttcgagaagcaccagtttacaagattgac 432
Db 436 TATGATCGGACACACACACAAGAGCCCTTCATCAGAGAAAGCCAGTTTGGCAAGACTGC 495
Qy 433 accattgcagctgataaagatttcaactcaaatggaatcttggggaccgtatctgaagctc 492
Db 496 ACCATCGCAGCTGATGAGAGCTTACGACGAGTGACATTGGACGGAATTCATGAACATC 555
Qy 493 aaactcgaatataagaaataggtctctgcaacaagaagagatttacttgaattcaa 552
Db 556 AACACTGAGATCCGGGATGATAGGGCCACATGACCAAGAAAGGGTTTTAACTTGACTTTCAG 615
Qy 553 gatgttgctgctgtgtgctcctgtgtctgtctgtgagaagtacttcaaaagtcgccaatt 612
Db 616 GATGTGGGTGCTTGCAATCCGCCCTCGTCTGTCTGTCTGTCTTACAAAGATGTCCACTIC 675
Qy 613 acagtgaaagatctggtctatgtttccagacaggtaccatg--gactcccaagtcctg 669
Db 676 ACCGTTGCAAACTATACCCAGTTCCTGACACACATTAATGGGGCTGATACGCTTCCCTG 735
Qy 670 gtggaggttaagaggtctgtgttcaacaattcttaagagaagatctccaagatgtac 729
Db 736 GTGGAAAGTTGAGAGCTTCGTGTCAACAACCTCAGAAAGAAAGATGTGCAAAAAGTAC 795
Qy 730 tgcagtagaagcgaagcgaagctgtgaccattggcgaagtgttcctgcgaatctggtcat 789
Db 796 TGTGGGGCAGATGTGTAAGTGCTGTGATGCCATTGGCAATGCTTATGCAACGCTGGGCAC 855
Qy 790 gaagaagaaggtttatgtgcaca 813
Db 856 GAGGACGACGAATGTGATGCCAA 879

RESULT 15
S57168
LOCUS S57168 4242 bp mRNA ROD 28-JUN-1993
DEFINITION Sek-Eph-related receptor protein tyrosine kinase [mice, mRNA, 4242
nt]
ACCESSION S57168
VERSION S57168.1 GI:298687
KEYWORDS
SOURCE
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4242)
AUTHORS Giliardi-Hebenstreit,P., Nieto,M.A., Frain,M., Mattei,M.G.,
Cheslier,A., Wilkinson,D.G. and Charney,P.
An Eph-related receptor protein tyrosine kinase gene segmentally
expressed in the developing mouse hindbrain
JOURNAL Oncogene 8 (4), 1103 (1993)
MEDLINE 93205393
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gi298687 127779] from the original journal article.
This sequence comes from Fig. 5.
ERRATUM Giliardi-Hebenstreit et al., Oncogene (1992)7, 2499-2507.

FEATURES Location/Qualifiers
source 1..4242

gene /organism="Mus sp."
/db_xref="taxon:10095"
58..3018
/gene="Sek"
/note="Bph-related receptor protein tyrosine kinase"
58..3018
/gene="Sek"
CDS

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 11:20:11 ; Search time 1358.94 Seconds
(without alignments)
259.489 Million cell updates/sec

Title: US-09-104-340-6

Perfect score: 87

Sequence: 1 atgagtgtcagctctccat.....ttccgcagccttccatgaa 87

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 202611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*

45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_est45:*
80: gb_est46:*
81: gb_est47:*
82: gb_gss1:*
83: gb_gss2:*
84: gb_gss3:*
85: gb_gss4:*
86: em_gss1:*
87: em_gss2:*
88: em_gss3:*
89: em_gss4:*
90: gb_gss5:*
91: gb_gss6:*
92: gb_gss7:*
93: gb_gss8:*
94: gb_gss9:*
95: gb_gss10:*
96: em_gss5:*
97: em_gss7:*
98: em_gss8:*
99: em_gss9:*
100: em_gss10:*
101: em_gss11:*
102: gb_gss10:*
103: gb_gss11:*
104: em_gss12:*
105: gb_gss12:*
106: gb_gss13:*
107: gb_gss14:*
108: gb_gss15:*
109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

Query

SUMMARIES

Unpublished (1997)
On Jan 14, 1998 this sequence replaced g1:1798438

Unpublished (1997)
On Jan 14, 1998 this sequence version replaced g1:1798438.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmett-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLT at:
www.bio.lnlnl.gov/dbp/image/image.html

Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 373.
Location/Qualifiers
1. .427

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1469977"
/clone_1id="NCL_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatma Bonaldo. "

```

AA752361 225 bp mRNA EST 20-JAN-1998
96GS0872 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
cDNA clone 96GS0872, mRNA sequence.
AA752361
AA752361.1 GI:2799372
EST.
Oryza sativa.
Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Oryza.
1 (bases 1 to 225)
Nahn,B.H., Kim,J.K., Cheong,U.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
On May 8, 1995 this sequence version replaced gi:801205.

```

Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@suno20.aeti.re.kr
Submitted by Baek Hie Nam, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnam@bserver.myongji.ac.kr
Seq primer: M13 Reverse primer.
Location/Qualifiers
1..225
/organism="Oryza sativa"
/cultivar="Milyang23"
/db_xref="taxon:4530"
/clone="96GS0872"
/clone_lib="Rice Immature Seed Lambda ZAPII CDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; site.2:
XhoI; Directional CDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
53 a 69 c 45 g 58 t
33.1%; Score 28.8; DB 38; Length 225;
1 Similarity 65.6%; Pred. No. 77;
42; Conservative 0; Mismatches 22; Indels 0; Gaps 0
acc 64
aac 94
aac 94

```

AO850374 407 bp DNA GSS 15-OCT-1999
 LMAuFV1_lm30b08.v1 Leishmania major FV1 random genomic library
 Leishmania major genomic clone LMAuFV1_lm30b08 5', genomic survey
 sequence.
 AO850374
 AO850374.1 GI:6055022
 GSS
 Leishmania major.
 Leishmania major
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Leishmania.
 1 (bases 1 to 407)
 Akopyants,N.S., Beverley,S.M., Clifton,S., Marra,M., Hillier,L.,
 Chitwalla,A., Page,D., Martin,J., Wylie,T., Blistain,A.,
 Schmitt,A., Person,B., Theising,B., Ritter,E., Ronko,I.,
 Bennett,J., Cole,R., Underwood,R., Cardenas,M., Gibbons,M.,
 Harey,N., McCann,R., Tsagarisvilli,R., Williams,T., Jackson,Y.,
 Bowers,Y., Swaler,T., Waterston,R. and Wilson,R.
 WashU Leishmania Project
 Unpublished (1999)
 On Mar 23, 1999 this sequence version replaced gi:3333768.
 other GSS: lm30b08.x1
 Contact: Akopyants, NS / Beverley, SM
 WashU Leishmania Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewartson.wustl.edu
 Library construction: Natalia S. Akopyants, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 if using this information please cite:
 N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
 Friedlin strain VI genome by shotgun sequencing' and the Washington
 University Genome Sequencing Center For information on obtaining

QY	8	gtcagctctccatctccctccctccagctgtctgtctgcagacagcttcggggaacta	67
Db	172	ggcactctctctcctcagacctctctcctcaattctccctcttccctcctcagctgtgggctctgg	113
QY	68	ttccgcag	75
Db	112	tactgctg	105
RESULT	7		
AV393461/c			
LOCUS			
DEFINITION	AV393461 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii	EST	21-JAN-2000
ACCESSION	AV393461		
VERSION	AV393461.1	GI:6547677	
KEYWORDS	EST.		
SOURCE	Chlamydomonas reinhardtii.		
ORGANISM	Chlamydomonas reinhardtii.		
REFERENCE	Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;		
AUTHORS	Chlamydomonadaceae; Chlamydomonas.		
TITLE	1 (bases 1 to 473)		
JOURNAL	Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S.		
COMMENT	A large Scale Structural Analysis of cDNAs in a Unicellular Green		
	Alga, Chlamydomonas reinhardtii. I. Generation of 3433		
	Non-redundant Expressed Sequence Tags		
	DNAs. Res. 6, 369-373 (1999)		
	On Jul 9, 1999 this sequence version replaced gi:5434219.		
	Contact: Yasukazu Nakamura		
	The First Laboratory for Plant Gene Research		
	Kazusa DNA Research Institute		
	Yana 1532-3, Kiserazu, Chiba 292-0812, Japan		
	Email: ynakamu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/		
FEATURES	Location/Qualifiers		
source	1..473		
	/organism="Chlamydomonas reinhardtii"		
	/strain="C9"		
	/db_xref="taxon:3055"		
	/clone="C107e07.L"		
	/clone_11b="Chlamydomonas reinhardtii C9"		
	/dev_stage="photoautotrophic growth"		
	/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:		
	xhoI."		
BASE COUNT	83 a 151 c 151 g 88 t		
ORIGIN			
Query Match	32.2%; Score 28; DB 74; Length 473;		
Best Local Similarity	66.7%; Pred. No. 1.6e+02;		
Matches	40; Conservative 0; Mismatches 20; Indels 0; Gaps 0.		
QY	2	tggatgtcagctccatccatccctccctctctcagctgtctgtctgcagacagcttcggg	61
Db	264	tggatgtcagctccatccatccctccctctctcagctgtctgtctgcagacagcttcggg	205
RESULT	8		
AM230735/c			
LOCUS			
DEFINITION	AM230735 518 bp mRNA EST 10-DEC-1999		
ACCESSION	AM230735		
VERSION	AM230735.1	GI:6560031	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 518)		
	NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
	National Cancer Institute, Cancer Genome Anatomy Project (CCGAP).		
	Tumor Gene Index		

JOURNAL

COMMENT

Unpublished (1997)

On Jul 9, 1999 this sequence version replaced gi:5434208.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LNLN at: www-bio.1nl.gov/bbrp/image/image.html

MG1:102804

Seq primer: -40RP from Glbco

High quality sequence stop: 442.

Location/Qualifiers

1. 518

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:2647592"

/clone_1id="NCI CGAP_Mam1"

/tissue_type="tumor, biopsy sample"

/dev_stage="3 months, virgin"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

169 a 116 c 163 g 68 t 2 others

BASE COUNT

ORIGIN

	Query Match	32.2%	Score 28;	DB 74;	Length 518;				
	Best Local Similarity	66.7%	Pred. No. 1.7e+02;						
Matches	40;	Conservative	0;	Mismatches	20;	Indels	0;	Gaps	0;

OY	Db	Accession	Version	KeyWords	Source	Organism	Reference	Authors
9	AV153845/c	AV153845	307 bp	mRNA	EST	08-JUL-1999		
LOCUS	DEFINITION	AV153845 Mus musculus hippocampus C57BL/6J adult Mus musculus CDNA clone 29000558C14, mRNA sequence.						
ACCESSION	VERSION	AV153845	AV153845.1	GI:5359051				
KEYWORDS	EST.							
SOURCE	house mouse.							
ORGANISM	Mus musculus							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
REFERENCE	1 (bases 1 to 307)							
AUTHORS	Carninci,P., Shibata,K., Ozawa,Y., Kono,H., Itoh,M., Alizawa,K., Akhira,S., Akiyama,J., Fukuda,S., Fukuishi,I.Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itch,M., Izawa,M., Kawai,J., Kiluchi,N., Kojima,Y., Matsuyama,T., Nitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y., Tomihata,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.							
TITLE	Riken Mouse ESTs							
JOURNAL	Unpublished (1999)							
COMMENT	On May 18, 1998 this sequence version replaced gi:3137133. Contact: Chie Owa Genome Science Laboratory RIKEN							

3-1-1 Koyadaï, Tsukuba, Ibaraki 305-0074, Japan
Tel.: 81-298-36-9145
Fax: 81-298-36-9098

VERSION	AA282730.1	GI:1925656
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
	Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE	1 (bases 1 to 402)	
AUTHORS	NCI-CCAP http://www.nccl.nlm.nih.gov/ncicgap .	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	On May 8, 1995 this sequence version replaced gi:80900. Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 960 Std Error: 0.00 Seq primer: -28m3 rev2 ET from Amersham High quality sequence stop: 395. Location/Qualifiers	
FEATURES	Source	
	1..402	
	/organism="Homo sapiens"	
	/db_xref="GDB:5854427"	
	/db_xref="taxon:9606"	
	/clone_image="IMAGE:704703"	
	/clone_id="NCI_CGAP_GCB1"	
	/tissue_type="germinal center B cell"	
	/lab_host="DH10B"	
	/note="Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staud (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGGGAGGCGGCCCTCATTTTTTTTTTTTTT-3'] Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."	
BASE COUNT	102 a 82 c 108 g 110 t	
ORIGIN		
Query Match	31.7%; Score 27.6; DB 31; Length 402;	
Best Local Similarity	60.8%; Pred. No.2e+02; Indels 0; Gaps 0;	
Matches	45; Conservative 0; Mismatches 29;	
OY	2 ttgattgtcagctccatcctcctcttcagtctgtttctgcagacttcggcg 61	
Db	281 TCGACCATTCCCACATTCCTTGTGCACATCAGCATTAACACATCCCACTTCTGC 222	
OY	62 aactgatctcgcgacg 75	
Db	221 ATGTGATCCCTCAG 208	
RESULT 13		
LOCUS	A1869632 419 bp mRNA EST 30-AUG-1999	
DEFINITION	w199d07.x1 NCI_CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2433037 3'.	
ACCESSION	A1869632	
VERSION	A1869632.1 GI:5543600	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
	Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE	1 (bases 1 to 419)	
AUTHORS	NCI/NINDS-CGAP http://www.nccl.nlm.nih.gov/ncicgap .	

JOURNAL	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
COMMENT	Unpublished (1998) On Jun 22, 1998 this sequence version replaced g1:3247580. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bernaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINM at: www-bio.llnl.gov/bdrrp/image/image.html
FEATURES	Seq primer: -40UP from GIBCO High quality sequence stop: 412.
SOURCE	Location/Qualifiers 1..419 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2433037" /clone_id="NCI_CGAP_Brn25" /tissue_type="anaplastic oligodendroglioma" /lab_host="DH10B" /note="Organ: brain; Vector: pTZ19-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGAGCGCCGCATAGGTGTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTZ19 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bernaldo."
BASE COUNT	96 a 131 c 104 g 88 t
ORIGIN	
Query Match	31.7%; Score 27.6; DB 61; Length 419;
Best Local Similarity	60.8%; Pred. No.2e+02; 29; Indels 0; Gaps 0;
Matches	45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
Dn	14 tctcatcctcccttccttcagctgctgtcttcgcagacttcgggaactgatccgc 73 180 TCTCAGGCTTAGAGCTTCTCCAGAGCCCCACACACAGGCCAAGCTTGGGAACTGAGC 239
QY	74 agccttccaatgaa 87 Db 240 AGGCCTCGAGCAA 253
RESULT 14	
A1992021	
LOCUS	w644b02.x1 NCI-CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2500011 3', mRNA EST 08-SEP-1999
DEFINITION	mRNA sequence.
ACCESSION	A1992021
VERSION	A1992021.1 GI:5838926
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 484)
TITLE	NCI/RINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTCAP), Tumor Gene Index Unpublished (1998) On Dec 20, 1995 this sequence version replaced g1:1133839.
JOURNAL	
COMMENT	

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from G1bco
High quality sequence stop: 471.

FEATURES
source
Location/Qualifiers
1..484

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2500011"
/clone_1lb="NCI-CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCACTCTGAGTGGAGCGCCGACATGATGTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 116 a 141 c 124 g 103 t
ORIGIN

Query Match 31.7%; Score 27.6; DB 63; Length 484;
Best Local Similarity 60.8%; Pred. No. 2.1e+02;

Matches 45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 14 tctccatctctcctcctcctcagctcgtctgtctgcacagctcgggaactgattccgc 73
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 174 TCTCCAGCCTCAGCTTCCCGAGCCCGACACCGCCAGCCAGCTCTGGAGACTCGAGC 233

Qy 74 agccttccaatgaa 87
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 234 AGGCTCTGGAGCA 247

RESULT 15

FR0019242

LOCUS FR0019242 549 bp DNA GSS 09-DEC-1997

DEFINITION F. rubripes GSS sequence, clone 027G17Ag10, genomic survey sequence.

ACCESSION AL012136

VERSION AL012136.1 GI:2677569

KEYWORDS GSS: genome survey sequence.

SOURCE Fugu rubripes.

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;

Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;

Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.

1 (bases 1 to 549)

Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umanila,Y.,

Williams,G. and Brenner,S.

Direct Submission

Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource

Centre Hinxton, Cambridge, CB10 1SB. Email: blonh@hngmp.mrc.ac.uk

Vector: pBluescript II KS

V_type: phagemid

PRIMER: KS

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic

sequence.

FEATURES
source
Location/Qualifiers
1..549

/organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone_1lb="cosmid 027G17"
/clone="027G17Ag10"

BASE COUNT 169 a 131 c 98 g 140 t 11 others
ORIGIN

Query Match 31.7%; Score 27.6; DB 82; Length 549;
Best Local Similarity 67.2%; Pred. No. 2.2e+02;

Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 9 tcaagctccatctcctcctcctcctcagctcgtctgtctgcacagctcgggaactg 66
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 82 TCAGCTGCTCTTCCTCCACTTCAGCAGTGTGGTTTTCCTGCTTACGGGTCCTG 139

Search completed: May 15, 2000, 11:20:15
Job time: 19138 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2000, 15:18:09 ; Search time 1681.72 Seconds
(without alignments)
-160.230 Million cell updates/sec

Title: US-09-104-340-6

Perfect score: 87
Sequence: 1 atgagatgtcagctctccat.....ttccgcagcttccaatga 87

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5414606 segs, -1548632823 residues

Total number of hits satisfying chosen parameters: 10829192

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 4% summaries

Database :

Pending_Patents_NA.*
1: /cgn2_6/ptodata/2/pna/US0810A.COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US0810B.COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US0810C.COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US0810D.COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US0810E.COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US0810F.COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US0810G.COMB.seq.*
8: /cgn2_6/ptodata/2/pna/US0810H.COMB.seq.*
9: /cgn2_6/ptodata/2/pna/US0810I.COMB.seq.*
10: /cgn2_6/ptodata/2/pna/US0810J.COMB.seq.*
11: /cgn2_6/ptodata/2/pna/US0810K.COMB.seq.*
12: /cgn2_6/ptodata/2/pna/US0810L.COMB.seq.*
13: /cgn2_6/ptodata/2/pna/US0810M.COMB.seq.*
14: /cgn2_6/ptodata/2/pna/US0810N.COMB.seq.*
15: /cgn2_6/ptodata/2/pna/US0810O.COMB.seq.*
16: /cgn2_6/ptodata/2/pna/US0810P.COMB.seq.*
17: /cgn2_6/ptodata/2/pna/US0810Q.COMB.seq.*
18: /cgn2_6/ptodata/2/pna/US0810R.COMB.seq.*
19: /cgn2_6/ptodata/2/pna/US0810S.COMB.seq.*
20: /cgn2_6/ptodata/2/pna/US0810T.COMB.seq.*
21: /cgn2_6/ptodata/2/pna/US0810U.COMB.seq.*
22: /cgn2_6/ptodata/2/pna/US0810V.COMB.seq.*
23: /cgn2_6/ptodata/2/pna/US0810W.COMB.seq.*
24: /cgn2_6/ptodata/2/pna/US0810X.COMB.seq.*
25: /cgn2_6/ptodata/2/pna/US0810Y.COMB.seq.*
26: /cgn2_6/ptodata/2/pna/US0810Z.COMB.seq.*
27: /cgn2_6/ptodata/2/pna/US0811A.COMB.seq.*
28: /cgn2_6/ptodata/2/pna/US0811B.COMB.seq.*
29: /cgn2_6/ptodata/2/pna/US0811C.COMB.seq.*
30: /cgn2_6/ptodata/2/pna/US0811D.COMB.seq.*
31: /cgn2_6/ptodata/2/pna/US0811E.COMB.seq.*
32: /cgn2_6/ptodata/2/pna/US0811F.COMB.seq.*
33: /cgn2_6/ptodata/2/pna/US0811G.COMB.seq.*
34: /cgn2_6/ptodata/2/pna/US0811H.COMB.seq.*
35: /cgn2_6/ptodata/2/pna/US0811I.COMB.seq.*
36: /cgn2_6/ptodata/2/pna/US0811J.COMB.seq.*
37: /cgn2_6/ptodata/2/pna/US0811K.COMB.seq.*
38: /cgn2_6/ptodata/2/pna/US0811L.COMB.seq.*
39: /cgn2_6/ptodata/2/pna/US0811M.COMB.seq.*
40: /cgn2_6/ptodata/2/pna/US0811N.COMB.seq.*
41: /cgn2_6/ptodata/2/pna/US0811O.COMB.seq.*
42: /cgn2_6/ptodata/2/pna/US0811P.COMB.seq.*
43: /cgn2_6/ptodata/2/pna/US0811Q.COMB.seq.*
44: /cgn2_6/ptodata/2/pna/US0811R.COMB.seq.*

45: /cgn2_6/ptodata/2/pna/US092C.COMB.seq.*
46: /cgn2_6/ptodata/2/pna/US092D.COMB.seq.*
47: /cgn2_6/ptodata/2/pna/US092E.COMB.seq.*
48: /cgn2_6/ptodata/2/pna/US092F.COMB.seq.*
49: /cgn2_6/ptodata/2/pna/US092G.COMB.seq.*
50: /cgn2_6/ptodata/2/pna/US092H.COMB.seq.*
51: /cgn2_6/ptodata/2/pna/US092I.COMB.seq.*
52: /cgn2_6/ptodata/2/pna/US092J.COMB.seq.*
53: /cgn2_6/ptodata/2/pna/US092K.COMB.seq.*
54: /cgn2_6/ptodata/2/pna/US092L.COMB.seq.*
55: /cgn2_6/ptodata/2/pna/US092M.COMB.seq.*
56: /cgn2_6/ptodata/2/pna/US092N.COMB.seq.*
57: /cgn2_6/ptodata/2/pna/US092O.COMB.seq.*
58: /cgn2_6/ptodata/2/pna/US092P.COMB.seq.*
59: /cgn2_6/ptodata/2/pna/US092Q.COMB.seq.*
60: /cgn2_6/ptodata/2/pna/US092R.COMB.seq.*
61: /cgn2_6/ptodata/2/pna/US092S.COMB.seq.*
62: /cgn2_6/ptodata/2/pna/US092T.COMB.seq.*
63: /cgn2_6/ptodata/2/pna/US092U.COMB.seq.*
64: /cgn2_6/ptodata/2/pna/US092V.COMB.seq.*
65: /cgn2_6/ptodata/2/pna/US092W.COMB.seq.*
66: /cgn2_6/ptodata/2/pna/US092X.COMB.seq.*
67: /cgn2_6/ptodata/2/pna/US092Y.COMB.seq.*
68: /cgn2_6/ptodata/2/pna/US092Z.COMB.seq.*
69: /cgn2_6/ptodata/2/pna/US093A.COMB.seq.*
70: /cgn2_6/ptodata/2/pna/US093B.COMB.seq.*
71: /cgn2_6/ptodata/2/pna/US093C.COMB.seq.*
72: /cgn2_6/ptodata/2/pna/US093D.COMB.seq.*
73: /cgn2_6/ptodata/2/pna/US093E.COMB.seq.*
74: /cgn2_6/ptodata/2/pna/US093F.COMB.seq.*
75: /cgn2_6/ptodata/2/pna/US093G.COMB.seq.*
76: /cgn2_6/ptodata/2/pna/US093H.COMB.seq.*
77: /cgn2_6/ptodata/2/pna/US093I.COMB.seq.*
78: /cgn2_6/ptodata/2/pna/US093J.COMB.seq.*
79: /cgn2_6/ptodata/2/pna/US093K.COMB.seq.*
80: /cgn2_6/ptodata/2/pna/US093L.COMB.seq.*
81: /cgn2_6/ptodata/2/pna/US093M.COMB.seq.*
82: /cgn2_6/ptodata/2/pna/US093N.COMB.seq.*
83: /cgn2_6/ptodata/2/pna/US093O.COMB.seq.*
84: /cgn2_6/ptodata/2/pna/US093P.COMB.seq.*
85: /cgn2_6/ptodata/2/pna/US093Q.COMB.seq.*
86: /cgn2_6/ptodata/2/pna/US093R.COMB.seq.*
87: /cgn2_6/ptodata/2/pna/US093S.COMB.seq.*
88: /cgn2_6/ptodata/2/pna/US093T.COMB.seq.*
89: /cgn2_6/ptodata/2/pna/US093U.COMB.seq.*
90: /cgn2_6/ptodata/2/pna/US093V.COMB.seq.*
91: /cgn2_6/ptodata/2/pna/US093W.COMB.seq.*
92: /cgn2_6/ptodata/2/pna/US093X.COMB.seq.*
93: /cgn2_6/ptodata/2/pna/US093Y.COMB.seq.*
94: /cgn2_6/ptodata/2/pna/US093Z.COMB.seq.*
95: /cgn2_6/ptodata/2/pna/US094A.COMB.seq.*
96: /cgn2_6/ptodata/2/pna/US094B.COMB.seq.*
97: /cgn2_6/ptodata/2/pna/US094C.COMB.seq.*
98: /cgn2_6/ptodata/2/pna/US094D.COMB.seq.*
99: /cgn2_6/ptodata/2/pna/US094E.COMB.seq.*
100: /cgn2_6/ptodata/2/pna/US094F.COMB.seq.*
101: /cgn2_6/ptodata/2/pna/US094G.COMB.seq.*
102: /cgn2_6/ptodata/2/pna/US094H.COMB.seq.*
103: /cgn2_6/ptodata/2/pna/US094I.COMB.seq.*
104: /cgn2_6/ptodata/2/pna/US094J.COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	87	40	US-09-104-340-6
2	87	100.0	813	40	US-09-104-340-5
3	31	35.6	453	92	US-60-172-375-1200


```
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
US-60-183-791-6260
```

```
Query Match          32.4% Score 28.2; DB 95; Length 1454;
Best Local Similarity 64.6% Pred. No. 1.1e+02;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
```

```
QY 6 ttgtacgtccatccctcctctcagctgctgtctcgagctcgaggact 65
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1338 TTCCTCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 1279
```

```
QY 66 gattc 70
   |||
DB 1278 CCTTC 1274
```

```
RESULT 13
US-09-531-113-33845/C
; Sequence 33845, Application US/09531113
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15761)B
; CURRENT APPLICATION NUMBER: US/09/531,113
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 48629
; SEQ ID NO 33845
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700892085H1
US-09-531-113-33845
```

```
Query Match          32.2% Score 28; DB 103; Length 174;
Best Local Similarity 77.3% Pred. No. 89;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 10 cagctctccatccctcctctcagctgctgtctcgagacag 53
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 59 CAGTTTCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC 16
```

```
RESULT 14
US-60-144-084-16459/C
; Sequence 16459, Application US/60144084
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Buehler, Robert E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Coombs, Brian E.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Nelson, Donald E.
; APPLICANT: Shukla, Hridayabhramjam
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(15444)B
; CURRENT APPLICATION NUMBER: US/60/144,084
; CURRENT FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 47776
; SEQ ID NO 16459
; LENGTH: 344
```

```
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3109-014-Q1-K1-A10
US-60-144-084-16459
```

```
Query Match          32.2% Score 28; DB 86; Length 344;
Best Local Similarity 77.3% Pred. No. 99;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 10 cagctctccatccctcctctcagctgctgtctcgagacag 53
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 122 CAGTTTCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 79
```

```
RESULT 15
US-60-144-084-17798/C
; Sequence 17798, Application US/60144084
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Buehler, Robert E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Coombs, Brian E.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Nelson, Donald E.
; APPLICANT: Shukla, Hridayabhramjam
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(15444)B
; CURRENT APPLICATION NUMBER: US/60/144,084
; CURRENT FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 47776
; SEQ ID NO 17798
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3109-053-Q1-K1-D9
US-60-144-084-17798
```

```
Query Match          32.2% Score 28; DB 86; Length 391;
Best Local Similarity 77.3% Pred. No. 1e+02;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 10 cagctctccatccctcctctcagctgctgtctcgagacag 53
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 76 CAGTTTCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC 33
```

Search completed: May 13, 2000, 15:18:39
Job time: 5212 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 12:05:01 ; Search time 102.62 Seconds
(without alignments)
107.646 Million cell updates/sec

Title: US-09-104-340-6

Perfect score: 87
Sequence: 1 atgattgcagctctcatcat.....ttccgcagctctcatatgaa 87

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 226296 seqs, 63486255 residues

Total number of hits satisfying chosen parameters: 452592

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/1na/5C.COMB.seq: *
4: /cgn2_6/ptodata/2/1na/5D.COMB.seq: *
5: /cgn2_6/ptodata/2/1na/6.COMB.seq: *
6: /cgn2_6/ptodata/2/1na/PCUS.COMB.seq: *
7: /cgn2_6/ptodata/2/1na/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	3132	1 US-08-167-919A-9	Sequence 9, Appl1
2	87	100.0	3132	5 US-08-715-106-9	Sequence 9, Appl1
3	27.2	31.3	324	3 US-08-619-542B-34	Sequence 34, Appl1
4	26	29.9	1893	7 5438126-1	Patent No. 5438126
5	25.6	29.4	318	3 US-08-619-542B-36	Sequence 36, Appl1
6	25.6	29.4	323	3 US-08-619-542B-37	Sequence 37, Appl1
7	25.2	29.0	950	3 US-08-901-200A-14	Sequence 14, Appl1
8	25.2	29.0	1003	1 US-07-800-364B-13	Sequence 13, Appl1
9	25.2	29.0	1003	3 US-07-989-847-11	Sequence 11, Appl1
10	25.2	29.0	1723	1 US-07-841-646-28	Sequence 28, Appl1
11	25.2	29.0	1723	1 US-07-901-703-10	Sequence 10, Appl1
12	25.2	29.0	1723	1 US-08-147-023-28	Sequence 28, Appl1
13	25.2	29.0	1723	1 US-08-206-864-3	Sequence 3, Appl1
14	25.2	29.0	1723	1 US-08-278-729A-20	Sequence 20, Appl1
15	25.2	29.0	1723	1 US-08-480-528A-7	Sequence 7, Appl1
16	25.2	29.0	1723	1 US-08-479-666-7	Sequence 7, Appl1
17	25.2	29.0	1723	1 US-08-155-343A-20	Sequence 20, Appl1
18	25.2	29.0	1723	1 US-08-406-612-20	Sequence 20, Appl1
19	25.2	29.0	1723	2 US-08-643-563A-20	Sequence 20, Appl1
20	25.2	29.0	1723	2 US-08-447-570-28	Sequence 28, Appl1
21	25.2	29.0	1723	2 US-08-643-763A-20	Sequence 20, Appl1
22	25.2	29.0	1723	2 US-08-463-623-20	Sequence 20, Appl1
23	25.2	29.0	1723	2 US-08-451-953A-20	Sequence 20, Appl1
24	25.2	29.0	1723	3 US-08-459-346-5	Sequence 5, Appl1
25	25.2	29.0	1723	3 US-08-445-468A-20	Sequence 20, Appl1
26	25.2	29.0	1723	3 US-08-901-200A-7	Sequence 7, Appl1
27	25.2	29.0	1723	3 US-08-449-700-28	Sequence 28, Appl1

28	25.2	29.0	1723	4 US-08-449-699A-28	Sequence 28, Appl1
29	25.2	29.0	1723	4 US-08-461-397A-20	Sequence 20, Appl1
30	25.2	29.0	1723	4 US-08-912-088-20	Sequence 20, Appl1
31	25.2	29.0	1723	5 US-08-278-730A-20	Sequence 20, Appl1
32	25.2	29.0	1723	6 PCT-US92-01968-20	Sequence 20, Appl1
33	25.2	29.0	1723	6 PCT-US93-05446-10	Sequence 10, Appl1
34	25.2	29.0	1723	6 PCT-US93-07189-5	Sequence 5, Appl1
35	25.2	29.0	1723	6 PCT-US93-07190-20	Sequence 20, Appl1
36	25.2	29.0	1723	6 PCT-US93-07231-20	Sequence 20, Appl1
37	25.2	29.0	1723	6 PCT-US93-08742-20	Sequence 20, Appl1
38	25.2	29.0	1723	6 PCT-US93-08808-20	Sequence 20, Appl1
39	25.2	29.0	1723	6 PCT-US93-08885-20	Sequence 20, Appl1
40	25.2	29.0	1723	6 PCT-US93-10520-7	Sequence 7, Appl1
41	25.2	29.0	1941	6 PCT-US91-07635-5	Sequence 5, Appl1
42	25.2	29.0	6418	1 US-08-480-528A-11	Sequence 11, Appl1
43	25.2	29.0	6418	1 US-08-479-666-11	Sequence 11, Appl1
44	25.2	29.0	6418	6 PCT-US93-10520-11	Sequence 11, Appl1
45	25.2	28.7	2467	4 US-08-701-240-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-167-919A-9
; Sequence 9, Application US/08167919A
; Patent No. 5674691
; GENERAL INFORMATION:
; APPLICANT: Boyd, Andrew W.
; APPLICANT: Simpson, Richard J.
; APPLICANT: Wicks, Ian
; APPLICANT: Ward, Larry D.
; APPLICANT: Wilkinson, David
; TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167, 919A
; FILING DATE: 18-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK6841 (AU)
; FILING DATE: 21-JUN-1991
; PRIOR APPLICATION DATA: PK9992 (AU)
; APPLICATION NUMBER: PK9992 (AU)
; FILING DATE: 12-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU92/00294
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3132 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..3048
US-08-167-919A-9

Query Match 100.0%; Score 87; DB 1; Length 3132;
Best Local Similarity 100.0%; Pred. No. 4,6e-21;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgagtttcagctctccatccctcctctcctcagctgctctgcttcgacagcttcggg 60
|||||
DB 100 ATGATGTGACAGCTCTCCATCCTCCCTTCCTTCAGCTGCTGTCTGTCGACAGCTTCGGG 159
|||||
OY 61 gaactgattccgacagcttcgaatgaa 87
|||||
DB 160 GAACGTGATTCGCGACGCTTCGAATGAA 186

RESULT 2

US-08-715-106-9
Sequence 9, Application US/08715106
Patent No. 6020306
GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..3048
US-08-715-106-9

Query Match 100.0%; Score 87; DB 5; Length 3132;
Best Local Similarity 100.0%; Pred. No. 4,6e-21;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgagtttcagctctccatccctcctcctcagctgctctgcttcgacagcttcggg 60
|||||
DB 100 ATGATGTGACAGCTCTCCATCCTCCCTTCCTTCAGCTGCTGTCTGTCGACAGCTTCGGG 159
|||||
OY 61 gaactgattccgacagcttcgaatgaa 87
|||||
DB 160 GAACGTGATTCGCGACGCTTCGAATGAA 186

RESULT 3

US-08-619-542B-34/C
Sequence 34, Application US/08619542B
Patent No. 5830662
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University in the City
APPLICANT: of New York
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
TITLE OF INVENTION: CDNA LIBRARIES
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,542B
FILING DATE: June 21, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 324 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 12..311
US-08-619-542B-34

Query Match 31.3%; Score 27.2; DB 3; Length 324;
Best Local Similarity 67.9%; Pred. No. 0.6;
Matches 38; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```

QY      62 aactgattccgcagccttc 81
      ||||| | | | | |

```

Db 215 AACTCACCCTCTCATGCC 196

RESULT 7

US-08-901-200A-14
; Sequence 14, Application US/08901200A
; Patent No. 5834071
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H. L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/901,200A
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-076DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 950 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "A GAP OCCURS BETWEEN
; OTHER INFORMATION: POSITION 884 IN SEQ ID NO: 11 AND POSITION 1 IN THIS SEQUENCE"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 204..393
; OTHER INFORMATION: /note= "EXON TWO"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 466..930
; OTHER INFORMATION: /note= "EXON THREE"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..950
; OTHER INFORMATION: /note= "HOP-2 genomic sequence"
US-08-901-200A-14

Query Match

Best Local Similarity 29.0%; Score 25.2; DB 3; Length 950;
Best Local Similarity 57.7%; Pred. No. 4.2;
Matches 45; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 6 ttatcagctcatcctcctctcagctctcgttctctgacagctcggggagact 65
Db 313 TTTACAGGTCCTCCAGCCTCTGCTCAACAGACCTCCACGTCGATGTTCCAGGT 372

QY 66 gatcccgagcctcccaa 83
Db 373 GGTCCAGAGAGACTCCA 390

RESULT 8

US-07-800-364B-13
; Sequence 13, Application US/07800364B
; Patent No. 568678
; GENERAL INFORMATION:
; APPLICANT: Hewick, Rodney M.
; APPLICANT: Wang, Jack H.
; APPLICANT: Wozney, John M.
; APPLICANT: Celeste, Anthony J.
; TITLE OF INVENTION: Bone and Cartilage Inductive Proteins
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/800,364B
; FILING DATE: 26-NOV-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5182A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1003 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Human Heart
; IMMEDIATE SOURCE:
; LIBRARY: Human heart cDNA library stratagene catalog
; LIBRARY: #936208
; CLONE: hH38
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 8..850
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 427..843
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 1..997
US-07-800-364B-13

Query Match

Best Local Similarity 29.0%; Score 25.2; DB 1; Length 1003;
Best Local Similarity 57.7%; Pred. No. 4.3;
Matches 45; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Oy 6 ttgtcagctcccaatcccccctcttcagctgctcgtctcgcagagcttcggagact 65
 Db 88 TTACAAGTGGCCAGCAGTCCACCTGCTCACAAGGACCTCCACCTCAGCATGTTCCAGT 147
 Oy 66 gattccgcagacttccca 83
 Db 148 GGTCCAGGAGCAGTCCA 165

RESULT

```

1Sequence 11. Application US/07989847
2Patient No. 5866364
3
4GENERAL INFORMATION:
5APPLICANT:  Israel, David
6APPLICANT:  Appelbaum, Neil M.
7TITLE OF INVENTION:  Recombinant Bone Morphogenetic Protein
8TITLE OF INVENTION:  Heterodimers, Compositions and Methods of Use
9NUMBER OF SEQUENCES:  30
10CORRESPONDENCE ADDRESS:
11ADDRESSEE:  Legal Affairs, Genetics Institute, Inc.
12STREET:  87 Cambridgepark Drive
13CITY:  Cambridge
14STATE:  MA
15COUNTRY:  USA
16ZIP:  02140-2387
17COMPUTER READABLE FORM:
18MEDIUM TYPE:  Tape
19COMPUTER:  IBM PC compatible
20OPERATING SYSTEM:  PC-DOS/MS-DOS
21SOFTWARE:  PatentIn Release #1.0, Version #1.25
22CURRENT APPLICATION DATA:
23APPLICATION NUMBER:  US/07/989,847
24FILING DATE:
25CLASSIFICATION:  436
26ATTORNEY/AGENT INFORMATION:
27NAME:  Kaplins, Ellen J.
28REGISTRATION NUMBER:  32,245
29REFERENCE/DOCKET NUMBER:  GI-5192B
30TELECOMMUNICATION INFORMATION:
31TELEPHONE:  617-876-1170
32TELEFAX:  617-876-5851
33INFORMATION FOR SEQ. ID NO:  11:
34SEQUENCE CHARACTERISTICS:
35LENGTH:  1003 base pairs
36TYPE:  nucleic acid
37STRANDEDNESS:  double
38TOPOLOGY:  circular
39MOLECULE TYPE:  cDNA to mRNA
40HYPOTHETICAL:  NO
41ORIGINAL SOURCE:
42ORGANISM:  Homo sapiens
43TISSUE TYPE:  Human Heart
44IMMEDIATE SOURCE:
45LIBRARY:  Human heart cDNA library stratagene catalog
46CLONE:  hn38
47POSITION IN GENOME:
48UNITS:  bp
49FEATURE:
50NAME/KEY:  CDS
51LOCATION:  8..850
52FEATURE:
53NAME/KEY:  mat_peptide
54LOCATION:  427..843
55FEATURE:
56NAME/KEY:  mRNA
57LOCATION:  1..997
58US-07-989-847-11

```

Query Match	29.08;	Score 25.2;	DB 3;	Length 1003;
Best Local Similarity	57.78;	Pred. NO. 4.3;		

Matches	45;	Conservative	0;	Mismatches	33;	Indels	0;	Gaps	0;
Oy	6	tttgtagcttcacatcccctccctctctagctgcctggttcacagacattcggggaact	65						
Db	88	TTACAAGGTGCCACATCATCAACCTCTCAACAGACCTCCACGTCAGCATGTTCAGGT	147						
Oy	66	gattccgcagaccttcaca	83						
Db	148	GCTCCAGAGCAGTCCAA	165						

RESULT 10

US-07-841,646-26
Sequence 28, Application US/07841646
Patent No. 5266683
GENERAL INFORMATION:
APPLICANT: OPPERMAN, ENGMANN
APPLICANT: OZKANYAK, HENIN
APPLICANT: KUERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 33 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,646
FILING DATE: 19920221
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1723 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: HIPPOCAMPUS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 490..1696
; OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product="hop2-p"
; OTHER INFORMATION: /note="hop2 (cDNA)"
;
US-07-841-646-28

Query Match      29.0%; Score 25.2; DB 1; Length 1723;
Best Local Similarity 57.7%; Pred. No. 5.1;
Matches 45; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 6 ttgtcagctctcatcctctctcttcagctgctctgttctcgacagcttcggggaact 65
DB 933 ttTACAAGGTGCCAGACCTGCTCTCAACAGACCTCCACGATGTTCCAGGT 992
QY 66 gattccgcagccttccaa 83
DB 993 GGTCCAGAGACGTCCA 1010

RESULT 11
US-07-901-703-10
; Sequence 10, Application US/07901703
; Patent No. 5344654
; GENERAL INFORMATION:
; APPLICANT: RUEGER, DAVID C
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZAKAYNAK, ENGIN
; TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
; TITLE OF INVENTION: OSTEOGENIC PROPERTIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,703
; FILING DATE: 19920616
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, ESO, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1723 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: HIPPOCAMPUS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 490..1696
; OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product="hop2-p"
; OTHER INFORMATION: /note="hop2 (cDNA)"
;
US-07-901-703-10

Query Match      29.0%; Score 25.2; DB 1; Length 1723;
Best Local Similarity 57.7%; Pred. No. 5.1;
Matches 45; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 6 ttgtcagctctcatcctctctcttcagctgctctgttctcgacagcttcggggaact 65
DB 933 ttTACAAGGTGCCAGACCTGCTCTCAACAGACCTCCACGATGTTCCAGGT 992
QY 66 gattccgcagccttccaa 83
DB 993 GGTCCAGAGACGTCCA 1010

RESULT 12
US-08-147-023-28
; Sequence 23, Application US/08147023
; Patent No. 5468845
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZAKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H. L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,023
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
```

```

1      FILING DATE: 20-DEC-1991
2      PRIOR APPLICATION DATA:
3      APPLICATION NUMBER: US 827,052
4      FILING DATE: 28-JAN-1992
5      PRIOR APPLICATION DATA:
6      APPLICATION NUMBER: US 660,162
7      FILING DATE: 22-FEB-1991
8      PRIOR APPLICATION DATA:
9      APPLICATION NUMBER: US 621,988
10     FILING DATE: 04-DEC-1990
11     PRIOR APPLICATION DATA:
12     APPLICATION NUMBER: US 621,849
13     FILING DATE: 04-DEC-1990
14     PRIOR APPLICATION DATA:
15     APPLICATION NUMBER: US 616,374
16     FILING DATE: 21-NOV-1990
17     PRIOR APPLICATION DATA:
18     APPLICATION NUMBER: US 600,024
19     FILING DATE: 18-OCT-1990
20     PRIOR APPLICATION DATA:
21     APPLICATION NUMBER: US 599,543
22     FILING DATE: 18-OCT-1990
23     PRIOR APPLICATION DATA:
24     APPLICATION NUMBER: US 579,865
25     FILING DATE: 07-SEP-1990
26     PRIOR APPLICATION DATA:
27     APPLICATION NUMBER: US 569,920
28     FILING DATE: 20-AUG-1990
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: US 483,913
31     FILING DATE: 22-FEB-1990
32     PRIOR APPLICATION DATA:
33     APPLICATION NUMBER: US 422,613
34     FILING DATE: 17-OCT-1989
35     PRIOR APPLICATION DATA:
36     APPLICATION NUMBER: US 315,342
37     FILING DATE: 23-FEB-1989
38     PRIOR APPLICATION DATA:
39     APPLICATION NUMBER: US 232,630
40     FILING DATE: 15-AUG-1988
41     PRIOR APPLICATION DATA:
42     APPLICATION NUMBER: US 179,460
43     FILING DATE: 08-APR-1988
44     ATTORNEY/AGENT INFORMATION:
45     NAME: PITCHER, EDMUND R.
46     REGISTRATION NUMBER: 27,829
47     REFERENCE/DOCKET NUMBER: CRP-001CP6
48     TELECOMMUNICATION INFORMATION:
49     TELEPHONE: 617/248-7000
50     TELEFAX: 617/248-7100
51     INFORMATION FOR SEQ ID NO: 28:
52     SEQUENCE CHARACTERISTICS:
53     LENGTH: 1723 base pairs
54     TYPE: nucleic acid
55     STRANDEDNESS: single
56     TOPOLOGY: linear
57     MOLECULE TYPE: cDNA
58     ORIGINAL SOURCE:
59     ORGANISM: Homo sapiens
60     TISSUE TYPE: HIPPOCAMPUS
61     FEATURE:
62     NAME/KEY: CDS
63     LOCATION: 490..1696
64     OTHER INFORMATION: /function="OSMEGENCENTIC PROTEIN"
65     OTHER INFORMATION: /product="hop2-p2"
66     OTHER INFORMATION: /note="hop2 (cDNA)"
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870

```

Qy	6	tttgcagctccatctctctctctcctcctcagctctctgtctctgacagctcgggagact	65
Db	933	TTTAAAGTGGCCAGCATCCACCTGCTCTCAAGAGACCCCTCAGCTCAGATGTTCCAGT	932
Qy	66	gattccgcagcctctccaa	83
Db	993	GGTCCAGAGACGATCCAA	1010

```

13 RESULT
14 US-08-206-864-3
15 : Sequence 3, Application US/08206864
16 Patent No. 5610021
17 : GENERAL INFORMATION:
18 APPLICANT: RUEGER, DAVID C
19 APPLICANT: JONES, WILLIAM K
20 APPLICANT: TUCKER, RONALD F
21 APPLICANT: OPPERMAN, HERMAN
22 APPLICANT: OKAYMAK, ENGIN
23 APPLICANT: KUBERASAMPAH, THANGAVEL
24 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
25 NUMBER OF SEQUENCES: 6
26 RECOMBINANT OSTEOGENIC PROTEIN PRODUCTION
27 : CORRESPONDENCE ADDRESSES:
28 ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES,
29 ADDRESSEE: INC.
30 STREET: 45 SOUTH STREET
31 CITY: HOPKINTON
32 STATE: MA
33 COUNTRY: USA
34 ZIP: 01748
35 : COMPUTER READABLE FORM:
36 MEDIUM TYPE: Floppy disk
37 COMPUTER: IBM PC compatible
38 OPERATING SYSTEM: PC-DOS/MS-DOS
39 SOFTWARE: Patentln Release #1.0, Version #1.25
40 CURRENT APPLICATION DATA:
41 APPLICATION NUMBER: US/08/206,864
42 FILING DATE:
43 CLASSIFICATION: 530
44 PRIOR APPLICATION DATA:
45 APPLICATION NUMBER: US 08/027,070
46 FILING DATE: 04-MAR-1993
47 PRIOR APPLICATION DATA:
48 APPLICATION NUMBER: US 07/841,646
49 FILING DATE: 21-FEB-1992
50 ATTORNEY/AGENT INFORMATION:
51 NAME: PITCHER, EDMUND R
52 REGISTRATION NUMBER: 27,829
53 REFERENCE/DOCKET NUMBER: CAP-096
54 TELECOMMUNICATION INFORMATION:
55 TELEPHONE: 617/7000
56 TELEFAX: 617/248-7100
57 INFORMATION FOR SEQ ID NO: 3:
58 : SEQUENCE CHARACTERISTICS:
59 LENGTH: 1723 base pairs
60 TYPE: nucleic acid
61 STRANDEDNESS: single
62 TOPOLOGY: linear
63 MOLECULE TYPE: cDNA
64 ORIGINAL SOURCE:
65 ORGANISM: Homo sapiens
66 TISSUE TYPE: HIPPOCAMPUS
67 FEATURE:
68 NAME/KEY: CDS
69 LOCATION: 490..1696
70 OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
71 OTHER INFORMATION: /product= "hop2-p"
72 OTHER INFORMATION: /note= "hop2 (cDNA)"
73
74 US-08-206-864-3

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 12:08:19 ; Search time 111.14 Seconds
(without alignments)
195.849 Million cell updates/sec

Title: US-09-104-340-6

Perfect score: 87
Sequence: 1 atgagttgtcagcttccat.....ttccgcagcctccaatgaa 87

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	3132	1	HEK coding sequenc
2	27.2	31.3	1088	1	Ferritin CDNA. A p
3	27.2	31.3	5562	1	Human calcin chan
4	27	31.0	110000	1	Continuation (10 o
5	26	29.9	1866	1	Human secreted pro
6	26	29.9	1893	1	Human thyroid horm
7	25.6	29.4	360	1	Human secreted pro
8	25.4	29.2	1269	1	Human secreted pro
9	25.4	29.2	1562	1	Human derived long
10	25.2	29.0	1002	1	Human BMP-8 gene.
11	25.2	29.0	1723	1	Human osteogenic p
12	25.2	29.0	1723	1	Human osteogenic p
13	25.2	29.0	1723	1	Human osteogenic p
14	25.2	29.0	1723	1	Human OP-2. Morpho
15	25.2	29.0	1723	1	Morphogen hOP2 cod
16	25.2	29.0	1723	1	Sequence encoding
17	25.2	29.0	1723	1	hOP2 CDNA. Morphog
18	25.2	29.0	1723	1	hOP2 CDNA. Use mor
19	25.2	29.0	1723	1	Human osteogenic p
20	25.2	29.0	1723	1	Human OP-2. Morpho
21	25.2	29.0	1723	1	Human OP-2. Mainta
22	25.2	29.0	1723	1	Human OP-2. Use of
23	25.2	29.0	1723	1	Osteogenic protein
24	25.2	29.0	1723	1	hOP2-PP prepro for
25	25.2	29.0	1723	1	hOP-2 CDNA. Antibo
26	25.2	29.0	1723	1	Human osteogenic p
27	25.2	29.0	1723	1	Human hipoCampal
28	25.2	29.0	1723	1	CDNA encoding huma
29	25.2	29.0	1723	1	Human OP-2 CDNA. T
30	25.2	29.0	1723	1	Human osteogenic p
31	25.2	29.0	1723	1	Human osteogenic p
32	25.2	29.0	1723	1	Human osteogenic p
33	25.2	29.0	1723	1	CDNA encoding prep
34	25.2	29.0	2358	1	Mouse Fas-binding

35	25.2	29.0	6418	1	O65395
36	25	28.7	2467	1	T61862
37	25	28.7	6327	1	T32301
38	24.6	28.3	2883	1	T58898
39	24.4	28.0	244	1	X39537
40	24.4	28.0	4931	1	V29584
41	24	27.6	2658	1	T60339
42	24	27.6	3225	1	T15234
43	24	27.6	3225	1	T94637
44	24	27.6	6373	1	V74538
45	23.8	27.4	875	1	X39853

Osteogenic protein
Human glial tumor
Dermatocystitis sp
C-Delta-1 gene (al
Human secreted pro
Homo sapiens sulph
Pumpkin ent-Kauren
Tumor necrosis fac
TNF-R1-DD ligand p
Staphylococcus aur
Gastric cancer ass

ALIGNMENTS

RESULT 1	
Q34513	Q34513 standard; DNA: 3132 BP.
AC	Q34513:
DT	24-MAY-1993 (first entry)
DE	HEK coding sequence.
KW	Primer: expression vector; extracellular domain; human; HEK;
KW	eph/erbB-like; kinase; pre-B; cell; T; tumour; lymphoid; LK63;
KW	Lila-1; JM; epithelial; Hela; receptor-type; thymidine kinase;
KW	TK; ligand; B-cellular response; growth; differentiation; ss.
OS	Synthetic.
FH	Key
FT	Location/Qualifiers
FT	5'utr
FT	1..99
FT	/*tag= a
FT	100..3051
FT	/*tag= b
FT	3052..3132
FT	/*tag= c
FT	100..159
FT	/*tag= d
FT	1723..1795
FT	/*tag= e
FT	/*note= "Potential transmembrane region"
FT	160..216
FT	/*tag= f
FT	/*note= "Purified HEK protein #1"
FT	2617..2679
FT	/*tag= g
FT	/*note= "Purified HEK protein #2"
FT	W09300425-A.
PD	07-JAN-1993.
PR	19-JUN-1992; AU0294.
PR	21-JUN-1991; AU-006841.
PR	12-DEC-1991; AU-009992.
PA	(HALL-) HALL INST MEDICAL RES WALTER & ELITA.
PI	Boyd AD, Simpson R, Ward LD, Wicks I, Wilkinson D;
DR	WPI; 93-036373/04.
DR	P-PSDB; R31466.
PT	Receptor-type tyrosine kinase reactive with monoclonal antibody
PT	III-A4 - is Eph-ERK-like kinase, useful for phosphorylating
PT	proteins in modulating pre-B, B and T cell function, in cancer
PT	therapy etc.
PS	Claim 6; Fig 1; 58pp; English.
CC	This sequence encodes human eph/erbB-like kinase (HEK). HEK is
CC	expressed in both pre-B cells and T cell lines and in a number of
CC	tumours of human origin, eg. lymphoid tumours LK63, Lila-1 and JM,
CC	and the epithelial tumour Hela. This receptor-type thymidine kinase
CC	(TK) and/or its ligands are useful as agents in modulation of the
CC	production and/or function of pre-B, B and T cells. The TK and its
CC	analogues have activity in transducing signals or in stimulating
CC	cellular responses such as growth and/or differentiation.
SO	Sequence 3132 BP; 888 A; 711 C; 759 G; 774 T;

Query Match 100.0%; Score 87; DB 1; Length 3132;
Best Local Similarity 100.0%; Pred. No. 3.9e-19;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 atgagatgacagctccacccctcctcctcagctgctgttcttcgacagcttcgag 60
DB 100 ATGAGATGACAGCTCCACCCCTCCTCCTCAGCTGCTGTCTCGACAGCTTCGGG 159
OY 61 gaactgattccgacagcttcacatga 87
DB 160 GAAGTGTATTCGAGCCTTCATGA 186

RESULT 2
T76750
ID T76750 standard; cDNA to mRNA; 1088 BP.
AC T76750;
DT 08-OCT-1997 (first entry)
DE Ferritin cDNA.
KW Plant; ferritin; acidic soil; diagnosis; agriculture; ds.
OS Acacia mangium.
FH Key Location/Qualifiers
FT cds 71..877
FT /tag= a
FT /product= Ferritin
FT transit_peptide 71..247
FT /tag= b
FT mat_peptide 248..874
FT /tag= c
FT poly_a_signal 1055..1059
FT /tag= d
FT misc_feature 1079..1088
FT /tag= e
FT /note= "PolyA_site"
PN J09140384-A.
PD 03-JUN-1997.
PF 20-NOV-1995; 323527.
PR 20-NOV-1995; JP-323527.
PA (NERTT-) NERTTAT RIN SAISEI GIJUNSU KENKYU KOMITAI.
DR WPI: 97-344897/32.
DR P-PSDB: W21736.
PT A plant ferritin gene induced in acidic soil - derived from Acacia
PS Plants, improves resistance to acidic growth conditions
PS Claim 1, Page 6-7: 99p; Japanese.
CC This sequence represents a plant ferritin gene. The plant ferritin
CC gene, whose production is induced in acidic soil, is involved in the
CC occurrence of disorders in a plant caused by acidic soil as well as
CC in improvements in the resistance of a plant to acidic conditions.
CC This gene can be used for breeding of plants highly resistant to acidic
CC soil. The cDNA or its fragment can also be used for diagnosis of a
CC plant planted in acidic soil by determining the expression of ferritin
CC in it. Ferritin can be expressed excessively by introducing the cDNA
CC of the invention into a plant in the sense direction to reinforce the
CC resistance of the plant to acidic soil. Therefore acidic soil which could
CC not be utilised for agricultural purposes can be utilised by the
CC resulting plants.
SQ Sequence 1088 BP; 273 A; 221 C; 254 G; 340 T;

Query Match 31.3%; Score 27.2; DB 1; Length 1088;
Best Local Similarity 64.1%; Pred. No. 3.9;
Matches 41; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY 16 tccatctctcctcctcagctgctgttcgacagcttcggggaacttcgag 75
DB 1 TTCAATCTCTCTCTTGAATTTCAATCTCTCTCGAGTTCGCTTCGAG 60
OY 76 cctt 79
DB 61 CTTT 64

RESULT 3
V57542
ID V57542 standard; cDNA; 5562 BP.
AC V57542;
```

```
DT 20-NOV-1998 (first entry)
DE Human calcium channel subunit alpha-1 partial sequence encoding cDNA.
KW Calcium channel subunit alpha-1; recombinant; alpha 2 delta;
KW beta calcium channel; agonist; antagonist; alpha-11 calcium channel;
KW histological assay; tissue distribution; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..5562
FT /tag= a
FT /product= "Human calcium channel subunit alpha-1
FT partial sequence"
PN M09838301-A1.
PD 03-SEP-1998.
PF 27-FEB-1998; CA0173.
PR 25-FEB-1998; US-030482.
PR 28-FEB-1997; US-039204.
PA (NEUR-) NEUROMED TECHNOLOGIES INC.
PT Ballile DL, Snutch TP;
DR WPI: 98-481203/41.
DR P-PSDB: W79161.
PT Newly identified calcium channel subunits alpha 11 and alpha 1H -
PT for development of cell lines which express the novel calcium
PT channels, useful for screening channel (antagonists
PS Claim 2, pages 26-33, 45pp; English.
CC This represents a cDNA from BAC Bx206c7 encoding a partial sequence of a
CC human calcium channel subunit alpha-1. The invention provides isolated
CC DNA fragments coding for novel calcium channel subunits alpha-11 and
CC alpha-1H. An eukaryotic cell transiently or stably transformed with an
CC expression vector containing the calcium subunits encoding DNA fragments
CC can be used for expressing the calcium channel. The cells are optionally
CC further transformed to express alpha 2 delta or beta calcium channel or
CC both the proteins. The transformed cells are useful for identifying
CC compounds capable of acting as agonists or antagonists for the alpha-11
CC calcium channel. The nucleic acid sequences can be used in histological
CC assay to determine the tissue distribution of the novel calcium channel
CC subunits.
SQ Sequence 5562 BP; 1060 A; 1757 C; 1654 G; 1091 T;
```

```
Query Match 31.3%; Score 27.2; DB 1; Length 5562;
Best Local Similarity 72.9%; Pred. No. 5.6;
Matches 35; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 14 tctcacctcctcctcctcagctgctgttcgacagcttcggg 61
DB 5258 TCTCCCTTCGCTCCAGTCAGCTCTCTTGTGTCAACATGTTTGG 5305
```

```
RESULT 4
V21209.09/C
Continuation (10 of 17) of V21209 from base 900001 (Methanococcus jannaschii circular
WP Sequence split into 17 fragments LOCUS V21209 Accession V21209
WP Fragment Name Begin End
WP V21209_00 1 110000
WP V21209_01 100001 210000
WP V21209_02 200001 310000
WP V21209_03 300001 410000
WP V21209_04 400001 510000
WP V21209_05 500001 610000
WP V21209_06 600001 710000
WP V21209_07 700001 810000
WP V21209_08 800001 910000
WP V21209_09 900001 1010000
WP V21209_10 1000001 1110000
WP V21209_11 1100001 1210000
WP V21209_12 1200001 1310000
WP V21209_13 1300001 1410000
WP V21209_14 1400001 1510000
WP V21209_15 1500001 1610000
WP V21209_16 1600001 1664976
```

Query Match 31.0%; Score 27; DB 1; Length 110000;

	Best Local Similarity	60.0%	Pred. No. 12:	
Matches	45:	Conservative	0:	Mismatches 30: Indels 0: Gaps 0:
Oy	5	attgtcagctccacccctccctcctcagctgctcgttctgcagacgctcggaac	64	
Db	33054	ATTGATTCCTCTACATTCACAAACCTCTCTCTTTTCTTGTAGCTAAACTTCACATAAC	32995	
Oy	65	tgattccgacgacct	79	
Db	32994	TCATTCAATAGCTT	32980	
RESULT	5			
ID	V84466/C			
AC	V84466 standard; DNA; 1866 BP.			
DT	01-MAR-1999 (first entry)			
DE	Human secreted protein gene 56 clone HE20F09.			
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;			
KW	developmental abnormality; asthma; lymphocytic disease; brain; hepatic; lymphoma;			
KW	immune system; ischaemic shock; Alzheimer's disease; osteoarthritis; AIDS;			
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;			
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;			
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.			
OS	Homo sapiens.			
PN	WO9854963-A2.			
PD	10-DEC-1998.			
PF	04-JUN-1998: U11422.			
PR	18-DEC-1997: US-070923.			
PR	06-JUN-1997: US-048877.			
PR	06-JUN-1997: US-048881.			
PR	06-JUN-1997: US-048884.			
PR	06-JUN-1997: US-048893.			
PR	06-JUN-1997: US-048896.			
PR	06-JUN-1997: US-048899.			
PR	06-JUN-1997: US-048915.			
PR	06-JUN-1997: US-048949.			
PR	06-JUN-1997: US-048964.			
PR	06-JUN-1997: US-048972.			
PR	06-JUN-1997: US-049020.			
PR	06-JUN-1997: US-049375.			
PR	05-SEP-1997: US-057628.			
PR	05-SEP-1997: US-057635.			
PR	05-SEP-1997: US-057644.			
PR	05-SEP-1997: US-057647.			
PR	05-SEP-1997: US-057650.			
PR	05-SEP-1997: US-057661.			
PR	05-SEP-1997: US-057667.			
PR	05-SEP-1997: US-057761.			
PR	05-SEP-1997: US-057764.			
PR	05-SEP-1997: US-057770.			
PR	05-SEP-1997: US-057775.			
PR	05-SEP-1997: US-057778.			
PR	06-JUN-1997: US-048875.			
PR	06-JUN-1997: US-048878.			
PR	06-JUN-1997: US-048882.			
PR	06-JUN-1997: US-048885.			
PR	06-JUN-1997: US-048894.			
PR	06-JUN-1997: US-048897.			
PR	06-JUN-1997: US-048900.			
PR	06-JUN-1997: US-048916.			
PR	06-JUN-1997: US-048962.			
PR	06-JUN-1997: US-048970.			
PR	06-JUN-1997: US-048974.			
PR	06-JUN-1997: US-049373.			
PR	05-SEP-1997: US-057584.			
PR	05-SEP-1997: US-057642.			
PR	05-SEP-1997: US-057645.			
PR	05-SEP-1997: US-057648.			
PR	05-SEP-1997: US-057651.			

PR 05-SEP-1997; US-057662.
PR 05-SEP-1997; US-057668.
PR 05-SEP-1997; US-057762.
PR 05-SEP-1997; US-057765.
PR 05-SEP-1997; US-057771.
PR 05-SEP-1997; US-057776.
PR 06-JUN-1997; US-048876.
PR 06-JUN-1997; US-048880.
PR 06-JUN-1997; US-048883.
PR 06-JUN-1997; US-048892.
PR 06-JUN-1997; US-048895.
PR 06-JUN-1997; US-048898.
PR 06-JUN-1997; US-048901.
PR 06-JUN-1997; US-048917.
PR 06-JUN-1997; US-048963.
PR 06-JUN-1997; US-048971.
PR 06-JUN-1997; US-049019.
PR 06-JUN-1997; US-049374.
PR 05-SEP-1997; US-057637.
PR 05-SEP-1997; US-057634.
PR 05-SEP-1997; US-057643.
PR 05-SEP-1997; US-057646.
PR 05-SEP-1997; US-057649.
PR 05-SEP-1997; US-057654.
PR 05-SEP-1997; US-057656.
PR 05-SEP-1997; US-057666.
PR 05-SEP-1997; US-057760.
PR 05-SEP-1997; US-057763.
PR 05-SEP-1997; US-057769.
PR 05-SEP-1997; US-057774.
PR 05-SEP-1997; US-057777.
PR (HUMA-) HUMAN GENOME SCI INC.
PA Biewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA,
PI Fan P, Feng P, Ferlie AM, Fischer CL, Florence C,
PI Florence K, Greene JM, Hu J, Kyaw H, Lafleur DM,
PI Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM,
PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
DR WPI: 99-059865/05.
DR P-PSDB: W88589, W88807, W88808, W88809, W88810, W88811.
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
PS Claim 4; Page 323-324; 772pp; English.
CC The invention relates to nucleic acid sequences (V84411 to V84633)
CC encoding human secreted proteins (W8534 to W8756). The secreted protein
CC gene sequences are deposited with the ATCC under deposit numbers ATCC
CC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
CC cells comprising recombinant vectors containing the nucleic acid
CC sequences are used for the recombinant production of the secreted
CC proteins. The polynucleotide and amino acid sequences are useful for are
CC useful for preventing, treating or ameliorating medical conditions e.g.
CC by protein or gene therapy. Pathological conditions can be also diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the polynucleotides, based on
CC which tissues they are most highly expressed in, and include developing
CC products for the diagnosis or treatment of cancer, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC restenosis, prostate diseases, obesity, disorders involving osteoclasts
CC such as osteoporosis, arthritis or malignancies, diseases of testes, lung
CC or thymus, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners.
CC The present sequence represents a gene encoding a human secreted protein
CC (see descriptor line for gene number and clone identification).
SQ Sequence 1866 BP; 484 A; 458 C; 397 G; 524 T;

Query Match	29.98;	Score 26;	DB 1;	Length 1866;
Best Local Similarity	59.58;	Pred. No. 11;		
Matches 44;	Conservative 0;	Mismatches 30;	Indels 0;	Gaps 0;

```

OY 1 atgagatgcagctccatcctcctcctcctcagctcgtctgttcacagcttcggg 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 105 AAGGCATCTACTCTCTCATTTGCTCTACATCCAAAGATGCTGTGTCTACAGCCCTGAG 46
OY 61 gaactcattccgca 74
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 45 GAAACAGCTTTGGCA 32

RESULT 6
ID 095110/c
AC 095110: standard; cDNA: 1893 BP.
DE 06-MAR-1996 (first entry)
KW Human thyroid hormone receptor alpha-1 cDNA.
KW Human thyroid hormone receptor; alpha-1; htr-alpha-1; analysis;
KW assays; therapeutic agents; antibodies; affinity purification;
KW detection; quantification; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 73..1305
FT US5438126-A.
PD 01-AUG-1995.
PF 11-SEP-1989; 405342.
PR 11-SEP-1989; US-405342.
PR 03-FEB-1992; US-830766.
PA (ARCH) ARCH DEV CORP.
PI Degroot LJ, Nakai A;
DR WPI: 95-274923/36.
DR P-PSDB: R78318.
PT New human thyroid hormone receptor nucleic acid - used to develop
PT Prods. for use in analysis, assays and therapeutic agents
PS Claim 1; Fig 1; 7p; English.
CC 095110 encodes R78318 human thyroid hormone receptor alpha-1 (htr-
CC alpha-1). The nucleic acid can be used to develop prods. for use in
CC analysis assays and therapeutic agents. htr-alpha-1 can be used in
CC tests for thyroid function, or for producing antibodies for use in
CC affinity purific., detection and quantification.
SQ Sequence 1893 BP; 461 A; 531 C; 551 G; 350 T;

Query Match 29.9%; Score 26; DB 1; Length 1893;
Best Local Similarity 62.1%; Pred. No. 11;
Matches 41; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 17 ccatacctcctcctcagctcgtctcgttcgacagcttcggggaactgattccgacg 76
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1594 CCTTCCCTTACTCTTGAGAGAGTGGGTCTGGAGACTGCAGACACAGCTCCCCAGC 1535
OY 77 ctcca 82
    | | | | |
DB 1534 CTCCCA 1529

RESULT 7
ID X00663
AC X00663:
DE 25-MAR-1999 (first entry)
KW Human secreted protein gene 53 clone HBWCL41.
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
PN WO9842738-A1.
PD 01-OCT-1998.

```

```

PF 19-MAR-1998; U05311.
PR 30-MAY-1997; US-050937.
PR 21-MAR-1997; US-041276.
PR 21-MAR-1997; US-041277.
PR 21-MAR-1997; US-041281.
PR 21-MAR-1997; US-042344.
PR 30-MAY-1997; US-048069.
PR 30-MAY-1997; US-048094.
PR 30-MAY-1997; US-048095.
PR 30-MAY-1997; US-048096.
PR 30-MAY-1997; US-048099.
PR 30-MAY-1997; US-048131.
PR 30-MAY-1997; US-048135.
PR 30-MAY-1997; US-048154.
PR 30-MAY-1997; US-048160.
PR 30-MAY-1997; US-048186.
PR 30-MAY-1997; US-048187.
PR 30-MAY-1997; US-048188.
PR 30-MAY-1997; US-048350.
PR 30-MAY-1997; US-048351.
PR 30-MAY-1997; US-048352.
PR 30-MAY-1997; US-048355.
PR 05-AUG-1997; US-054804.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA,
PI Greene JM, Hu JS, Lafleur DM, Moore PA, Ni J, Olsen HS,
PI Rosen CA, Ruben SM, Shi Y, Young P;
DR WPI: 99-070066/06.
DR P-PSDB: W67859.
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancer, neurological
PT disorders, immune diseases, inflammation or blood disorders
PS Claim 1; Page 215; 385p; English.
CC This sequence represents a nucleic acid molecule which encodes a secreted
CC human protein. The gene number, and the clone it is derived from, are
CC detailed in the descriptor line. The gene can be used to generate fusion
CC proteins by linking to the gene to a human immunoglobulin Fc portion
CC (e.g. X00602) for increasing the stability of the fused protein as
CC compared to the human protein only.
CC The invention relates to 87 novel genes and their fragments (nucleic acid
CC sequences: X00611-X00724; amino acid sequences W67807-W68004) which
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also, pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 87 polynucleotides, based on
CC which tissues they are most highly expressed in (see X00611 for described
CC uses).
SQ Sequence 360 BP; 102 A; 89 C; 76 G; 91 T;

Query Match 29.4%; Score 25.6; DB 1; Length 360;
Best Local Similarity 63.8%; Pred. No. 9.9;
Matches 37; Conservative 1; Mismatches 20; Indels 0; Gaps 0;

OY 30 tctcagctcgtctgttcgacagcttcggggaactgattccgacgctccaatgaa 87
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 44 TGTAAAGCCCGCAGCTCCCGCAGCTCCCGGAGATCTGCGCCTCTTACATGAA 101

RESULT 8
ID T94563
AC T94563:
DE 22-APR-1998 (first entry)
KW Human derived long chain DNA novel gene.
KW Human; long chain DNA; antibody; nervous disorder; detection;
KW inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..1269
FT /*tag= a
FT /product= "long chain DNA protein"

```


FT /note= "no stop codon given"
PN W09737018-A1.
PD 09-OCT-1997.
PR 19-MAR-1997; J00919.
PR 03-APR-1996; JP-081304.
PA (ASAH) ASAH KASEI KOGYO KK.
PI Kato C, Takada Y;
DR WPI; 97-503103/46.
DR P-PSDB; W32797.
PT Human long chain DNA and antibodies which bind to the peptide(s) -
PS is potentially useful in treating nervous disorders
PS Claim 3; Page 91-92; 109pp; Japanese.
CC The present sequence represents human derived long chain DNA comprising
CC at least a peptide-encoding region. Peptides encoded by the human
CC derived long chain DNA, may be used for detecting substances which bind
CC to the peptides, and for detecting substances which suppress or inhibit
CC binding to these peptides. The peptides and their inhibitors are
CC potentially useful in treating nervous disorders.
SO Sequence 1269 BP; 263 A; 413 C; 285 G; 308 T;

Query Match 29.2%; Score 25.4; DB 1; Length 1269;
Best Local Similarity 58.7%; Pred. No. 15;
Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 10 cagctccatccctcctcctcagctgctgttcctgacagcttcgggaactgatt 69
DB 736 CTGCTCTACATCCTCCCTCTCATCATCTGTGCTTACGCTGCTGCGCAGAGAA 795
OY 70 ccgcagcttccaat 84
DB 796 CTGTGGCTGTGTAAT 810

RESULT 9
T94564
ID T94564 standard; DNA: 1562 BP.
AC T94564;
DT 22-APR-1998 (first entry)
DE Human derived long chain DNA novel gene.
KW Human; long chain DNA; antibody; nervous disorder; detection;
KW Inhibitor; ss.
OS Homo sapiens.
FH Key
FT CDS
FT Location/Qualifiers
FT 168..1439
FT /*tag= a
FT /product= "long chain DNA protein"

PN W09737018-A1.
PD 09-OCT-1997.
PR 19-MAR-1997; J00919.
PR 03-APR-1996; JP-081304.
PA (ASAH) ASAH KASEI KOGYO KK.
PI Kato C, Takada Y;
DR WPI; 97-503103/46.
DR P-PSDB; W32797.
PT Human long chain DNA and antibodies which bind to the peptide(s) -
PS is potentially useful in treating nervous disorders
PS Claim 4; Page 92-93; 109pp; Japanese.
CC The present sequence represents human derived long chain DNA comprising
CC at least a peptide-encoding region. Peptides encoded by the human
CC derived long chain DNA, may be used for detecting substances which bind
CC to the peptides, and for detecting substances which suppress or inhibit
CC binding to these peptides. The peptides and their inhibitors are
CC potentially useful in treating nervous disorders.
SO Sequence 1362 BP; 318 A; 506 C; 389 G; 349 T;

Query Match 29.2%; Score 25.4; DB 1; Length 1562;
Best Local Similarity 58.7%; Pred. No. 16;
Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 10 cagctccatccctcctcctcagctgctgttcctgacagcttcgggaactgatt 69
DB 736 CTGCTCTACATCCTCCCTCTCATCATCTGTGCTTACGCTGCTGCGCAGAGAA 795

DB 903 CTGCTCTACATCCTCCCTCTCATCATCTGTGCTTACGCTGCTGCGCAGAGAA 962
OY 70 ccgcagcttccaat 84
DB 963 CTGTGGCTGTGTAAT 977

RESULT 10
Q41296
ID Q41296 standard; DNA: 1002 BP.
AC Q41296;
DT 13-SEP-1993 (first entry)
DE Human BMP-8 gene.
KW Bone morphogenetic protein; bone defect treatment; healing; wound;
KW injury; tissue repair; osteoporosis; burns; incisions; ulcers;
KW neuronal survival increase; fracture reduction; cartilage growth;
KW induction; ss.
OS Homo sapiens.
FH Key
FT CDS
FT Location/Qualifiers
FT 8..850
FT /*tag= a
FT mat_peptide 427..843
FT /*tag= b
FT mrna 1..997
FT /*tag= c

PN W09109229-A.
PD 13-MAR-1993.
PF 02-NOV-1992; U09430.
PR 04-NOV-1991; US-787496.
PR 07-APR-1992; US-864692.
PA (GENY) GENETICS INST INC.
PI Israel D, Wolfman NM;
DR WPI; 93-167696/20.
DR P-PSDB; R36737.
PT Recombinant hetero-dimeric BMP proteins - are useful in treating
PT bone defects, healing bone injury and in wound healing
PS Disclosure: Fig 6; 16pp; English.
CC The sequence is that encoding the human bone morphogenetic protein
CC BMP-8. It may be used in the prodn. of a recombinant heterodimeric
CC protein having bone stimulating activity. This heterodimer is
CC encoded by a sequence encoding BMP-2 or BMP-4 or a fragment and a
CC sequence encoding a second protein or fragment. BMP-8. It may be
CC used in compns. for wound healing, tissue repair, and in similar
CC compns. which have been indicated for the use of individual BMPs.
CC Increased potency of the heterodimer over individual BMPs may permit
CC lower dosages to be administered. A heterodimeric protein which
CC induces cartilage and/or bone growth in circumstances where bone
CC is not normally formed, has applications in the healing of bone
CC fractures and cartilage defects in humans and other animals. The
CC heterodimer may have prophylactic use in closed as well as open
CC fracture reduction and also in the improved fixation of artificial
CC joints. De novo bone formation induced by an osteogenic agent
CC contributes to the repair of congenital, trauma induced or oncologic
CC resection induced craniofacial defects, and also is useful in cosmetic
CC plastic surgery. It may be used in the treatment of periodontal
CC disease and in other tooth repair processes. It may also be useful
CC in the treatment of osteoporosis, wound healing (e.g. burns,
CC incisions and ulcers) and related tissue repair, and may increase
CC neuronal survival and be useful in the transplantation and treatment
CC of conditions exhibiting a decrease in neuronal survival. It may be
CC combined with other agents beneficial to the bone and/or cartilage
CC defect, wound or tissue in question, e.g. BGF, PdgF, TGF-alpha,
CC TGF-beta and insulin-like growth factor
SO Sequence 1002 BP; 196 A; 330 C; 285 G; 191 T;

Query Match 29.0%; Score 25.2; DB 1; Length 1002;
Best Local Similarity 57.7%; Pred. No. 17;
Matches 45; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 6 ttgtacgctccatccctcctcctcagctgctgttcctgacagcttcgggaact 65
DB 88 TTACAGAGTGGCCAGCATCCTCTCTACAGAGACCTCTCCAGTCAGATGTTCCAGGT 147

QY 66 gattccgcagcctcccaa 83
 DB 148 GGTCAGAGAGACTCCAA 165

RESULT 11
 Q28737
 ID Q28737 standard; cDNA; 1723 BP.
 AC Q28737;
 DT 26-FEB-1993 (first entry)
 DE Human osteogenic protein hop2 coding sequence.
 KW Morphogen; morphogenic protein.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 490..1698
 FT /tag= a
 FT /product= hop2
 FT W09215323-A.
 PN 17-SEP-1992.
 PD 11-MAR-1992; U01968.
 PR 11-MAR-1991; US-667274.
 PA (CREA-) CREATIVE BIOMOLECULES INC.
 PI Cohen CM, Kuberassampath T, Oppermann H, Pang RHL, Rueger DC;
 DR P-PDB; R27291.
 CC Compens. for increasing progenitor cell population - contain a
 PT morphogen to induce proliferation, useful for inhibiting
 CC neoplastic growth. Inducing tissue repair and in diagnosis of
 PT tissue dysfunction
 PS Disclosure; Page 102-104; 132pp; English.
 CC Mature hop2 is one of the preferred known morphogens which can be
 CC used in the manufacture of pharmaceuticals for inducing non-
 CC chondrogenic mammalian tissue growth; progenitor cell proliferation
 CC and hepatic tissue growth and for maintaining the phenotypic
 CC expression of differentiated cells in a mammal. Morphogenic
 CC compositions of the invention can also be used to treat blood
 CC disorders and impaired or lost immune function. Morphogens sharing
 CC at least 70% homology with hop2 are included.
 SQ Sequence 1723 BP; 265 A; 624 C; 576 G; 258 T;

Query Match 29.0%; Score 25.2; DB 1; Length 1723;
 Best Local Similarity 57.7%; Pred. No. 19;
 Matches 45; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 6 tigtacgctccatctctctctctcagctgctgtcttcagacgctcgaggact 65
 DB 933 TTACAAAGGTGCCCCAGCATTCACCTGCTCAACAGAGACCTCCAGCATGTTCAGGT 992

QY 66 gattccgcagcctcccaa 83
 DB 993 GGTCAGAGAGACTCCAA 1010

RESULT 12
 Q38946
 ID Q38946 standard; cDNA; 1723 BP.
 AC Q38946;
 DT 21-JUL-1993 (first entry)
 DE Human osteogenic protein 2 (hop-2) gene.
 KW Bone; loss; increase; fracture; post-menopausal; senile;
 KW osteoporosis; hyperparathyroidism; skeletal microstructure defects;
 KW chronic renal failure; kidney disease; osteomalacia; vitamin D;
 KW deficiency-induced osteopenia, osteoporosis; Paget's disease;
 KW bone mass; imbalance; resorption; formation; dialysis; calcium;
 KW phosphate; metabolism; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 490..1696
 FT /tag= a
 FT /note= "hop-2"
 FT W09305751-A.

PD 01-APR-1993. 007432.
 PF 28-AUG-1992; U07432.
 PR 30-AUG-1991; US-752764.
 PR 30-AUG-1991; US-752857.
 PR 30-AUG-1991; US-752861.
 PR 31-JUL-1992; US-923780.
 PA (CREA-) CREATIVE BIOMOLECULES INC.
 PI Cohen CM, Kuberassampath T, Oppermann H, Ozkaynak E,
 PI Pang RHL, Rueger DC, Smart JE;
 DR WPI: 93-117208/14.
 CC Use of morphogenic or in-vivo morphogenic-stimulating agent - to
 PT prevent bone loss or increase, used for treating bone fractures,
 PT post-menopausal or senile osteoporosis, hyperparathyroidism etc.
 PS Disclosure; Page 115-117; 162pp; English.
 CC The sequence is that encoding human osteogenic protein 2 (hop-2) a
 CC morphogenically active protein which may be used as part of a
 CC method for treating a bone fracture or a disease which causes or
 CC results in bone fractures or other defects in skeletal
 CC microstructure. Such diseases include chronic renal failure and
 CC other kidney diseases, osteomalacia, vitamin D deficiency-induced
 CC osteopenia or osteoporosis, postmenopausal or senile osteoporosis,
 CC hyperparathyroidism and Paget's disease. The methods can be used for
 CC protecting individuals at risk for loss of bone mass such as
 CC postmenopausal females, aged individuals and individuals undergoing
 CC dialysis. The loss of bone mass may result from an imbalance in bone
 CC resorption or bone formation, an imbalance of calcium or phosphate
 CC metabolism, a vitamin D imbalance or be nutritionally or hormonally
 CC induced.
 SQ Sequence 1723 BP; 266 A; 624 C; 576 G; 257 T;

Query Match 29.0%; Score 25.2; DB 1; Length 1723;
 Best Local Similarity 57.7%; Pred. No. 19;
 Matches 45; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 6 tigtacgctccatctctctctctcagctgctgtcttcagacgctcgaggact 65
 DB 933 TTACAAAGGTGCCCCAGCATTCACCTGCTCAACAGAGACCTCCAGCATGTTCAGGT 992

QY 66 gattccgcagcctcccaa 83
 DB 993 GGTCAGAGAGACTCCAA 1010

RESULT 13
 Q38735
 ID Q38735 standard; cDNA; 1723 BP.
 AC Q38735;
 DT 15-JUL-1993 (first entry)
 DE Human OP-2.
 KW morphogenic; osteogenic protein; developmental cascade; hop-2;
 KW inflammation; anti-inflammatory; Transforming Growth Factor;
 KW TGF-beta super-family; hippocampus; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 490..1698
 FT /tag= a
 FT /note= "hop2"
 FT mat-peptide 1279..1695
 FT /tag= b
 FT /note= "contains conserved 7 cysteine skeleton"
 FT W09304692-A.
 PN 18-MAR-1993.
 PD 28-AUG-1992; U07358.
 PR 30-AUG-1991; US-752764.
 PR 30-AUG-1991; US-752861.
 PR 30-AUG-1991; US-753059.
 PA (CREA-) CREATIVE BIOMOLECULES INC.
 PI Cohen CM, Kuberassampath T, Oppermann H, Ozkaynak E;
 PI Pang RHL, Rueger DC, Smart JE;
 DR WPI: 93-100652/12.
 DR P-PDB; R33410.
 PT Morphogen-induced modulation of inflammatory response - and

PT resulting tissue damage, e.g. in autoimmune diseases, diabetes,
PT asthma, ischemia reperfusion injury, etc.
PS Claim 26; Page 119-121; 165pp; English.
CC Human osteogenic protein (OP)-2 is a preferred morphogen for use in
CC treating tissue damage in e.g. inflammatory disease, autoimmune
CC disease, arthritis, psoriasis, dermatitis, diabetes and emphysema.
CC Proteins having at least 70% homology with OP-2 amino acid
CC sequences can also be used. See R33400 for mature hOP-2.
SQ Sequence 1723 BP; 266 A; 625 C; 574 G; 258 T;

Query Match 29.0%; Score 25.2; DB 1; Length 1723;
Best Local Similarity 57.7%; Pred. No. 19;
Matches 45; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 6 ttgtacgtcttcacatcccttccttcagctgctgtgttcacagattcggggaact 65
DB 933 TTACAAGGTGCCAGATCCACTGCTCAACAGACCCCTCCAGTCAGATGTTCCAGGT 992
OY 66 gattccgcagcctccca 83
DB 993 GGTCACGAGCAGCTCAA 1010

RESULT 14
ID 038859 standard; DNA: 1723 BP.
AC 038859;

DE 13-UTL-1993 (first entry)
DE Morphogen hOP2 coding sequence.
KW Morphogen; homodimer; stimulate; proliferation; progenitor cell;
KW differentiation; growth; redifferentiation; transformation; human;
KW mouse; Drosophila; Xenopus; committed cells; hippocampus; ss.
OS Homo sapiens.

FT Key Location/Qualifiers
FT cds 490..1698
FT /*tag= a

PN W09305172-A.
PD 18-MAR-1993.
PR 28-AUG-1992; U07359.
PR 30-AUG-1991; US-752861.
PA (CREA)-CREATIVE BIOMOLECULES INC.
PI Cohen CN, Kuberasampath T, Oppermann H, Ozkaynak E, Pang RHL;
PI Rueger DC, Smart JE;
DR WPI; 93-100993/12.
DR P-PSDB; R33993.

PT Screening cpds. to determine ability to modulate effective concn.
PT of a morphogen - by assaying test tissue type cells for parameter
PS indicative of a prodn. level change of morphogen
PS Disclosure; Page 95-97; 132pp; English.

CC This sequence encodes the human morphogen hOP2, isolated from the
CC hippocampus. This morphogen is inactive when reduced but is active
CC as an oxidised homodimer and when oxidised in combination with other
CC morphogens. These morphogens are capable of stimulating proliferation
CC of progenitor cell, stimulating the differentiation of progenitor
CC cells, stimulating the proliferation of differentiated cells and
CC supporting the growth and maintenance of differentiated cells,
CC including the redifferentiation of transformed cells. These
CC morphogens may also be capable of inducing redifferentiation of
CC committed cells under appropriate environmental conditions.
SQ Sequence 1723 BP; 270 A; 624 C; 572 G; 257 T;

Query Match 29.0%; Score 25.2; DB 1; Length 1723;
Best Local Similarity 57.7%; Pred. No. 19;
Matches 45; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 6 ttgtacgtcttcacatcccttccttcagctgctgtgttcacagattcggggaact 65
DB 933 TTACAAGGTGCCAGATCCACTGCTCAACAGACCCCTCCAGTCAGATGTTCCAGGT 992
OY 66 gattccgcagcctccca 83
DB 993 GGTCACGAGCAGCTCAA 1010

DB 993 GGTCACGAGCAGCTCAA 1010

RESULT 15

ID 053155 standard; cDNA: 1723 BP.
AC 053155;

DE 06-JUN-1994 (first entry)
DE Sequence encoding human osteogenic protein OP2.
DE Osteogenic protein; bone; cartilage; matrix; osteoarthritis;
KW repair; vascularisation; mineralisation; differentiation; ss.
OS Homo sapiens.

FT Key Location/Qualifiers
FT cds 490..1696
FT /*tag= a
FT /product= Osteogenic protein OP2.

PN US5266683-A.
PD 30-NOV-1993.
PR 08-APR-1988; 179406.
PR 08-APR-1988; US-179406.
PR 15-AUG-1988; US-232630.
PR 23-FEB-1989; US-315342.
PR 17-OCT-1989; US-422613.
PR 17-OCT-1989; US-422699.
PR 22-FEB-1990; US-483913.
PR 20-AUG-1990; US-569920.
PR 07-SEP-1990; US-579865.
PR 18-OCT-1990; US-599543.
PR 18-OCT-1990; US-600024.
PA 04-DEC-1990; US-621849.
PA 04-DEC-1990; US-621988.
PA 22-FEB-1991; US-660162.
PA 20-DEC-1991; US-810560.
PA 28-JAN-1992; US-827052.
PA 21-FEB-1992; US-841646.
PI Kuberasampath T, Oppermann H, Ozkaynak E, Pang RHL;
PI Rueger DC;
DR WPI; 93-365405/49.
DR P-PSDB; R44759.

PT New pure mammalian osteogenic proteins - induce cartilage and
PT endochondral bone formation when in association with a matrix
PS Claim 26; Columns 143-148; 128pp; English.
CC The osteogenic protein when in association with a matrix can induce
CC at the locus of an implant the full development cascade of
CC endochondral bone formation including vascularisation,
CC mineralisation and bone marrow differentiation. The osteogenic
CC protein can also be used to repair both bone and cartilage in the
CC treatment of osteoarthritis. This sequence encodes the pre-pro
CC form of the protein.
SQ Sequence 1723 BP; 265 A; 624 C; 577 G; 257 T;

Query Match 29.0%; Score 25.2; DB 1; Length 1723;
Best Local Similarity 57.7%; Pred. No. 19;
Matches 45; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 6 ttgtacgtcttcacatcccttccttcagctgctgtgttcacagattcggggaact 65
DB 933 TTACAAGGTGCCAGATCCACTGCTCAACAGACCCCTCCAGTCAGATGTTCCAGGT 992
OY 66 gattccgcagcctccca 83
DB 993 GGTCACGAGCAGCTCAA 1010

Search completed: May 15, 2000, 12:08:28
Job time: 4587 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 11:42:02 ; Search time 1225.64 Seconds
(without alignments)
-69.052 Million cell updates/sec

Title: US-09-104-340-6

Perfect score: 87
Sequence: 1 atggatgtcagcttccat.....ttccgcagcttccaatgaa 87

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da1:*
2: gb_da2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pl3:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sts:*
14: gb_sy:*
15: gb_un:*
16: gb_vl:*
17: em_fun:*
18: em_hum1:*
19: em_hum2:*
20: em_in:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_sy:*
30: em_un:*
31: em_vl:*
32: gb_hcgl:*
33: gb_hcgl2:*
34: gb_hcgl3:*
35: gb_hcgl4:*
36: gb_hcgl5:*
37: gb_hcgl6:*
38: em_hum3:*
39: em_hum4:*
40: gb_pr4:*
41: gb_hcgl7:*
42: gb_hcgl8:*
43: gb_hcgl9:*
44: gb_hcgl10:*
45: gb_hcgl11:*

45: gb_hcgl7:*
46: em_hcgl1:*
47: em_hcgl2:*
48: em_hcgl3:*
49: em_hcgl4:*
50: gb_pl3:*
51: gb_pr5:*
52: gb_hcgl8:*
53: gb_hcgl9:*
54: gb_hcgl10:*
55: gb_hcgl11:*
56: gb_hcgl12:*
57: gb_hcgl13:*
58: gb_hcgl14:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	87	100.0	3132	5 A28003	A28003 H.sapiens H
2	87	100.0	3132	5 I68018	I68018 Sequence 9
3	87	100.0	3149	9 HUMHEK	M83941 Human recep
4	61.4	70.6	2032	12 MUSMEK4SE	M68515 Mouse eph-r
5	61.4	70.6	3077	12 MUSMEK4	U69278 Rattus norv
6	61.4	70.6	3197	12 MUSMEK4	M68513 Mouse eph-r
7	29	33.3	53997	44 AC021186	AC021186 Homo sapi
8	28.8	33.1	84551	35 AC004295	AC004295 Drosophi
9	28.8	33.1	120625	43 AC017563	AC017563 Drosophi
10	28.6	32.9	119118	11 HSRIR7CCL	AC017563 Drosophi
11	28.4	32.6	183716	53 AC017104	AL049760 Human DNA
12	28.2	32.4	90299	11 HS72E17	AC017104 Homo sapi
13	28.2	32.4	187701	44 AC010485	AL033523 Human DNA
14	28.2	32.4	211385	33 AL138881	AC010485 Homo sapi
15	28.2	32.4	307834	44 AC010475	AL138881 Homo sapi
16	28	32.2	3031	12 MM027398	AC010475 Homo sapi
17	28	32.2	38532	1 SCE94	U27398 Mus musculu
18	28	32.2	74654	45 AC021405	AL049628 Streptomy
19	27.8	32.0	1760	2 AF190426	AC021405 Homo sapi
20	27.6	31.7	5382	34 ARDMNIC	AF190426 Brwalia h
21	27.6	31.7	117270	9 HSRGFRAG	D10747 Acropora do
22	27.6	31.7	117270	11 AC005316	Y13801 Homo sapien
23	27.6	31.7	146834	45 AC019360	AC005316 Human Chr
24	27.6	31.7	171950	40 AC005317	AC019360 Homo sapi
25	27.6	31.7	191988	45 AC021446	AC005317 Human Chr
26	27.6	31.7	208079	43 AC013391	AC021446 Mus muscu
27	27.4	31.5	113253	42 AC010121	AC013391 Homo sapi
28	27.4	31.5	169516	42 AC013934	AC010121 Drosophi
29	27.4	31.5	178609	55 AC011060	AC013934 Drosophi
30	27.4	31.5	179563	45 AC006433	AC011060 Homo sapi
31	27.4	31.5	180593	33 AC005282	AC006433 Homo sapi
32	27.4	31.5	213879	57 AC011612	AC005282 Homo sapi
33	27.4	31.5	251664	57 AC011607	AC011612 Homo sapi
34	27.2	31.3	319	9 HDUALPHUB	AC011607 Homo sapi
35	27.2	31.3	324	5 AR051317	L11645 Homo sapien
36	27.2	31.3	1088	5 EL13168	AR051317 Sequence
37	27.2	31.3	6405	9 AB032946	EL13168 Acacia mang
38	27.2	31.3	6510	11 AF005392	AB032946 Homo sapi
39	27.2	31.3	6740	40 AF129133	AF005392 Homo sapi
40	27.2	31.3	6990	40 AF142567	AF129133 Homo sapi
41	27.2	31.3	7768	40 AF051946	AF142567 Homo sapi
42	27.2	31.3	7898	40 AF073931	AF051946 Homo sapi
43	27.2	31.3	31756	11 HSN53A9	AF073931 Homo sapi
44	27.2	31.3	45896	11 HSB29P11	HSN53A9 Human DNA
45	27.2	31.3	52097	33 HS357D8	AL050312 Human DNA

ALIGNMENTS

```
RESULT 1
A28003 1 3132 bp DNA PAT 25-SEP-1995
LOCUS A28003 H.sapiens HEK gene.
DEFINITION H.sapiens HEK gene.
ACCESSION A28003
VERSION A28003.1 GI:1247486
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3132)
AUTHORS A NOVEL RECEPTOR-TYPE TYROSINE KINASE AND USE THEREOF
JOURNAL Patent: WO 9300425-A 7 07-JAN-1993;
FEATURES
source Location/Qualifiers
1..3132
/organism="Homo sapiens"
/db_xref="taxon:9606"
/gene="HEK"
100..3051
/gene="HEK"
100..3051
/gene="HEK"
/codon_start=1
/protein_id="CAA01906.1"
/db_xref="GI:1247487"
/translation="MDCQLSTILLSCSYLDSFGELIPQPSNEVNLDSKTIOGELGM
ISYPSHGEIISGVDEHYPIRTYQCNVMDISQNNMLRTNVPKNSAKIYVELKFT
LRDCNSIPVLGTCKETENLYMESDDHGVKREKQFTKIDTADSEFTQDLGDR
ILKNTETREVGCVNKKGFYLAQDVACVALSVAVKRCPEYKKNLAMPDTPM
DSQSLVEVAGSCVNNKEDPPRMKSTGEMVLVPGKSCNAGYERQFMCOACRPG
FYKALDGNMKCAKPPHSSSTOEDGSMNCENNYFRADDPSPMACTRPPSPRNVIS
NINETSVIDLMSWPLDTGGRKDYTFNICKCGMNIKOCEPCSPNRYFLPROGLTNT
TYTVDLAHTNTYFEIDAVNGVSELSPPRQAAVSTTNQAAPSVTLIKDRSTR
NSISLSMOPREHNGIILDEYKATYKQEDERTYTLRAGINVTISLKPDTIYVQ
IRKRTAGIGTNSRKFEFTSPDSFISSESSVVAIAAVALIILTVIYLVLR
FCGYKSKHADKRLHFGNGHLPLGLRTYVDPHTEPTQAVHEFAKELDATNISID
KTVGAGEFEVCSGRKLPSKKEISVALTKIKYGEKORDFLGASIMGQDHSNI
IRLEGVATSKPMYIVTEYWMENGLSPFRKHDAQPTVQLGLMGLASGMKYLSDM
GYVHRDLAARNILINSNLVCYKSDPGLISLTPRAATYTRGKPIKMTSPKAIAY
RKFTSASDVMSIGIYVMEVMSYGERPWEKSNODYIKAVDEGRILPPMDCPALYOL
MDCQKDRNNRKPKEQIYSILDKLIRNPGSLKITTSAAARSNLLDSDNDISFR
TTGDMWNGVRIAHCKEIFTGVEISSCDTIKISTDDMKRVGVTVGPQKIISSIKAL
ETQSKNGPVPV"
BASE COUNT 888 a 709 c 761 g 774 t
ORIGIN
```

```
REFERENCE 1 (bases 1 to 3132)
AUTHORS Boyd,A.W., Simpson,R.John, Wicks,I., Ward,I.David and Wilkinson,D.
TITLE Method of screening for ligands to a receptor-tyrosine kinase
JOURNAL Patent: US 5674691-A 9 07-OCT-1997;
FEATURES
source Location/Qualifiers
1..3132
/organism="unknown"
BASE COUNT 888 a 709 c 761 g 774 t
ORIGIN
```

Query Match 100.0%; Score 87; DB 5; Length 3132;
Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 atgattgtaagcttcacatccctcctcctcgaagcgtctctgttcgacagcttcgg 60
|||||
DB 100 ATGATTGTAGCTTCACATCCCTCCTCTCTGAGCTGCTGTCTCGACAGCTTG 159
|||||
QY 61 gaactgattccgacgacctccaatgaa 87
|||||
DB 160 GAACGTGATCCGACGCTTCCATGAA 186
|||||
```

RESULT 3
LOCUS HUMHEK 3149 bp mRNA PRI 31-DEC-1994
DEFINITION Human receptor tyrosine kinase (HEK) mRNA, complete cds.
ACCESSION M83941
VERSION M83941.1 GI:183931
KEYWORDS receptor protein-tyrosine kinase.
SOURCE Homo sapiens lymphoid tumor cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3149)
AUTHORS Wicks,I.P., Wilkinson,D., Salvaris,E. and Boyd,A.W.
TITLE Molecular cloning of HEK, the gene encoding a receptor tyrosine
kinase expressed by human lymphoid tumor cell lines
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (5), 1611-1615 (1992)
FEATURES
source Location/Qualifiers
1..3149
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="LK63"
/tissue_type="Lymphoid tumor"
101..3052
/gene="HEK"
101..3052
/gene="HEK"
/codon_start=1
/product="receptor protein kinase"
/protein_id="AA58633.1"
/db_xref="GI:183932"
/translation="MDCQLSTILLSCSYLDSFGELIPQPSNEVNLDSKTIOGELGM
ISYPSHGEIISGVDEHYPIRTYQCNVMDISQNNMLRTNVPKNSAKIYVELKFT
LRDCNSIPVLGTCKETENLYMESDDHGVKREKQFTKIDTADSEFTQDLGDR
ILKNTETREVGCVNKKGFYLAQDVACVALSVAVKRCPEYKKNLAMPDTPM
DSQSLVEVAGSCVNNKEDPPRMKSTGEMVLVPGKSCNAGYERQFMCOACRPG
FYKALDGNMKCAKPPHSSSTOEDGSMNCENNYFRADDPSPMACTRPPSPRNVIS
NINETSVIDLMSWPLDTGGRKDYTFNICKCGMNIKOCEPCSPNRYFLPROGLTNT
TYTVDLAHTNTYFEIDAVNGVSELSPPRQAAVSTTNQAAPSVTLIKDRSTR
NSISLSMOPREHNGIILDEYKATYKQEDERTYTLRAGINVTISLKPDTIYVQ
IRKRTAGIGTNSRKFEFTSPDSFISSESSVVAIAAVALIILTVIYLVLR
FCGYKSKHADKRLHFGNGHLPLGLRTYVDPHTEPTQAVHEFAKELDATNISID
KTVGAGEFEVCSGRKLPSKKEISVALTKIKYGEKORDFLGASIMGQDHSNI
IRLEGVATSKPMYIVTEYWMENGLSPFRKHDAQPTVQLGLMGLASGMKYLSDM
GYVHRDLAARNILINSNLVCYKSDPGLISLTPRAATYTRGKPIKMTSPKAIAY
RKFTSASDVMSIGIYVMEVMSYGERPWEKSNODYIKAVDEGRILPPMDCPALYOL
MDCQKDRNNRKPKEQIYSILDKLIRNPGSLKITTSAAARSNLLDSDNDISFR
TTGDMWNGVRIAHCKEIFTGVEISSCDTIKISTDDMKRVGVTVGPQKIISSIKAL
ETQSKNGPVPV"

Db 35 ATGAGTTGCACCTCTCCATCCATCCCTGTTGGCTGCTGCTCCTCAGCTCCTCAGG 94
Qy 61 gaactgattccgcagcctccatga 87
||||| ||| ||||| |||
Db 95 GAAGCTGAGTCACAGCCTTCACAGAA 121
RESULT 6
LOCUS MUSMEK4 3197 bp mRNA ROD 15-FEB-1994
DEFINITION Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.
ACCESSION M68513
VERSION M68513.1 GI:199119
KEYWORDS receptor tyrosine kinase.
SOURCE Mus musculus (strain IRC x Swiss Webster) 11.5 day embryo embryo cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3197)
AUTHORS Sajjadi,F.G., Pasquale,E.B. and Subraman,S.
TITLE Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor
JOURNAL New Biol. 3, 769-778 (1991)
MEDLINE 92031278
FEATURES
source 1..3197
location/Qualifiers
/organism="Mus musculus"
/strain="IRC x Swiss Webster"
/db_xref="taxon:10090"
/dev_stage="11.5 day embryo"
/tissue_type="embryo"
89..3040
/gene="Mek4"
89..3040
/gene="Mek4"
/codon_start=1
/product="receptor tyrosine kinase"
/protein_id="AAA39521.1"
/db_xref="GI:199120"
/translation="MDCHLSIVLAGCCVLSGSGELSPSPSENVNLDSKITQGEIGW
LSPHGWELISGVDEHPTPIRTYQVCNWDHSSQNNWLTNNVNPNSAKIVELKFT
LADNSIPLYLGTCKEFTNLXYMESDGHGKFRHQFTKIDIDADESTQDLDRIL
IKLNTIREVGVNKKGFYLAQDVACALVSRVYFKCFYKALNMPDTPMD
SOSLVEKSGCVNNSKEDEPPRMNCSGEGEMLVPIGKTCNMGYERGPICQARPF
YKASGAACAKCAPHSSQDQESNMNRCENNYPAEKDPPMACAPRPSAPRYSN
INETSIIIDMSPLDTGGRKDTTNNICKCGMNRQCEPCSPNRFPLRQGLNNT
VVTDLAHTNTFEIDAVNGVSELSPPROTAASITTNQAPSPVMTIKDRTSRN
SISLWQEPENHNGIILDYEVYQKQEDSTYILRAGTNTVTSLSKPTTYFOI
RARTAGYCTGNTKEFEFSPDSFSGNSHVMIAISAAVAIIVLYVTVLGRF
CGYHKSKEAEKRLHFGNGHLKPLRLTYDPHYEDPTQAVHEPAKRLDNTNSID
KYVGAEEGVESGKILPSKREISVAITKLVGYTEKORPDLCEASTMGOPDPNT
ILLEGVYTKSEKEMTVTEYMENGLSDSLFRKHDAQTVYIQLVGMRLGINSKGLISDM
GVVHRLAARNLILNSNLCKVSDFLSVLEDDPEAATTGGAIPRIWTSPEMSY
RFTSASDVMSYGIWLEWMSYGERYSQMSQDYIKADERYRLPPMDCPALYFH
MLDCWQDRNNRPFEOIYSILDKILRNGSLKITSAAARSNLLDQSNVDIATFH
TTGDMNGMRITAHCKEIFGTVEYSSCDTIAKISTDMKVKGVTVVGPOKKIISTKAL
ETQSKNGPPV"
BASE COUNT 907 a 767 c 775 g 748 t
ORIGIN
Query Match 70.6%; Score 61.4; DB 12; Length 3197;
Best Local Similarity 81.6%; Pred.No.5.5e-10;
Matches 71; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 149 GAAGTGAAGCCACAGCCTTCACAGAA 175
||||| ||| ||||| |||
RESULT 7
LOCUS AC021186
DEFINITION Homo sapiens clone RP11-744D14, LOW-PASS SEQUENCE SAMPLING.
AC021186
ACCESSION AC021186
VERSION AC021186.1 GI:6693396
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 53997)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 53997)
REFERENCE Waterston,R.H.
AUTHORS Direct Submission
TITLE Submitted (14-JAN-2000) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT
* NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlapping relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1
* 389: contig of 389 bp in length
* 390
* 399: gap of unknown length
* 400
* 1367: contig of 968 bp in length
* 1368
* 1377: gap of unknown length
* 1378
* 2389: contig of 1012 bp in length
* 2390
* 2399: gap of unknown length
* 2400
* 3353: contig of 954 bp in length
* 3354
* 3364: gap of unknown length
* 4194: contig of 831 bp in length
* 4195
* 4204: gap of unknown length
* 4205
* 4674: contig of 470 bp in length
* 4675
* 4684: gap of unknown length
* 5046: contig of 362 bp in length
* 5047
* 5056: gap of unknown length
* 5057
* 5483: contig of 427 bp in length
* 5484
* 5493: gap of unknown length
* 5494
* 5647: contig of 154 bp in length
* 5648
* 5657: gap of unknown length
* 5658
* 6112: contig of 455 bp in length
* 6113
* 6122: gap of unknown length
* 6123
* 6972: contig of 850 bp in length
* 6973
* 6982: gap of unknown length
* 6983
* 7421: contig of 439 bp in length
* 7422
* 7431: gap of unknown length
* 7432
* 7835: contig of 404 bp in length
* 7836
* 7845: gap of unknown length
* 7846
* 8687: contig of 842 bp in length
* 8688
* 8697: gap of unknown length
* 8698
* 9143: contig of 446 bp in length
* 9144
* 9153: gap of unknown length
* 9154
* 9623: contig of 470 bp in length
* 9624
* 9633: gap of unknown length
* 9634
* 9766: contig of 133 bp in length
* 9767
* 9776: gap of unknown length
* 9777
* 10579: contig of 903 bp in length
* 10580
* 10689: gap of unknown length

* 10690 11095: contig of 406 bp in length
* 11096 11105: gap of unknown length
* 11106 11560: contig of 455 bp in length
* 11561 11570: gap of unknown length
* 11571 12357: contig of 787 bp in length
* 12358 12367: gap of unknown length
* 12368 12803: contig of 436 bp in length
* 12804 12813: gap of unknown length
* 12814 13287: contig of 474 bp in length
* 13288 13297: gap of unknown length
* 13298 13758: contig of 461 bp in length
* 13759 13768: gap of unknown length
* 13769 14181: contig of 413 bp in length
* 14182 14191: gap of unknown length
* 14192 14651: contig of 460 bp in length
* 14652 14661: gap of unknown length
* 14662 14986: contig of 325 bp in length
* 14987 14996: gap of unknown length
* 14997 15462: contig of 466 bp in length
* 15463 15472: gap of unknown length
* 15473 15947: contig of 475 bp in length
* 15948 15957: gap of unknown length
* 15958 16378: contig of 421 bp in length
* 16379 16388: gap of unknown length
* 16389 16857: contig of 469 bp in length
* 16858 16867: gap of unknown length
* 16868 17320: contig of 453 bp in length
* 17321 17330: gap of unknown length
* 17331 18171: contig of 841 bp in length
* 18172 18181: gap of unknown length
* 18182 19048: contig of 867 bp in length
* 19049 19058: gap of unknown length
* 19059 19973: contig of 915 bp in length
* 19974 19983: gap of unknown length
* 19984 20865: contig of 882 bp in length
* 20866 20875: gap of unknown length
* 20876 21718: contig of 843 bp in length
* 21719 21728: gap of unknown length
* 21729 22156: contig of 428 bp in length
* 22157 22624: gap of unknown length
* 22625 22634: gap of unknown length
* 22635 23571: contig of 937 bp in length
* 23572 23581: gap of unknown length
* 23582 24490: contig of 909 bp in length
* 24491 24500: gap of unknown length
* 24501 25316: contig of 816 bp in length
* 25317 25326: gap of unknown length
* 25327 26304: contig of 978 bp in length
* 26305 26314: gap of unknown length
* 26315 27085: contig of 771 bp in length
* 27086 27095: gap of unknown length
* 27096 27933: contig of 838 bp in length
* 27934 27943: gap of unknown length
* 27944 28199: contig of 256 bp in length
* 28200 28209: gap of unknown length
* 28201 28982: contig of 773 bp in length
* 28983 28992: gap of unknown length
* 28993 29273: contig of 281 bp in length
* 29274 29283: gap of unknown length
* 29284 29629: contig of 346 bp in length
* 29630 29639: gap of unknown length
* 29640 29826: contig of 187 bp in length
* 29827 29836: gap of unknown length
* 29837 30588: contig of 752 bp in length
* 30589 30598: gap of unknown length
* 30599 31194: contig of 596 bp in length
* 31195 31204: gap of unknown length
* 31205 31597: contig of 393 bp in length
* 31598 31607: gap of unknown length
* 31608 32529: contig of 922 bp in length
* 32530 32539: gap of unknown length
* 32540 33475: contig of 936 bp in length

* 33476 33485: gap of unknown length
* 33486 34146: contig of 661 bp in length
* 34147 34156: gap of unknown length
* 34157 35232: contig of 1076 bp in length
* 35233 35242: gap of unknown length
* 35243 35249: contig of 252 bp in length
* 35250 35504: gap of unknown length
* 35505 36453: contig of 949 bp in length
* 36454 36463: gap of unknown length
* 36464 37079: contig of 616 bp in length
* 37080 37089: gap of unknown length
* 37090 37907: contig of 818 bp in length
* 37908 37917: gap of unknown length
* 37918 38197: contig of 280 bp in length
* 38198 38207: gap of unknown length
* 38208 38528: contig of 321 bp in length
* 38529 38538: gap of unknown length
* 38539 39502: contig of 964 bp in length
* 39503 39512: gap of unknown length
* 39513 40424: contig of 912 bp in length
* 40425 40434: gap of unknown length
* 40435 40645: contig of 215 bp in length
* 40650 40659: gap of unknown length
* 40660 41601: contig of 942 bp in length
* 41602 41611: gap of unknown length
* 41612 42577: contig of 966 bp in length
* 42578 42587: gap of unknown length
* 42588 43372: contig of 785 bp in length
* 43373 43382: gap of unknown length
* 43383 44123: contig of 741 bp in length
* 44124 44133: gap of unknown length
* 44134 44428: contig of 295 bp in length
* 44429 44438: gap of unknown length
* 44439 45402: contig of 964 bp in length
* 45403 45412: gap of unknown length
* 45413 45580: contig of 168 bp in length
* 45581 45590: gap of unknown length
* 45591 45837: contig of 247 bp in length
* 45838 45847: gap of unknown length
* 45848 46006: contig of 159 bp in length
* 46007 46016: gap of unknown length
* 46017 46221: contig of 205 bp in length
* 46222 46231: gap of unknown length
* 46232 47280: contig of 1049 bp in length
* 47281 47290: gap of unknown length
* 47291 48030: contig of 740 bp in length
* 48031 48040: gap of unknown length
* 48041 49181: contig of 1141 bp in length
* 49182 49191: gap of unknown length
* 49192 49814: contig of 623 bp in length
* 49815 49824: gap of unknown length
* 49825 50733: contig of 909 bp in length
* 50734 50743: gap of unknown length
* 50744 51515: contig of 772 bp in length
* 51516 51525: gap of unknown length
* 51526 51657: contig of 132 bp in length
* 51658 51667: gap of unknown length
* 52726 52736: contig of 1059 bp in length
* 52737 52899: contig of 163 bp in length

Query Match 33.38; Score 29; DB 44; Length 53997;
Best Local Similarity 63.88; Pred. No. 24;
Matches 44; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 13 ctctccaccccccctctcagctgctctgttctgcacaccttcgggaactgattccg 72
Db 6898 CTCCTCTCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGACACATTCCG 6957
OY 73 cagccttc 81
Db 6958 CCGCAGCC 6966

		RESULT	8
		AC004295	
		LOCUS	AC004295 84551 bp DNA INV 29-JUL-1998
		DEFINITION	Drosophila melanogaster DNA sequence (PI DS08374 (D180)), complete sequence.
		ACCESSION	AC004295 AC003461 AC003462 AC003463 AC003824 AC003464 AC003825
		VERSION	AC003465 AC003466 AC003467 AC003468 AC003469 AC003470
		SOURCE	AC004295.1 GI:3347818
		HITS	Drosophila melanogaster (subclones in tet from PI clone DS08374 (D180)) DNA. Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 84551) Celinker,S.E., George,R.A., Galle,R.F., Hoskins,R.A., Svirskas,R.R., Harris,N.L., Aghayani,A., Arcalana,T.T., Baxter,E., Blazej,R.G., Chavez,C., Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A., Hummatti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B., Lomocan,M.A., Mak,J., Mazda,P., Mok,M.S., Moshefi,I.A.R., Moshefi,M., Nixon,K., Pacledb,J.M., Park,S., Pfliederer,B., Punch,E., Snir,E., Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R., Zieran,L.L. and Kimmel,B. Sequencing of Drosophila chromosome 2R, region 55C1-55C4 Unpublished (1997) 2 (bases 1 to 84551) Celinker,S.E., George,R.A., Galle,R., Svirskas,R.R., Hoskins,R.A., Aghayani,A., Arcalana,T.T., Baxter,E., Blazej,R.G., Chavez,C., Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A., Hummatti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B., Lomocan,M.A., Mak,J., Mazda,P., Mok,M.S., Moshefi,I.A.R., Moshefi,M., Nixon,K., Pacledb,J.M., Park,S., Pfliederer,B., Punch,E., Snir,E., Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R., Zieran,L.L. and Kimmel,B.E. Direct Submission Submitted (07-MAR-1998) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Jul 29, 1998 this sequence version replaced gi:3334971. Sequence submitted by: Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory, MS 64-121 Berkeley, CA 94720 For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send email to drosophila@hgsc.lbl.gov. Library location: 22-88.
		FEATURES	Location/Qualifiers 1..84551 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /chromosome="2R" /map="55C1-55C4" /clone="PI_DS08374 (D180)" BASE COUNT 22625 a 19310 c 19295 g 23321 t ORIGIN
OY	14	tctccatcctcccttcagctgctgttctcgacagcttgagggaactgatcgcg	33.1%; Score 28.8; DB 35; Length 84551;
OY	Db	6538 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGGGAACCACTCGG	Best Local Similarity 65.6%; Pred. No. 30;
OY	74	ggcg 6601	Mismatches 22; Indels 0; Gaps 0;

[illegible]

human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr22>. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep/IMPORTANT: This sequence is not the entire insert of clone XX-PRY7CC1 it may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. The true left end of clone XX-PRY7CC1 is at 1 in this sequence. The true left end of clone CRA-217C2 is at 119019 in this sequence. The true right end of clone RP4-753W9 is at 50597 in this sequence.

FEATURES

source

1. .119118
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
/clone="XX-PRY7CC1"
12. .3186
/note="Cpg Island"
/evidence="not_experimental"
77. .504
/note="214 copies 2 mer 9g 55 conserved"
111. .500
/note="15 copies 26 mer 56 conserved"
369. .488
/note="3 copies 40 mer 76 conserved"
1585. .1620
/note="6 copies 6 mer gtaggt 86 conserved"
2485. .2644
/note="4 copies 40 mer 70 conserved"
2527. .2598
/note="12 copies 6 mer cccccc 69 conserved"
2593. .2608
/note="Single clone region"
2647. .2659
/note="Single clone region"
2719. .2726
/note="Single clone region"
2744. .2817
/note="37 copies 2 mer cc 66 conserved"
3678. .3707
/note="15 copies 2 mer tt 90 conserved"
3936. .4249
/note="Alusg repeat: matches 1. .307 of consensus"
4418. .4542
/note="Alusg repeat: matches 1. .276 of consensus"
5264. .5329
/note="Alu/FRAM repeat: matches 152. .276 of consensus"
5999. .6097
/note="MIR repeat: matches 70. .172 of consensus"
6121. .6177
/note="MER94 repeat: matches 47. .107 of consensus"
6178. .6472
/note="Alusg repeat: matches 1. .295 of consensus"
6473. .6500
/note="MER94 repeat: matches 27. .47 of consensus"
6501. .6797
/note="Aluy repeat: matches 1. .297 of consensus"
7334. .7400
/note="MER21B repeat: matches 706. .789 of consensus"
7779. .7894
/note="MER2 repeat: matches 18. .132 of consensus"
7895. .7975

repeat_region
8005. .8080
/note="MIR repeat: matches 269. .343 of consensus"
8105. .8229
/note="Alusg/x repeat: matches 9. .133 of consensus"
8257. .8415
/note="Alu/FRAM repeat: matches 149. .304 of consensus"
8630. .8919
/note="Alu/Alu repeat: matches 13. .300 of consensus"
9266. .9580
/note="Alusg repeat: matches 5. .313 of consensus"
9714. .9845
/note="MIR repeat: matches 105. .262 of consensus"
9973. .10170
/note="MIR repeat: matches 34. .240 of consensus"
10270. .10480
/note="L1MA10 repeat: matches 6135. .6322 of consensus"
10481. .10735
/note="Alusg repeat: matches 57. .311 of consensus"
10736. .10821
/note="L1MA10 repeat: matches 6045. .6135 of consensus"
10871. .11171
/note="Alu/Alu repeat: matches 1. .303 of consensus"
11190. .11487
/note="Alusx repeat: matches 1. .298 of consensus"
11610. .11726
/note="MIR repeat: matches 13. .134 of consensus"
12322. .12636
/note="Alusx repeat: matches 1. .312 of consensus"
13016. .13133
/note="L2 repeat: matches 2616. .2748 of consensus"
13419. .13704
/note="143 copies 2 mer 9g 59 conserved"
13432. .13769
/note="13 copies 26 mer 57 conserved"
13878. .14208
/note="MIR repeat: matches 6. .368 of consensus"
14224. .14886
/note="L1PA10 repeat: matches 5476. .6165 of consensus"
14893. .15204
/note="Alusg repeat: matches 1. .312 of consensus"
15226. .15335
/note="Lrp3 repeat: matches 5336. .5465 of consensus"
15336. .15446
/note="MIR repeat: matches 355. .464 of consensus"
15484. .15777
/note="Alusg repeat: matches 1. .295 of consensus"
complement(15768. .16376)
/note="match: GSS: Em: A0476535"
16387. .16541
/note="MIR repeat: matches 73. .226 of consensus"
17071. .17122
/note="26 copies 2 mer aa 73 conserved"
17222. .17308
/note="L2 repeat: matches 2652. .2738 of consensus"
17452. .17487
/note="18 copies 2 mer tg 91 conserved"
17599. .17908
/note="Aluy repeat: matches 1. .310 of consensus"
18508. .18616
/note="L1PA6 repeat: matches 6035. .6143 of consensus"
18668. .18965
/note="Alusx repeat: matches 1. .298 of consensus"
19069. .19100
/note="MIR repeat: matches 692. .723 of consensus"
19494. .19849
/note="MIR repeat: matches 927. .1296 of consensus"
19869. .20149
/note="Alu/Alu repeat: matches 18. .288 of consensus"
20218. .20385
/note="MIR repeat: matches 1. .180 of consensus"

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0562105
----- Summary Statistics -----

```

1. : 183776
/organism="Homo sapiens"

FEATURES	Location/Qualifiers
source	1. .183776
	/organism="Homo sapiens"

ADHORS	ADHORS
DOE JOINT GENOME INSTITUTE.	DOE JOINT GENOME INSTITUTE.
Sequencing of Human Chromosome 19	Sequencing of Human Chromosome 19
TITLE	TITLE

	/note="match: GSS: Em:AQ342290.1; match: STS: Em:G58015.1
feature	8184. .8478
feature	/note="match: GSS: Em:AQ101900"
feature	11636. .11917
feature	/note="match: STS: Em:P05237"
feature	complement(12136. .12380)
feature	/note="match: STS: Em:P01490"
feature	17034. .17305
feature	/note="match: GSS: Em:AQ122350"
feature	complement(17175. .17672)
feature	/note="match: STS: Em:G28114; match: STS: Em:T91135"
feature	complement(17272. .17672)
feature	/note="match: STS: Em:G25929"
feature	complement(41270. .41845)
feature	/note="match: STS: Em:PA131878"
feature	complement(41285. .41846)
feature	/note="match: STS: Em:G23248"
feature	41498. .41706
feature	/note="match: STS: Em:"P90903"
feature	complement(46466. .46874)
feature	/note="match: STS: Em:AA437255"
feature	complement(50974. .51452)
feature	/note="match: GSS: Em:AQ587947.1"
feature	53812. .54273
feature	/note="match: GSS: Em:AQ223851"
feature	complement(54830. .55149)
feature	/note="match: GSS: Em:AQ039120"
feature	55156. .55504
feature	/note="match: GSS: Em:AQ022131"
feature	55156. .55631
feature	/note="match: GSS: Em:B93140"
feature	55156. .55566
feature	/note="match: GSS: Em:AQ135812"
feature	69199. .69703
feature	/note="match: GSS: Em:AQ118077"
feature	complement(70389. .70829)
feature	/note="match: STS: Em:AA774466"
feature	complement(74369. .74765)
feature	/note="match: GSS: Em:AQ184450"
feature	80516. .81048
feature	/note="match: GSS: Em:AQ767778.1"
feature	24639 a 20192 c 20337 g 25131 t
ch	32.4%; Score 28.2; DB 11; Length 90299;
1 Similarity	59.3%; Pred. No. 47;
48; Conservative	0; Mismatches 33; Indels 0; Gaps 0.
gttcagcgtctccatcctcctcctctcatgctctgtttctcgacagcttgcgggaacty 66 tttcgcagccttccaatgaa 87 TTTCCATCGAGTGGAATCAA 75589	
AC010485	187701 bp DNA HTG 14-JAN-2000
Homo sapiens chromosome 19 clone C17B-H1_2329C7, WORKING DRAFT	
AC010485	SEQUENCE
AC010485.2 GI:6693194	
HTG: HTGS_PHASE1; HTGS_DRAFT.	
human.	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 187701) XOE Joint Genome Institute.	
Sequencing of Human Chromosome 19	

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 211385)
JOURNAL SImS.S.
Direct Submission
Submitted (05-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Feb 16, 2000 this sequence version replaced gi:6912160.
REMARKS: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in
progress and the release of this data is based on the understanding
that the sequence may change as work continues. The sequence may
be contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Contig_ID: 00006 Length: 9572bp
Contig_ID: 00011 Length: 1016bp
Contig_ID: 00022 Length: 1557bp
Contig_ID: 00032 Length: 2972bp
Contig_ID: 00050 Length: 4358bp
Contig_ID: 00051 Length: 5737bp
Contig_ID: 00052 Length: 1925bp
Contig_ID: 00082 Length: 4685bp
Contig_ID: 00185 Length: 4360bp
Contig_ID: 00199 Length: 2863bp
Contig_ID: 00206 Length: 6154bp
Contig_ID: 00210 Length: 2440bp
Contig_ID: 00238 Length: 2803bp
Contig_ID: 00243 Length: 1982bp
Contig_ID: 00263 Length: 4711bp
Contig_ID: 00281 Length: 6857bp
Contig_ID: 00295 Length: 3004bp
Contig_ID: 00313 Length: 3422bp
Contig_ID: 00337 Length: 2375bp
Contig_ID: 00386 Length: 2333bp
Contig_ID: 00464 Length: 4205bp
Contig_ID: 00472 Length: 1855bp
Contig_ID: 00473 Length: 3313bp
Contig_ID: 00484 Length: 3603bp
Contig_ID: 00493 Length: 1719bp
Contig_ID: 00499 Length: 4386bp
Contig_ID: 00506 Length: 1451bp
Contig_ID: 00508 Length: 1159bp
Contig_ID: 00518 Length: 3841bp
Contig_ID: 00546 Length: 1753bp
Contig_ID: 00549 Length: 3386bp
Contig_ID: 00550 Length: 1984bp
Contig_ID: 00551 Length: 2333bp
Contig_ID: 00564 Length: 3705bp
Contig_ID: 00580 Length: 4685bp
Contig_ID: 00581 Length: 3614bp
Contig_ID: 00621 Length: 6142bp
Contig_ID: 00649 Length: 4868bp
Contig_ID: 00651 Length: 3054bp
Contig_ID: 00654 Length: 1455bp
Contig_ID: 00666 Length: 1855bp
Contig_ID: 00726 Length: 2320bp
Contig_ID: 00737 Length: 4142bp
Contig_ID: 00774 Length: 3880bp
Contig_ID: 00876 Length: 2731bp
Contig_ID: 00889 Length: 3553bp
Contig_ID: 00906 Length: 9950bp
Contig_ID: 00916 Length: 2452bp
Contig_ID: 00955 Length: 1319bp
Contig_ID: 00955 Length: 2346bp.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
* be preserved. 9572: contig of 9572 bp in length
* 1
* 9573 10372: gap of 800 bp
* 10373 11388: contig of 1016 bp in length
* 11389 12188: gap of 800 bp
* 12189 13745: contig of 1557 bp in length
* 13746 14545: gap of 800 bp
* 14546 17517: contig of 2972 bp in length
* 17518 18317: gap of 800 bp
* 18318 22675: contig of 4358 bp in length
* 22676 23475: gap of 800 bp
* 23476 29212: contig of 5737 bp in length
* 29213 30012: gap of 800 bp
* 30013 31937: contig of 1925 bp in length
* 31938 32737: gap of 800 bp
* 32738 37422: contig of 4685 bp in length
* 37423 38222: gap of 800 bp
* 38223 42582: contig of 4360 bp in length
* 42583 43382: gap of 800 bp
* 43383 45245: contig of 2863 bp in length
* 45246 47045: gap of 800 bp
* 47046 53199: contig of 6154 bp in length
* 53200 53999: gap of 800 bp
* 54000 56439: contig of 2440 bp in length
* 56440 57239: gap of 800 bp
* 57240 60042: contig of 2803 bp in length
* 60043 60842: gap of 800 bp
* 60843 62824: contig of 1982 bp in length
* 62825 63624: gap of 800 bp
* 63625 68335: contig of 4711 bp in length
* 68336 69135: gap of 800 bp
* 69136 75992: contig of 6857 bp in length
* 75993 76792: gap of 800 bp
* 76793 79796: contig of 3004 bp in length
* 79797 80596: gap of 800 bp
* 80597 84018: contig of 3422 bp in length
* 84019 84818: gap of 800 bp
* 84819 87193: contig of 2375 bp in length
* 87194 87993: gap of 800 bp
* 87994 90326: contig of 2333 bp in length
* 90327 91126: gap of 800 bp
* 91127 95331: contig of 4205 bp in length
* 95332 96131: gap of 800 bp
* 96132 97986: contig of 1855 bp in length
* 97987 98786: gap of 800 bp
* 98787 102099: contig of 3313 bp in length
* 102100 102899: gap of 800 bp
* 102900 106502: contig of 3603 bp in length
* 106503 107302: gap of 800 bp
* 107303 109021: contig of 1719 bp in length
* 109022 109821: gap of 800 bp
* 109822 114207: contig of 4386 bp in length
* 114208 115007: gap of 800 bp
* 115008 116458: contig of 1451 bp in length
* 116459 117258: gap of 800 bp
* 117259 118417: contig of 1159 bp in length
* 118418 119217: gap of 800 bp
* 119218 123058: contig of 3841 bp in length
* 123059 123858: gap of 800 bp
* 123859 125613: contig of 1755 bp in length
* 125614 126413: gap of 800 bp
* 126414 129799: contig of 3386 bp in length
* 129800 130599: gap of 800 bp
* 130600 132583: contig of 1984 bp in length
* 132584 133383: gap of 800 bp
* 133384 135715: contig of 2332 bp in length
* 135716 136515: gap of 800 bp
* 136516 140220: contig of 3705 bp in length
* 140221 141020: gap of 800 bp
* 141021 145705: contig of 4685 bp in length
* 145706 146505: gap of 800 bp
* 146506 150119: contig of 3614 bp in length

* 38841 40042: contig of 1202 bp in length gap of unknown length
* 40043 41631: contig of 1589 bp in length gap of unknown length
* 41632 42937: contig of 1306 bp in length gap of unknown length
* 42938 44046: contig of 1109 bp in length gap of unknown length
* 44047 45451: contig of 1405 bp in length gap of unknown length
* 45452 47075: contig of 1624 bp in length gap of unknown length
* 47076 48875: contig of 1800 bp in length gap of unknown length
* 48876 50620: contig of 1745 bp in length gap of unknown length
* 50621 51956: contig of 1336 bp in length gap of unknown length
* 51957 53979: contig of 2023 bp in length gap of unknown length
* 53980 55408: contig of 1429 bp in length gap of unknown length
* 55409 56518: contig of 1110 bp in length gap of unknown length
* 56519 57895: contig of 1377 bp in length gap of unknown length
* 57896 59316: contig of 1421 bp in length gap of unknown length
* 59317 60803: contig of 1487 bp in length gap of unknown length
* 60804 62554: contig of 1751 bp in length gap of unknown length
* 62555 64100: contig of 1546 bp in length gap of unknown length
* 64101 66567: contig of 2467 bp in length gap of unknown length
* 66568 68184: contig of 1617 bp in length gap of unknown length
* 68185 70971: contig of 2787 bp in length gap of unknown length
* 70972 73787: contig of 2816 bp in length gap of unknown length
* 73788 76676: contig of 2889 bp in length gap of unknown length
* 76677 84224: contig of 7548 bp in length gap of unknown length
* 84225 98029: contig of 13805 bp in length gap of unknown length
* 98030 110318: contig of 12289 bp in length gap of unknown length
* 110319 119812: contig of 9494 bp in length gap of unknown length
* 119813 136488: contig of 16676 bp in length gap of unknown length
* 136489 150409: contig of 13921 bp in length gap of unknown length
* 150410 169220: contig of 18811 bp in length gap of unknown length
* 169221 197236: contig of 28016 bp in length gap of unknown length
* 197237 219772: contig of 22536 bp in length gap of unknown length
* 219773 247056: contig of 27284 bp in length gap of unknown length
* 247057 307834: contig of 60778 bp in length gap of unknown length
* Location/Qualifiers
* 1..307834
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="5"
* /clone="CITB-HI_2308B20"
* 87825 a 67908 c 67457 g 84063 t 581 others

ORIGIN

Query Match

Best Local Similarity 32.4%; Score 28.2; DB 44; Length 307834;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY

8 gtcagctctccatccctccctctcagctgctctcgcagagcttcggggaactga 67

Db 297411 GACAGCTTCCTCTCCCTCTCCCTCCAGCCTGCTGCTTCATACAGATTCGGGGCCATT 297352

QY

68 ttcgcagccttc 80

Db 297351 TCCCGCAGGATTC 297339

Search completed: May 15, 2000, 11:43:02
Job time: 18609 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 11:20:15 ; Search time 1358.94 Seconds
(without alignments)
196.854 Million cell updates/sec

Title: US-09-104-340-7

Perfect score: 66
Sequence: 1 gtcacatctactgattcaaa.....tctcttaccatcacatgag 66

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*

45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_est45:*
80: gb_est46:*
81: gb_est47:*
82: gb_gss1:*
83: gb_gss2:*
84: gb_gss3:*
85: gb_gss4:*
86: em_gss1:*
87: em_gss2:*
88: em_gss3:*
89: em_gss4:*
90: gb_gss5:*
91: gb_gss6:*
92: gb_gss7:*
93: gb_gss8:*
94: gb_gss9:*
95: em_gss5:*
96: em_gss6:*
97: em_gss7:*
98: em_gss8:*
99: em_gss9:*
100: em_gss10:*
101: em_gss11:*
102: gb_gss10:*
103: gb_gss11:*
104: em_gss12:*
105: gb_gss12:*
106: gb_gss13:*
107: gb_gss14:*
108: gb_gss15:*
109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result

Query

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	66	100.0	435	23	H38363	H38363 yps0g04.r1
2	30	45.5	306	33	AA586761	AA586761 n71c10.s
3	27.2	41.2	487	22	R62432	R62432 y952e11.s1
4	26.4	40.0	252	25	N87424	N87424 l3865f.Huma
5	26.2	39.7	835	69	AU080921	AU080921 AU080921
6	26	39.4	254	59	AV080438	AV080438 AV080438
7	25.8	39.1	341	28	AA125015	AA125015 mg73c06.r
8	25.8	39.1	364	20	AA212205	AA212205 mg80b06.r
9	25.8	39.1	394	25	AQ38519	AQ38519 HS_3118_B
10	25.8	39.1	416	26	W30350	W30350 mc25e10.r1
11	25.8	39.1	426	37	AA726779	AA726779 v042f03.r
12	25.8	39.1	434	34	AA103674	AA103674 mc40c10.r
13	25.8	39.1	438	34	AA466804	AA466804 v090g11.r
14	25.8	39.1	497	27	AA000659	AA000659 mg26a04.r
15	25.8	39.1	505	38	AA762271	AA762271 v060g01.r
16	25.8	39.1	551	28	AA123801	AA123801 mp96d07.r
17	25.2	38.2	462	107	AQ433555	AQ433555 HS_5060_A
18	25	37.9	567	108	AQ572153	AQ572153 HS_2108_B
19	24.8	37.6	361	41	AU016229	AU016229 AU016229
20	24.8	37.6	382	79	AW261956	AW261956 xq29d10.x
21	24.8	37.6	424	85	AQ718452	AQ718452 HS_5516_B
22	24.8	37.6	479	79	AW261950	AW261950 xq29c10.x
23	24.8	37.6	509	49	A1655503	A1655503 t13e07.x
24	24.8	37.6	534	49	A1655522	A1655522 t13e07.x
25	24.8	37.6	537	49	A1652683	A1652683 wb30e10.x
26	24.8	37.6	551	108	AQ541860	AQ541860 RPCI-11-3
27	24.6	37.3	235	73	AV345313	AV345313 AV345313
28	24.6	37.3	398	108	AQ522265	AQ522265 HS_5200_A
29	24.6	37.3	663	109	AO656077	AO656077 Sheared D
30	24.4	37.0	467	23	H17411	H17411 ym40c11.s1
31	24.2	36.7	191	49	A1645503	A1645503 v191h11.x
32	24.2	36.7	253	37	AA720125	AA720125 33318.Lam
33	24.2	36.7	461	91	AQ0861085	AQ0861085 nbcb0016E
34	24.2	36.7	487	34	A1195110	A1195110 u160g06.x
35	24.2	36.7	497	23	H55902	H55902 y702c08.s1
36	24	36.4	501	27	AA038832	AA038832 m155912.r
37	24	36.4	628	41	A1003549	A1003549 a18a09.s
38	23.8	36.1	269	32	AA376236	AA376236 EST8631
39	23.8	36.1	276	69	AV214670	AV214670 AV214670
40	23.8	36.1	440	24	H69538	H69538 y789c05.s1
41	23.8	36.1	461	25	N80340	N80340 y791n06.r1
42	23.8	36.1	535	109	AQ655614	AQ655614 Sheared D
43	23.8	36.1	536	85	AQ708302	AQ708302 HS_5569_A
44	23.8	36.1	565	24	N38130	N38130 19357.Lambda
45	23.8	36.1	733	62	AU077466	AU077466 AU077466

ALIGNMENTS

RESULT	1	435 bp	EST	16-AUG-1995
H38363	yp50g04.r1	Soares	retina N2b4HR	Homo sapiens
LOCUS	IMAGE:190902.5	similar to gb:M83941	TYROSINE-PROTEIN KINASE	
DEFINITION	RECEPTOR HEK PRECURSOR (HUMAN);	mRNA sequence.		
ACCESSION	H38363			
VERSION	H38363.1	GI:907862		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
AUTHORS	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
	Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,			
	Holman, M., Hultman, M., Kucuba, T., Le, M., Lennon, G., Marra, M.,			
	Paterson, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,			
	Tevaklis, E., Waterston, R., Williamson, A., Wohlmann, P., and			
	Wilson, R.			
TITLE	The MashU-Merck EST Project			
JOURNAL	Unpublished (1995)			

COMMENT

On May 5, 1995 this sequence version replaced gi:797807.
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Insert Size: 2663
 High quality sequence stops: 276
 Source: IMAGE Consortium, LNLN.
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.lnl.nyu.edu) for further information.
 Insert Length: 2663 Std Error: 0.00
 Seq primer: M13rev
 High quality sequence stop: 276.
 Location/Qualifiers
 1. 435

FEATURES

source
 /organism="Homo sapiens"
 /db_xref="GDB:3847311"
 /db_xref="taxon:9606"
 /clone="IMAGE:190902"
 /clone_1lb="Soares retina N2b4HR"
 /sex="male"
 /tissue="retina"
 /dev_stage="55 year old"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: eye; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGCGCGCGCTTTTCTTTTCTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). The retinas were obtained from a 55 year old
 Caucasian and total cellular poly(A)+ RNA was extracted 6
 hrs after their removal. The retina RNA was kindly
 provided by Roderick R. McInnes M.D. Ph.D. from the
 University of Toronto. Library constructed by Bento
 Soares and M.Fatima Bonaldo."

BASE COUNT

109 a 108 c 103 g 109 t 6 others

Query Match 100.0%; Score 66; DB 23; Length 435;
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	gtcaatctactggtatccaataaagggagctgggctgtatcttaccatca	60
DB	154	gtcaatctactggtatccaataaagggagctgggctgtatcttaccatca	213
OY	61	catggg	66
DB	214	catggg	219

RESULT	2	306 bp	EST	12-SEP-1997
AA586761/c	n71c10.s1	NCI-CGAP-Lar1	Homo sapiens	CDNA clone IMAGE:1089330.3'
LOCUS	AA586761			
DEFINITION	mRNA sequence.			
ACCESSION	AA586761			
VERSION	AA586761.1	GI:2397575		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
AUTHORS	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
JOURNAL	Tumor Gene Index			
	Unpublished (1997)			

COMMENT

On Nov 29, 1993 this sequence version replaced g1:430058.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
 Emmer-Buck, M.D., Ph.D.
 CDNA Library Preparation: Strategene, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www-bio.linn.gov/bdip/image/image.html

Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 298.

FEATURES

SOURCE

1.306
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1089330"
 /clone_lib="NCI CGAP Jar1"
 /tissue_type="larynx"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: larynx; Vector: Bluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
 011go dt. larynx. 5' adaptor sequence: 5' GATTTCGGCAGCAG
 3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
 Average insert size: 0.9 kb."
 93 a 77 c 62 g 74 t

BASE COUNT

93 a 77 c 62 g 74 t

Query Match

Best Local Similarity 45.5%; Score 30; DB 35; Length 306;
 Matches 39; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db

13 gattcaaaacatccaagggagctggctgagctctatccatccatcg 66
 237 GATCAACAACCATCTCTGGGGCTGAGACTGTCCTTTCCATACATG 184

RESULT 3

R62432 487 bp mRNA EST 26-MAY-1995
 LOCUS R62432
 DEFINITION Y652e11.s1 Soares infant brain INIB Homo sapiens CDNA clone
 IMAGE:36023 3', mRNA sequence.

ACCESSION R62432
 VERSION R62432.1 GI:834311
 KEYWORDS EST.

SOURCE

ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 487)
 Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevaekis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.

The WashU-Merck EST Project
 Unpublished (1995)
 On May 9, 1995 this sequence version replaced g1:804377.
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Insert Size: 2443

TITLE

JOURNAL

COMMENT

High quality sequence stops: 337 Source: IMAGE Consortium, LINL This
 clone is available royalty-free through LINL; contact the IMAGE
 Consortium (info@image.linn.gov) for further information.
 Insert Length: 2443 Std Error: 0.00

FEATURES

Seq primer: Promege -21ml3
 High quality sequence stop: 337.
 Location/Qualifiers
 1.487
 /organism="Homo sapiens"
 /db_xref="GDB:408524"
 /db_xref="taxon:9606"
 /clone="IMAGE:36023"
 /clone_lib="Soares infant brain INIB"
 /sex="female"
 /dev_stage="73 days post natal"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: whole brain; Vector: lafmid BA; Site_1: Not
 I; Site_2: Hind III; 1st strand CDNA was primed with a Not
 I - oligo(dt) primer [5';
 ACTCGAGAGATTGCGCGCCGCGAGAAATTTTTTTTTTTTTTTT 3'];
 double-stranded CDNA was ligated to Hind III adaptors
 (Pharmacia), digested with Not I and directionally cloned
 into the Not I and Hind III sites of the lafmid BA vector.
 Library went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

144 a 88 c 108 g 140 t 7 others

ORIGIN

Query Match 41.2%; Score 27.2; DB 22; Length 487;
 Best Local Similarity 67.9%; Pred. No. 5.8;
 Matches 38; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

4 aatctactggaattcaaacatccaagggagctggctgagctctatccatc 59
 332 AATCCACAGTTTTCATTAATTAACAGTGAACAGAGCTGGTGTCTTCAC 387

RESULT 4

N87424 252 bp mRNA EST 01-APR-1996
 LOCUS N87424
 DEFINITION L3865F Human fetal heart, Lambda ZAP Express Homo sapiens CDNA
 clone L3865 5' similar to RECEPTOR PROTEIN-TYROSINE KINASE (HER11),
 mRNA sequence.

ACCESSION N87424
 VERSION N87424.1 GI:1440626
 KEYWORDS EST.

SOURCE

ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 252)
 Liew C.C.

CDNAs from fetal heart (1996)
 Unpublished (1996)
 On May 9, 1995 this sequence version replaced g1:802248.
 Contact: Liew CC
 Department of Laboratory Medicine and Pathobiology
 University of Toronto
 Bantling Institute, 100 College St., Toronto, Ontario, M5G1L5
 Tel: 416/9788758
 Fax: 416/9785650
 Email: liewc@utcc.utoronto.ca

TITLE

JOURNAL

COMMENT

Seq primer: GAATTAACCTCTACATAAGG.
 Location/Qualifiers
 1.252

FEATURES

SOURCE

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="L3865"
 /clone_lib="Human fetal heart, Lambda ZAP Express"
 /lab_host="E. coli XL1-Blue"
 /note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
 XhoI; mRNA was purified from human fetal hearts (8-10
 weeks). CDNA was synthesized using a XhoI-011go dt
 adaptor-primer. EcoRI adaptors were ligated, followed by
 digestion with XhoI, for directional cloning into
 predigested lambda ZAP Express."

[illegible]

TITLE	The WashU-HHMI Mouse EST Project			
JOURNAL	Unpublished (1996)			
COMMENT	On Sep 12, 1996 this sequence version replaced g1.129758. Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:359010 Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 234. Location/Qualifiers 1. 341 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:584362" /clone_lib="Stratagene mouse melanoma (#937312)" /tissue_type="melanoma" /dev_stage="M2 cells" /lab_host="SOLR (kanamycin resistant)" /note="Organ: skin; Vector: pBluescript SK-; site_1: EcoRI; site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. From M2 cells, a highly metastatic derivative of the K-1735 (mouse) melanoma. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGACGAG 3' -3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3' "			
BASE COUNT	73 a	95 c	88 g	85 t
ORIGIN				
Query Match	39.1%;	Score 25.8;	DB 28;	Length 341;
Best Local Similarity	63.9%;	Pred. No. 19;		
Matches	39;	Conservative	0;	Mismatches 22; Indels 0; Gaps 0;
Oy	6	tctactgattcaaaacaattcaagggagctggcgctgatactcttatccatcagatg	65	
Db	75	tctactgattcactacacacaaagggggctggcgctgatactcttatccatcagatg	16	
Oy	66 g	66		
Db	15 G	15		
RESULT	8			
AA212205/c				
DEFINITION	AA212205 364 bp mRNA EST 31-JAN-1997			
LOCUS	mus0b06.r1 Stratagene mouse melanoma (#937312) Mus musculus cDNA			
CLONE IMAGE:51827 5'	similar to TR.G1184951 G1184951			
PHOSPHOTYROSINE INDEPENDENT LIGAND P62B FOR THE LCK SH2 DOMAIN				
B-CELL ISOFORM ; mRNA sequence.				
AA212205				
AA212205.1	GI:1810850			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 364) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. The WashU-HHMI Mouse EST Project			

JOURNAL Unpublished (1996)
On May 18, 1995 this sequence version replaced g1:811160.
COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNT; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:397675
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 287.

FEATURES
Source
Location/Organism
1..364
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:651827"
/clone_lib="Stratagene mouse melanoma (#937312)"
/tissue_type="melanoma"
/dev_stage="M2 cells"
/lab_host="SOLR (Kanamycin resistant)"
/note="Organ: skin; Vector: plusscript SK-; Site: 1;
ECORI: Site_2: XhoI: Cloned unidirectionally. Primer:
Oligo dt. From M2 cells; a highly metastatic derivative of
the K-1735 (mouse) melanoma. Average insert size: 1.0 kb;
Uni-ZAP XR vector: -5' adaptor sequence: 5' GAATTCGGCAGCGAG
3'-3' adaptor sequence: 5' CTCGAGTTTCTTTTTTTTTTTT 3'"

BASE COUNT 80 a 92 c 101 g 91 t

ORIGIN

Query Match 39.1%; Score 25.8; DB 30; Length 364;
Best Local Similarity 63.9%; Pred. No. 19;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Oy 6 ttctactgattcaaaaacaattcaaggaggctggcgtgatcttcattcatcacatg 65
||||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db 197 TCTACGTGATCAACTACACAAAGAGGGGTGGCTTGCCACAGCATCATGCANTG 138

Oy 66 g 66
|
Db 137 G 137

RESULT 9
A0338519 394 bp DNA GSS 12-JAN-1999
LOCUS A0338519 HS-3118_B1.C10_MR_CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=1118 Col=19 Row=F, genomic survey
sequence.
ACCESSION A0338519
VERSION A0338519.1 GI:4144535
KEYWORDS GGS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 394)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 3118 row: F column: 19
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence stop: 394.

FEATURES

source

1. .394
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="plate=3118 Col-19 Row=F"
 /clone_1lb="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 87 a 115 c 97 g 95 t
 ORIGIN

Query Match 39.1%; Score 25.8; DB 105; Length 394;
 Best Local Similarity 63.9%; Pred. No. 19;
 Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 5 atctactcgattcaaaacattcaaggagcgtggtgattcttattcattcatg 64
 Db 98 ATGTGTTGAACACACACACACACCGTGTGTGCTGTGATCCCTGCTGTGCCCTG 157

Qy 65 g 65
 Db 158 G 158

RESULT 10
 W30350/c 416 bp mRNA EST 11-SEP-1996
 LOCUS
 DEFINITION MC25510.1 r1 Soares mouse p3NM19.5 Mus musculus cDNA clone
 IMAGE:349578 5' similar to PIR:533561 S33561 ref(2) p protein -
 fruit fly ; mRNA sequence.

ACCESSION W30350
 VERSION W30350.1 GI:1310500
 KEYWORDS EST.

SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 416)
 AUTHORS Maira, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Apr 14, 1993 this sequence version replaced gl:692855.
 Contact: Maira M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:221378
 putative full length read
 Seq primer: E7primer
 High quality sequence stop: 414.

FEATURES

source

1. .416
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:349578"

/clone_1lb="Soares mouse p3NM19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pT7n3D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAGTGGAGCGGCGGCAATTTTTTTTTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7n3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."

BASE COUNT 86 a 111 c 115 g 104 t
 ORIGIN

Query Match 39.1%; Score 25.8; DB 26; Length 416;
 Best Local Similarity 63.9%; Pred. No. 19;
 Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 6 tctacttgattcaaaacattcaaggagcgtggtgattcttattcattcatg 65
 Db 213 TCTACGTGATGCACTACAGACAAAGGGGTGGCTTGCCACAGCACTATCACAAATG 154

Qy 66 g 66
 Db 153 G 153

RESULT 11
 AA726779 426 bp mRNA EST 02-JAN-1998
 LOCUS
 DEFINITION vU42f03.r1 Barstead mouse myotubes MRLB5 Mus musculus cDNA clone
 IMAGE:1194077 5' similar to TR:Q13502 Q13502 PHOSPHOTRISOME
 INDEPENDENT LIGAND P62B FOR THE LCK SH2 DOMAIN B-CELL ISOFORM ;
 mRNA sequence.

ACCESSION AA726779
 VERSION AA726779.1 GI:2744486
 KEYWORDS EST.

SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 426)
 AUTHORS Maira, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On May 5, 1995 this sequence version replaced gl:797862.
 Contact: Maira M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:641173
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 419.

FEATURES

source

1. .426
 /organism="Mus musculus"
 /strain="C3H"
 /db_xref="taxon:10090"
 /clone="IMAGE:1194077"
 /clone_1lb="Barstead mouse myotubes MRLB5"


```

/cell_line="C2C12"
/lab_host="DH10B"
/notes="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTGAAGTGGAGCGCCGCCCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AAATCGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT73 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."
BASE COUNT      99 a      115 c      109 g      103 t
ORIGIN

Query Match      39.1%; Score 25.8; DB 37; Length 426;
Best Local Similarity 63.9%; Pred. No. 19;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 6 tctactgattcaaaacattcaaggagctggcgtgcatctctatccatcatg 65
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 202 TCTATGATGATGCACTACACAGACAAAGGGGGTGGGGCTGTCTCCACAGCATCTACAAAG 143
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 66 g 66
DB 142 G 142

RESULT 12
AA103674/c
LOCUS      AA103674      434 bp      mRNA      EST      29-OCT-1996
DEFINITION m040c10.x1 l1a6 Tech mouse embryo 15 5dpc 10667012 Mus musculus
CDNA clone IMAGE:556050 5' similar to TR:G1184951 G1184951
PHOSPHORYLOSINE INDEPENDENT LIGAND PE2B FOR THE LCK SH2 DOMAIN
B-CELL ISOFORM ; mRNA sequence.
ACCESSION  AA103674
VERSION     AA103674.1 GI:1649894
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 434)
AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucab,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelsting,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE       The WashU-HMI Mouse EST Project
JOURNAL     Unpublished (1996)
COMMENT     On Nov 29, 1993 this sequence version replaced gi:430261.
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LIND ; contact the
IMAGE Consortium (info@image.lind.gov) for further information.
MGI:336842
Seq primer: -28M13 rev1 from Amersham
High quality sequence stop: 416.
Location/Qualifiers
1..434
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:556050"
/clone_1ib="l1a6 Tech mouse embryo 15 5dpc 10667012"
/tissue_type="embryo"

```

BASE COUNT	101 a	108 c	120 g	105 t	
ORIGIN					
Query Match	39.1%	Score 25.8;	DB 28;	Length 434;	
Best Local Similarity	63.9%;	Pred. No. 19;			
Matches 39;	Conservative 0;	Mismatches 22;	Indels 0;	Gaps 0;	
OY	6	tctactgattccaaacaaatccaagggagctggcgctgcgattcttccatcacatgg	65		
Db	268	TCCTAGTATGATCACTACACAGCAAAAGGGGGTGGGGCTGGCCACAGCATATCACAATG	209		
OY	66 g	1			
Db	208	G	208		
RESULT 13	AA466804/c				
LOCUS	AA466804	438 bp	mRNA	EST	11-JUN-1997
DEFINITION	v380g11.1 Soares mouse NBMH Mus musculus cDNA clone IMAGE:807908				
	5' similar to TR:G1184951 G1184951 PHOSPHORYROSINE INDEPENDENT				
ACCESSION	LIGAND PC2B FOR THE LCR SH2 DOMAIN B-CELL ISOFORM ; mRNA sequence.				
VERSION	AA466804				
KEYWORDS	AA466804.1	GI:2192944			
SOURCE	EST.				
ORGANISM	house mouse.				
	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 438)				
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,				
	Geisel,S., Kucada,T., Lacy,M., Le,M., Martin,J., Morris,M.,				
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,				
	Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and				
	Waterston,R.				
	The WashU-HHMI Mouse EST Project				
TITLE	Unpublished (1996)				
JOURNAL	On Jan 23, 1995 this sequence version replaced gi:637879.				
COMMENT	Contact: Marra M/Mouse EST Project				
	WashU-HHMI Mouse EST Project				
	Washington University School of Medicine				
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
	Tel: 314 286 1800				
	Fax: 314 286 1810				
	Email: mouseest@watson.wustl.edu				
	This clone is available royalty-free through LNL ; contact the				
	IMAGE Consortium (info@image.llnl.gov) for further information.				
	MG:44252				
	Putative full length read				
	vector to vector length is 511				
	Seq primer: -28ml3 rev2 ET from Amersham				
	High quality sequence stop: 409.				
FEATURES	location/Qualifiers				
SOURCE	1..438				
	/organism="Mus musculus"				
	/strain="C57BL/6J"				
	/db_xref="taxon:10090"				
	/clone="IMAGE:807908"				
	/clone_lib="Soares mouse NBMH"				
	/sex="male"				
	/tissue_type="heart"				
	/dev_stage="4 weeks"				
	/lab_host="DH10B"				
	/note="Vector: pRT3D-Pac (Pharmacia) with a modified				
	polylinker; site_1: Not I; site_2: Eco RI; 1st strand cDNA				
	was primed with a Not I - oligo(dt) primer [5'				
	TGTTACCAATCTGAAGTGGAGCGCCGCAAAAGTTTTTTTTTTTTTTTTTTTT				

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 12:05:03 ; Search time 102.62 seconds
(without alignments)
81.662 Million cell updates/sec

Title: US-09-104-340-7
Perfect score: 66
Sequence: 1 gtcaatctactggtatcaca.....tctctatcatcatcatggy 66

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 226296 seqs, 63486255 residues

Total number of hits satisfying chosen parameters: 452592

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/2/1na/5C.COMB.seq:*
- 4: /cgn2_6/ptodata/2/1na/5D.COMB.seq:*
- 5: /cgn2_6/ptodata/2/1na/6.COMB.seq:*
- 6: /cgn2_6/ptodata/2/1na/PT05.COMB.seq:*
- 7: /cgn2_6/ptodata/2/1na/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	3132	1 US-08-167-919A-9	Sequence 9, Appl1
2	66	100.0	3132	5 US-08-715-106-9	Sequence 9, Appl1
3	59.6	90.3	3254	1 US-08-162-809-15	Sequence 15, Appl1
4	34	51.5	3162	4 US-08-449-645A-12	Sequence 12, Appl1
5	34	51.5	3162	4 US-08-702-367A-12	Sequence 12, Appl1
6	34	51.5	3162	6 PCT-US95-04681-12	Sequence 12, Appl1
7	31.2	47.3	4529	4 US-08-449-645A-16	Sequence 16, Appl1
8	31.2	47.3	4529	4 US-08-702-367A-16	Sequence 16, Appl1
9	31.2	47.3	4529	6 PCT-US95-04681-16	Sequence 16, Appl1
10	29.2	44.2	3906	3 US-08-469-537A-102	Sequence 102, App
11	29.2	44.2	4165	2 US-08-440-248-1	Sequence 1, Appl1
12	29.2	44.2	4165	2 US-08-440-815-1	Sequence 1, Appl1
13	27	40.9	2323	6 PCT-US96-00419-6	Sequence 6, Appl1
14	27	40.9	2901	6 PCT-US96-00419-4	Sequence 4, Appl1
15	27	40.9	4304	6 PCT-US96-00419-1	Sequence 1, Appl1
16	26	39.4	4322	1 US-08-673-789-1	Sequence 1, Appl1
17	25.8	39.1	2005	1 US-08-208-108-1	Sequence 1, Appl1
18	23.2	35.2	2962	4 US-08-449-645A-10	Sequence 10, Appl1
19	23.2	35.2	2962	4 US-08-702-367A-10	Sequence 10, Appl1
20	23.2	35.2	2962	6 PCT-US95-04681-10	Sequence 10, Appl1
21	23	34.8	3116	4 US-08-449-645A-14	Sequence 14, Appl1
22	23	34.8	3116	4 US-08-702-367A-14	Sequence 14, Appl1
23	23	34.8	3116	6 PCT-US95-04681-14	Sequence 14, Appl1
24	23	34.8	3116	6 PCT-US95-04681-34	Sequence 34, Appl1
25	23	34.8	3348	6 PCT-US95-04228-34	Sequence 34, Appl1
26	22.2	33.6	3592	3 US-08-469-537A-100	Sequence 100, App
27	22.2	33.6	7286	6 PCT-US95-11684-1	Sequence 1, Appl1

28	21.8	33.0	867	2 US-08-368-852-14	Sequence 14, Appl1
29	21.8	33.0	867	3 US-08-525-940-14	Sequence 14, Appl1
30	21.8	33.0	867	4 US-08-976-838-14	Sequence 14, Appl1
31	21.8	33.0	2397	3 US-08-525-940-22	Sequence 22, Appl1
32	21.8	33.0	2397	4 US-08-976-838-22	Sequence 22, Appl1
33	21.8	33.0	2643	3 US-08-525-940-20	Sequence 20, Appl1
34	21.8	33.0	2643	4 US-08-976-838-20	Sequence 20, Appl1
35	21.8	33.0	2745	3 US-08-525-940-19	Sequence 19, Appl1
36	21.8	33.0	2745	4 US-08-976-838-19	Sequence 19, Appl1
37	21.8	33.0	2766	3 US-08-525-940-17	Sequence 17, Appl1
38	21.8	33.0	2766	4 US-08-976-838-17	Sequence 17, Appl1
39	21.8	33.0	2766	4 US-08-976-838-28	Sequence 28, Appl1
c	39	21.6	3776	1 US-08-162-809-7	Sequence 7, Appl1
41	21.6	32.7	4049	1 US-08-162-809-17	Sequence 17, Appl1
42	21.6	32.7	4097	1 US-08-162-809-11	Sequence 11, Appl1
43	21.4	32.4	372	1 US-08-442-542-5	Sequence 5, Appl1
44	21.4	32.4	420	3 US-08-449-287-3	Sequence 3, Appl1
45	21.4	32.4	777	4 US-08-860-882A-25	Sequence 25, Appl1

ALIGNMENTS

RESULT 1
US-08-167-919A-9
: Sequence 9, Application US/08167919A
: Patent No. 5674691
: GENERAL INFORMATION:
: APPLICANT: Boyd, Andrew W.
: APPLICANT: Simpson, Richard J.
: APPLICANT: Wicks, Ian
: APPLICANT: Ward, Larry D.
: APPLICANT: Wilkinson, David
: TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
: TITLE OF INVENTION: AND USE THEREOF
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Scully, Scott, Murphy & Presser
: STREET: 400 Garden City Plaza
: CITY: Garden City
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 11530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/167,919A
: FILING DATE: 18-APR-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PK6841 (AU)
: FILING DATE: 21-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PK9992 (AU)
: FILING DATE: 12-DEC-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/AU92/00294
: FILING DATE: 19-JUN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Digilio, Frank S.
: REGISTRATION NUMBER: 31,346
: REFERENCE/DOCKET NUMBER: 9159
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (516) 742-4343
: TELEFAX: (516) 742-4366
: TELEX: 230 901 SAMS UR
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3132 base pairs
: TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..3048
US-08-167-919A-9

Query Match 100.0%; Score 66; DB 1; Length 3132;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcacatctctggtatcaaaacaattcaaggagctggctgtatcttcatcatca 60
|||||
DB 187 gtcacatctctggtatcaaaacaattcaaggagctggctgtatcttcatcatca 246
QY 61 catggg 66
|||||
DB 247 CATGGG 252

RESULT 2

US-08-715-106-9
Sequence 9, Application US/08715106
Patent No. 6020306
GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK6992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGILIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..3048
US-08-715-106-9

Query Match 100.0%; Score 66; DB 5; Length 3132;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcacatctctggtatcaaaacaattcaaggagctggctgtatcttcatcatca 60
|||||
DB 187 gtcacatctctggtatcaaaacaattcaaggagctggctgtatcttcatcatca 246
QY 61 catggg 66
|||||
DB 247 CATGGG 252

RESULT 3

US-08-162-809-15
Sequence 15, Application US/08162809
Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjad, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3254 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 32..2980
US-08-162-809-15

Query Match 90.3%; Score 59.6; DB 1; Length 3254;
Best Local Similarity 93.9%; Pred. No. 4.4e-14;
Matches 62; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 gtcacatctctggtatcaaaacaattcaaggagctggctgtatcttcatcatca 60

Db 116 GTTATCTGCTGATCAAAAACATTCAGGGAGCTGGCTGATCTCCACCATCA 175
QY 61 catggg 66
Db 176 CATGGG 181

RESULT 4

US-08-449-645A-12
; Sequence 12, Application US/08449645A
; Patent No. 5981245
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; NUMBER OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,645A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2976
US-08-449-645A-12

Query Match 51.5%; Score 34; DB 4; Length 3162;
Best Local Similarity 69.7%; Pred. No. 0.00031;
Matches 46; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 gtcaactcactgagtcacaaacaaatcaaggagagctggagctctatccatca 60
Db 109 GTGATTTATTGATTCACGACACTGTCATGGGGAGCTGGATGATCTTTCCAAA 168
QY 61 catggg 66
Db 169 AATGGG 174

RESULT 5

US-08-702-367A-12
; Sequence 12, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; NUMBER OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2976
US-08-702-367A-12

Query Match 51.5%; Score 34; DB 4; Length 3162;
Best Local Similarity 69.7%; Pred. No. 0.00031;
Matches 46; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 gtcaactcactgagtcacaaacaaatcaaggagagctggagctctatccatca 60
Db 109 GTGATTTATTGATTCACGACACTGTCATGGGGAGCTGGATGATCTTTCCAAA 168
QY 61 catggg 66
Db 169 AATGGG 174

RESULT 6

PCT-US95-04681-12
; Sequence 12, Application PC/TUS9504681
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; NUMBER OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04681
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3162 base pairs

; APPLICATION NUMBER: PCT/US95/04681
 ; FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 186..3182
PCT-US95-04681-16

Query Match 47.3%; Score 31.2; DB 6; Length 4529;
Best Local Similarity 70.0%; Pred. No. 0.0041;
Matches 42; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 7 ctacgagttcaaaacattcaaggagctggctggtatcttctatccatcatgag 66
DB 288 CTGCTGATTCTTAAGCACACACAGAGTTGAGTGGATTCTCTCCACCACATGGG 347

RESULT 10
US-08-469-537A-102
Sequence 102, Application US/08469537A
Patent No. 5843749
GENERAL INFORMATION:
APPLICANT: Maisongier, et al.
TITLE OF INVENTION: EHK AND ROR TYROSINE
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: NY
COUNTRY: U.S.A.
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempster, Ph.D., Gall M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 3906 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA

FEATURE:
NAME/KEY: CDS
LOCATION: 476..3493
US-08-469-537A-102

Query Match 44.2%; Score 29.2; DB 3; Length 3906;
Best Local Similarity 65.2%; Pred. No. 0.023;
Matches 43; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 gtcaactactggtatcaaaacattcaaggagctggctggtatcttctatccatca 60
DB 662 GTGATTATTATGATTCGGCGACCTGTCTGGAGACCTTGATGATGCTTTTCCAAG 721

QY 61 catggg 66
DB 722 AATGGG 727

RESULT 11
US-08-442-248-1
Sequence 1, Application US/08442248
Patent No. 5759863
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,248
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-442-248-1

Query Match 44.2%; Score 29.2; DB 2; Length 4165;
Best Local Similarity 65.2%; Pred. No. 0.023;
Matches 43; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 gtcaactactggtatcaaaacattcaaggagctggctggtatcttctatccatca 60
DB 727 GTGATTATTATGATTCGGCGACCTGTCTGGAGACCTTGATGATGCTTTTCCAAG 786
QY 61 catggg 66

Db 787 AATGGG 792

RESULT 12
US-08-440-815-1
Sequence 1, Application US/08440815

Patent No. 5798448
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: At-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,815
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-815-1

Query Match 44.2%; Score 29.2; DB 2; Length 4165;
Best Local Similarity 65.2%; Pred. No. 0.023;
Matches 43; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 gtcattctcttgatgataaaacattcaaggagagctggtcgtctctatccatcata 60
DB 727 GTGATTATTGATTCGGCGACTGCTGGGAGACCTTGATGATTCCTTTCCAAAG 786

QY 61 catggy 66
DB 787 AATGGG 792

RESULT 13
PCT-US96-00419-6
Sequence 6, Application PC/TUS9600419

GENERAL INFORMATION:
APPLICANT: Thomas Closek, Axel Ullrich, Birgit
APPLICANT: Millaer
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00419
FILING DATE: January 3, 1995

CLASSIFICATION:
PRIOR APPLICATION DATA: Including application
PRIOR APPLICATION DATA: described below.
APPLICATION NUMBER: none

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2323
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic
PCT-US96-00419-6

Query Match 40.9%; Score 27; DB 6; Length 2323;
Best Local Similarity 66.1%; Pred. No. 0.14;
Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 8 tactgattcaaaacattcaaggagagctggtcgtctctatccatcatacatggy 66
DB 336 TACTGACTCGAAGACACAAACAAATGATTCCTCCTCCACCACTGGG 394

RESULT 14
PCT-US96-00419-4
Sequence 4, Application PC/TUS9600419

GENERAL INFORMATION:
APPLICANT: Thomas Closek, Axel Ullrich, Birgit
APPLICANT: Millaer
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00419
FILING DATE: January 3, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA: Including application
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: described below: none

APPLICATION NUMBER: none

FILING DATE: none

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 2901

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: nucleic

PCT-US96-00419-4

Query Match 40.9%; Score 27; DB 6; Length 2901;

Best Local Similarity 66.1%; Pred. No. 0.15;

Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 8 tacttgattcaaaacaattcaaggagctggctgtatctcttatcatcacatggg 66

DB 336 TACTGGACTCGAAGCACACAAACAAGATGGAATGATTTCTCTCCACCCAGTGGG 394

RESULT 15

PCT-US96-00419-1

Sequence 1, Application PC/TUS9600419

GENERAL INFORMATION:

APPLICANT: Thomas Closek, Axel Ullrich, Birgit

APPLICANT: Millaer

TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM compatible

OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/00419

FILING DATE: January 3, 1995

CLASSIFICATION:

PRIOR APPLICATION DATA: Including application

PRIOR APPLICATION DATA: described below: none

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4304

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: nucleic

PCT-US96-00419-1

Query Match 40.9%; Score 27; DB 6; Length 4304;

Best Local Similarity 66.1%; Pred. No. 0.16;

Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 8 tacttgattcaaaacaattcaaggagctggctgtatctcttatcatcacatggg 66

DB 336 TACTGGACTCGAAGCACACAAACAAGATGGAATGATTTCTCTCCACCCAGTGGG 394

Search completed: May 15, 2000, 12:05:06

Job time: 4425 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

Run on: May 15, 2000, 12:08:28 ; Search time 111.14 Seconds

(Without alignments)
148.575 Million cell updates/sec

Title: US-09-104-340-7

```

Perfect score: 86
Sequence: 1 gtaatctactgattcaaa.....tctctatcatcatcatggy 66

```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

```
Maximum DB seq length: 1000000
Minimum DB seq length: 0
```

Post-processing: Minimum Match 0g

Listing first 45 summaries

Database : N_Geneseq_36: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	66	100.0	3132	1	Q34513	HEK coding sequen
2	59.6	90.3	3254	1	O90659	Eph-related ptk Cat
3	34	51.5	3162	1	T02947	EPH-1-like receptor
4	31.6	47.9	3663	1	T72320	Embryonic stem cel
5	31.2	47.3	4529	1	T02949	EPH-1-like receptor
6	29.2	44.2	3906	1	V70207	Rat receptor tyros
7	29.2	44.2	4165	1	T18893	Rat REK7 cDNA. AL
8	27	40.9	2323	1	T33962	Mouse development
9	27	40.9	2901	1	T32961	Mouse development
10	27	40.9	4304	1	T32960	Mouse development
11	26	39.4	4322	1	V58192	Mouse BSK receptor
12	25.8	39.1	2005	1	O71303	Mouse osteoblast-
13	23.2	35.8	2962	1	T02946	EPH-1-like receptor
14	23	34.8	3116	1	T02948	EPH-1-like receptor
15	23	34.8	3348	1	T03100	Protein tyrosine-k
16	22.4	33.9	110000	1	T58840_2	Continuation (3 of
17	22.4	33.9	110000	1	T58840_3	Continuation (4 of
18	22.2	33.6	1000	1	V45121	Mus musculus cereb
19	22.2	33.6	3592	1	V70208	Rat receptor tyros
20	22.2	33.6	7286	1	T14547	Cytoskeleton gene, C
21	22.2	33.6	12923	1	N90338	Sequence of human
22	22	33.3	1228	1	T04180	scfv-pp coding seq
23	22	33.3	1758	1	V84573	Human secreted pte
24	21.8	33.0	320	1	O60056	Human brain Express
25	21.8	33.0	530	1	N80105	X mutant of L-A de
26	21.8	33.0	867	1	T99064	nhpc coding sequ
27	21.8	33.0	867	1	X01374	T-lymphocyte prote
28	21.8	33.0	2397	1	X01386	T-lymphocyte prote
29	21.8	33.0	2643	1	X01385	T-lymphocyte prote
30	21.8	33.0	2745	1	X01384	T-lymphocyte prote
31	21.8	33.0	2766	1	X01383	T-lymphocyte prote
32	21.8	33.0	2819	1	V19910	Human pro-protein
33	21.8	33.0	13365	1	X20554	Polynucleotide seq
34	21.6	32.7	2187	1	Q12399	Human hepatocyte g

C	35	21.6	32.7	2187	1	Q22146	Complete human HGF
C	36	21.6	32.7	2187	1	V20546	Human recombinant
C	37	21.6	32.7	2187	1	X15186	Nucleic acid encod
C	38	21.6	32.7	2394	1	Q22143	Human HGF gene par
C	39	21.6	32.7	2395	1	Q12397	Human hepatocyte g
C	40	21.6	32.7	3105	1	T07308	Receptor tyrosine
C	41	21.6	32.7	3105	1	T84528	Mouse Ndk tyrosine
C	42	21.6	32.7	3751	1	O62461	Human embryonal K1
C	43	21.6	32.7	3776	1	O90655	Eph-related ptk Ce
C	44	21.6	32.7	4049	1	O90660	Eph-related ptk Ce
C	45	21.6	32.7	4097	1	Q90657	Eph-related ptk Ce

ALIGNMENTS

RESULT	1
ID	034513 standard; DNA; 3132 BP.
AC	034513;
DT	24-MAY-1993 (first entry)
DE	HEK coding sequence.
KM	Primer: expression vector: extracellular domain; human; HEK;
KW	epb/elk-like; kinase; pre-B; cell; T; tumour; lymphoid; LK63;
KW	Lila-1; JM; B-cellular; Hela; receptor-type; thymidine kinase;
KW	TK; ligand; B-cellular response; growth; differentiation; ss.
OS	Synthetic.
PH	Key
FT	5'utr
FT	location/Qualifiers
FT	1..99
FT	/*tag= a
FT	100..3051
FT	/*tag= b
FT	3052..3132
FT	/*tag= c
FT	100..159
FT	/*tag= d
FT	1723..1795
FT	/*tag= e
FT	/*note= "Potential transmembrane region"
FT	160..216
FT	/*tag= f
FT	/*note= "Purified HEK protein #1"
FT	2617..2679
FT	/*tag= g
FT	/*note= "Purified HEK protein #2"
PA	MO9300425-A.
PN	07-JAN-1993.
PF	19-JUN-1992; AU0294.
PR	21-JUN-1991; AU-006841.
PR	12-DEC-1991; AU-009392.
PR	(HAL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI	Boyd AD, Simpson R, Ward LD, Wicks I, Wilkinson D;
PI	WPI; 93-036373/04.
DR	P-PSDB; R31466.
PT	Receptor-type tyrosine kinase reactive with monoclonal antibody
PT	III-A4 - is EPB-ELK-like kinase, useful for phosphorylating
PT	proteins in modulating pre-B, B and T cell function, in cancer
PT	therapy etc.
PS	Claim 6; Fig 1; 58pp; English.
PS	This sequence encodes human epb/elk-like kinase (HEK). HEK is
CC	expressed in both pre-B cells and T cell lines and in a number of
CC	tumours of human origin. eg. lymphoid tumours LK63, Lila-1 and JM,
CC	and the epithelial tumour Hela. This receptor-type thymidine kinase
CC	(TK) and/or its ligands are useful as agents in modulation of the
CC	production and/or function of pre-B, B and T cells. The TK and its
CC	analogs have activity in transducing signals or in stimulating
CC	cellular responses such as growth and/or differentiation.
SO	Sequence 3132 BP; 888 A; 711 C; 759 G; 774 T;

Query Match	100.0%;	Score 66;	DB 1;	Length 3132;
Best Local Similarity	100.0%;	Pred. No. 2.1e-16;		
Matches	66;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0

```

QY 1 gtcacatctactgattcaaaaacatccaaggaggctggctgcatctctatccatca 60
    |||||||
DB 187 GTCATCTACTGATTCAAAAACATTCAAGGGAGCTGGGACTGAGCTCTTATCCATCA 246

QY 61 catggg 66
    |||||
DB 247 CATGGG 252

RESULT 2
Q90659
ID 090659 standard: DNA; 3254 BP.
AC 090659;
DT 11-NOV-1995 (first entry)
DE Eph-related PTK Cdk4.
KW Cdk4; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
    prognosis; ss.
OS Gallus sp.
FH Key Location/Qualifiers
FT cds 32..2980
    /*tag= a
PN W09515375-A.
PD 08-JUN-1995.
PF 07-SEP-1994; U10140.
PR 03-DEC-1993; US-162809.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PI Pasquale EB, Sajjadl FG;
DR WPI; 95-215256/28.
PT P-PSDB; R75711.
PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
    cancer.
PS Disclosure: Page 85-89; 129pp; English.
CC Probes derived from the Eph-related PTKs Cdk4 (Q90659) and Cdk5
    (Q90660) were used to isolate novel cDNA clones (Q90652-58.
CC Q90661-62) from chicken embryo and embryonic brain libraries.
CC Cdk4 is highly expressed in the chicken developing brain and
    CC embryonic tissues, as well as in the adult brain and retina.
SQ Sequence 3254 BP; 926 A; 737 C; 796 G; 795 T;

Query Match 90.3%; Score 59.6; DB 1; Length 3254;
Best Local Similarity 93.9%; Pred. No. 6.3e-14;
Matches 62; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 gtcacatctactgattcaaaaacatccaaggaggctggctgcatctctatccatca 60
    |||||||
DB 116 GTCATCTACTGATTCAAAAACATTCAAGGGAGCTGGGACTGAGCTCTTATCCATCA 175

QY 61 catggg 66
    |||||
DB 176 CATGGG 181

RESULT 3
T02947
ID T02947 standard: cDNA; 3162 BP.
AC T02947;
DT 16-APR-1996 (first entry)
DE EPH-like receptor protein tyrosine kinase HEK7 cDNA.
KW EPH-like receptor protein tyrosine kinase; PTK; HEK7;
    human eph-like kinase; therapy; diagnosis; vector; antibody; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..2976
    /*tag= a
PN W09528484-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04681.
PR 15-APR-1994; US-229509.
PA (AMGE-) AMGEN INC.
PI Fox GM, Jling S, Welcher AA;
DR WPI; 95-37379/48.

```

```

DR P-PSDB; R85090.
PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -
    PT and related vectors, host cells, proteins, antibodies etc., used
    PT diagnostically and therapeutically to modulate receptor activation
    or prodn.
PS Claim 1; Page 49-54; 133pp; English.
CC cDNAs (T02946-49) coding for 4 novel human EPH-like receptor protein
    CC tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively,
    CC were isolated from a human foetal brain cDNA library using a directed
    CC PCR approach with primers (see T02960-61) based on conserved regions of
    CC receptor PTKs and Eph-like receptor PTKs. HEK5, HEK7 and HEK8 show
    CC extensive homology to the catalytic domain of chicken EPH-like
    CC receptors Cdk5, Cdk7 and Cdk8. HEK11 shows no homology to any known
    CC EPH-like receptor. The isolated cDNAs are used for prodn. of
    CC recombinant HEKs and chimeric receptors, in hybridisation assays, and
    CC to detect abnormalities in HEK receptor genes.
SQ Sequence 3162 BP; 921 A; 667 C; 775 G; 799 T;

Query Match 51.5%; Score 34; DB 1; Length 3162;
Best Local Similarity 69.7%; Pred. No. 0.00049;
Matches 46; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 gtcacatctactgattcaaaaacatccaaggaggctggctgcatctctatccatca 60
    |||||||
DB 109 GTCATCTACTGATTCAAAAACATTCAAGGGAGCTGGGACTGAGCTCTTATCCATCA 168

QY 61 catggg 66
    |||||
DB 169 CATGGG 174

RESULT 4
T72320
ID T72320 standard: DNA; 3663 BP.
AC T72320;
DT 15-SEP-1997 (first entry)
DE Embryonic stem cell kinase (Esk) cDNA.
KW Embryonic stem cell kinase; receptor tyrosine kinase; mucositis;
    KM epithelium; signal transduction; gene therapy; diagnosis; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT cds 355..3288
    /*tag= a
FT signal_peptide 355..432
    /*tag= b
FT mat_peptide 433..3285
    /*tag= c
PN W09723629-A1.
PD 03-JUL-1997.
PF 20-DEC-1996; A00826.
PR 22-DEC-1995; AU-007277.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Boyd AM, Lickliter J;
DR WPI; 97-351065/32.
PT P-PSDB; W19258.
PT DNA encoding embryonic stem cell kinase, receptor tyrosine kinase -
    PT for production of modulators and antibodies, useful to treat
    PT mucositis and other disorders involving epithelium
PS Claim 4; Page 48-54; 98pp; English.
CC An isolated nucleic acid molecule (T72320) codes for novel mouse
    CC embryonic stem cell kinase (Esk), a receptor tyrosine kinase that
    CC belongs to the Eph subfamily. To isolate the molecule, RNA from
    CC the murine embryonic stem cell line W9.5 was subjected to RT-PCR
    CC using primers (see also T72321-24) based on conserved Eph
    CC sequences. A labelled probe from an isolated clone was used to
    CC screen a mouse liver cDNA library, identifying a single clone that
    CC included the complete coding region of Esk. The gene for murine
    CC Esk is located on bands B1 and B2 of chromosome 6. Esk nucleic
    CC acids can be used to produce recombinant Esk polypeptides, develop
    CC probes, and as sense and antisense molecules for diagnosis or
    CC therapy.
SQ Sequence 3663 BP; 869 A; 976 C; 1015 G; 801 T;

```

```
Query Match          47.9%; Score 31.6; DB 1; Length 3663;
Best Local Similarity 69.4%; Pred. No. 0.0044;
Matches 43; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Oy 1 gtaactctactgattcaaaacaattcaaggagctggtgattcttatccatca 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 439 gtcactctaatgacacacacacacacacacacacacacacacacacacac 498
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Oy 61 ca 62
Db 499 GA 500

RESULT 5
T02949
ID T02949 standard; cDNA; 4529 BP.
AC T02949;
DT 16-APR-1996 (first entry)
DE Eph-1-like receptor protein tyrosine kinase HEK11 cDNA.
KW Eph-1-like receptor protein tyrosine kinase; PTK; HEK11;
KW human eph-1-like kinase; therapy; diagnosis; antibody; vector; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 186..3182
FT /*tag= a
PN MO9528484-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04681.
PR 15-APR-1994; US-229509.
PA (AMGE-) AMGEN INC.
PI Fox GM, Jing S, Welcher AA;
DR WPI: 95-373799/48.
DR P-PSDB: R85092.
PT New nucleic acid encoding Eph-1-like receptor tyrosine kinase(s) -
PT and related vectors, host cells, proteins, antibodies etc., used
PT diagnostically and therapeutically to modulate receptor activation
PT or prodm.
PS Claim 1; Page 66-71; 133pp; English.
CC CDNA (T02946-49) coding for 4 novel human Eph-1-like receptor protein
CC tyrosine kinases; HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively,
CC were isolated from a human foetal brain cDNA library using a directed
CC PCR approach with primers (see T02960-61) based on conserved regions of
CC receptor PTKs and Eph-1-like receptor PTKs. HEK5, HEK7 and HEK8 show
CC extensive homology to the catalytic domain of chicken Eph-1-like
CC receptors Csk5, Csk7 and Csk8. HEK11 shows no homology to any known
CC Eph-1-like receptor. The isolated cDNAs are used for prodm. of
CC recombinant HEKs and chimeric receptors, in hybridisation assays, and
CC to detect abnormalities in HEK receptor genes.
SQ Sequence 4529 BP; 1449 A; 834 C; 1000 G; 1246 T;
```

```
Query Match          47.3%; Score 31.2; DB 1; Length 4529;
Best Local Similarity 70.0%; Pred. No. 0.0066;
Matches 42; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Oy 7 ctacgattcaaaacaattcaaggagctggtgattcttatccatccatgag 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 288 ctctgcatcttcaaaacacacacacacacacacacacacacacacacacac 347
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

RESULT 6
V70207
ID V70207 standard; DNA; 3906 BP.
AC V70207;
DT 11-FEB-1999 (first entry)
DE Rat receptor tyrosine kinase Etk-1 encoding DNA.
KW Receptor tyrosine kinase; Ror-1; Ror-2; Etk-1; Etk-2; detection;
KW neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
KW binding protein; BDNF; NT-3; diagnosis; ss.
OS Rattus sp.
FH Key Location/Qualifiers
```

```
FT CDS 476..3493
FT /*tag= a
PN US5843749-A.
PD 01-DEC-1998.
PF 06-JUN-1995; 469537.
PR 17-MAR-1995; US-406247.
PR 26-JUL-1991; US-736559.
PR 28-OCT-1993; US-144992.
PR 06-JUN-1995; US-469537.
PA (REG-) REGENERON PHARM INC.
PI Maisompierre PC, Maslakowski P, Yancopoulos GD;
DR WPI: 99-044584/04.
DR P-PSDB: W83147.
PT DNA encoding receptor tyrosine kinase proteins - and corresponding
PT proteins
PS Claim 5; Fig 22; 194pp; English.
CC The present invention describes nucleic acid molecules for ror-1,
CC ror-2, etk-1 and etk-2. Also described are the corresponding proteins:
CC Ror-1; Ror-2; Etk-1; and Etk-2. The proteins are orphan receptor
CC tyrosine kinases. The present sequence encodes rat Etk-1.
SQ Sequence 3906 BP; 1097 A; 876 C; 990 G; 943 T;
```

```
Query Match          44.2%; Score 29.2; DB 1; Length 3906;
Best Local Similarity 65.2%; Pred. No. 0.038;
Matches 43; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Oy 1 gtaactctactgattcaaaacaattcaaggagctggtgattcttatccatca 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 662 gttgaattattgagatcgacacacacacacacacacacacacacacacacac 721
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Oy 61 catggg 66
    |||||
Db 722 AATGGG 727
```

```
RESULT 7
T18893
ID T18893 standard; cDNA; 4165 BP.
AC T18893;
DT 05-JAN-1997 (first entry)
DE Rat REK7 cDNA.
KW REK7; eph-related tyrosine kinase receptor; AL-1; ligand;
KW neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis;
KW ss.
OS Rattus sp.
FH Key Location/Qualifiers
FT cds 541..3327
FT /*tag= a
FT signal_peptide 541..711
FT /*tag= b
FT mat_peptide 712..3324
FT /*tag= c
PN WO9613518-A1.
PD 09-MAY-1996.
PF 26-OCT-1995; U14016.
PR 27-OCT-1994; US-330128.
PR 07-JUN-1995; US-486449.
PA (GETH ) GENENTECH INC.
PI Caras IW, Winslow JW;
DR WPI: 96-239448/24.
DR P-PSDB: R97853.
PT AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in
PT treatment and diagnosis of neuronal disorders and
PT angiogenesis-related conditions.
PS Example 1; Page 47-49; 75pp; English.
CC A cDNA clone (T18893) codes for rat REK7 (R97853), an eph-related
CC tyrosine kinase receptor, for which AL-1 (see also W97854) is a
CC ligand. It was isolated using degenerate receptor tyrosine kinase
CC primers (T18894-96) to amplify cDNAs of an adult mouse hippocampal
CC cDNA library. A PCR fragment was used as a probe to isolate the
CC full-length REK7 cDNA from a rat hippocampal cDNA library. An
CC REK-1gG fusion was used to screen cultured cell lines for surface
```



```

PR 11-JUN-1996: US-673789.
PA (KROM/) KROMER L F.
PA (SCHU/) SCHULZ N T.
PA (WOUU/) WOUDE G F V.
PA (ZHOV/) ZHOU R.
PI Kromer LF, Schulz NT, Woude GFV, Zhou R;
DR WPI: 98-541751/46.
P-PSDS: W71628.
PT Isolated nucleic acid sequence encoding protein - used in Bsk
PT nucleic acid probe, used in detecting alterations in level of Bsk
PT messenger-RNA in biological samples isolated from mammal afflicted
PT with disease
PS Claim 2; Fig 2; 72pp; English.
CC The present sequence encodes mouse Bsk, which is a receptor-like
CC tyrosine kinase. The nucleic acid sequence encoding Bsk can be used
CC Bsk nucleic acid probes, which can be used in detecting alterations in
CC the level of Bsk messenger-RNA (mRNA) in biological samples isolated
CC from a mammal afflicted with a disease, such as neurodegenerative
CC diseases or disorders and neoplasms. The nucleic acid sequence can
CC be delivered into the limbic system of patients with limbic system
CC neurodegenerative disease, disorder or injury, to promote or enhance
CC limbic system neuron regeneration or growth. Such neurodegenerative
CC diseases include, chromosomal abnormalities, degenerative growth and
CC development disorders, viral infections, bacterial infections, brain
CC injuries, neoplastic conditions, Alzheimer's disease, epilepsy,
CC schizophrenia, or stroke and cerebral ischaemia.
SQ Sequence 4322 BP; 1260 A; 887 C; 1055 G; 1120 T;

Query Match 39.4%; Score 26; DB 1; Length 4322;
Best Local Similarity 62.1%; Pred. No. 0.67;
Matches 41; Conservative 0; Mismatches 25; Indels 0; Gaps

QY 1 gtcattctacgtggttcaaaaacatccaaggagctggcgtgacattcatcactca 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
604 GTGATTGTGTTGGATGCGCCACATCGTATGSGGGGACCTTGATGAGATTGTTCCAAAG 663
QY 61 catggg 66
Db |||||
664 AACGGG 669

RESULT 12
Q71303/C
ID 071303 standard; cDNA to mRNA; 2005 BP.
AC 071303:
DT 11-APR-1995 (first entry)
DE Mouse osteoblast-specific factor-6 cDNA.
KW osteoblast-specific factor; OSF-6; mouse; murine;
KM bone metabolic disease; diagnosis; therapy; ds.
OS Mus musculus.
FH Key Location/Qualifiers
FT cds 22..1350
FT /tag= a
FT /product= OSF-6

PN EP-614974-A.
PD 14-SEP-1994.
PF 28-FEB-1994; 102992.
PR 10-MAR-1993; JP-048875.
PA (FAKH/) HOECHST JAPAN LTD.
PA (Aman E, Kawai S, Kikuno R, Okazaki M, Takeshita S;
DR WPI: 94-781304/35.
P-PSDS: R60536.
PT New osteoblast specific factor -6 - active as a transcription
PT control factor in bone formation, used for treating bone
PT metabolic diseases
PS Claim 2; Page 8-11; 18pp; English.
CC Two cDNA libraries were prepared, one from murine osteoblast-like
CC cell line MC3T3-E1 and the other from mouse hepatic tissues. Double-
CC stranded fragments of 300 bp were obtained using a random extension
CC primer and were blunt-ended. The ds linker ATO5-1/2 was ligated to
CC the MC3T3-E1 cDNA and the ds linker ATO5-4/5 was ligated to liver
CC cDNA. PCR amplification of each product was performed using ATO5-1

```

CC (Q71304) or AROS-4 (Q71305), respectively. DNA specific for
 CC MC3T3-E1 was obtained by subtraction of sequences also found in the
 CC liver library, then amplification with AROS-1. This was a first
 CC step in the cloning procedure for isolating a MC3T3-E1 specific
 CC clone, coding for OSF-6 (see Q71303).
 SQ Sequence 2005 BP; 485 A; 534 C; 552 G; 434 T;

Query Match 39.1%; Score 25.8; DB 1; Length 2005;
 Best Local Similarity 63.9%; Pred. No. 0.65;
 Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 6 ttacttgattcaaaacattcaaggagctggctgattcttcatcacatg 65
 DB 1402 TCTAGCTGATCGACTACAGCAAGAGGGGCTGGCGCTGCACAGCATTATCAGATG 1343
 OY 66 g 66
 DB 1342 G 1342

RESULT 13
 T02946
 ID T02946 standard; cDNA; 2962 BP.

AC T02946: 16-APR-1996 (first entry)
 DE EPH-like receptor protein tyrosine kinase HEK5 cDNA.
 KW EPH-like receptor protein tyrosine kinase; PTK; HEK5;
 KM human eph-like kinase; therapy; diagnosis; antibody; vector; ss.
 OS Homo sapiens.

PH Key Location/Qualifiers
 FT cds 1..2913
 FT /*tag= a
 FT WO9528484-A1.
 PD 26-OCT-1995.
 PF 14-APR-1995; U04681.
 PR 15-APR-1994; US-229509.
 PI (AMGE-) AMGEN INC.
 PA Fox GM, Jing S, Welcher AA;
 DR WPI: 95-373799/48.
 DR P-PSDB: R85089.

PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -
 PT and related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation
 PT or prodn.
 PS Claim 1: Page 41-45; 133pp; English.
 CC cDNAs (T02946-49) coding for 4 novel human EPH-like receptor protein
 CC tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively,
 CC were isolated from a human foetal brain cDNA library using a directed
 CC PCR approach with primers (see T02960-61) based on conserved regions of
 CC receptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show
 CC extensive homology to the catalytic domain of chicken EPH-like
 CC receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known
 CC EPH-like receptor. The isolated cDNAs are used for prodn. of
 CC recombinant HEKs and chimeric receptors, in hybridisation assays, and
 CC to detect abnormalities in HEK receptor genes.
 SQ Sequence 2962 BP; 654 A; 914 C; 827 G; 567 T;

Query Match 35.2%; Score 23.2; DB 1; Length 2962;
 Best Local Similarity 61.7%; Pred. No. 7.3;
 Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY 7 ctacttgattcaaaacattcaaggagctggctgattcttcatcacatg 66
 DB 25 CTATGACTCCACTACAGAGAGTGTGAGCTGGCTGATGTGATCTCATCAGGG 84

RESULT 14
 T02948
 ID T02948 standard; cDNA; 3116 BP.
 AC T02948: 16-APR-1996 (first entry)

DE EPH-like receptor protein tyrosine kinase HEK8 cDNA.
 KW EPH-like receptor protein tyrosine kinase; PTK; HEK8;
 KM human eph-like kinase; therapy; diagnosis; antibody; vector; ss.
 OS Homo sapiens.

PH Key Location/Qualifiers
 FT cds 34..2994
 FT /*tag= a
 FT WO9528484-A1.
 PD 26-OCT-1995.
 PF 14-APR-1995; U04681.
 PR 15-APR-1994; US-229509.
 PI (AMGE-) AMGEN INC.
 PA Fox GM, Jing S, Welcher AA;
 DR WPI: 95-373799/48.
 DR P-PSDB: R85091.

PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -
 PT and related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation
 PT or prodn.
 PS Claim 1: Page 57-62; 133pp; English.
 CC cDNAs (T02946-49) coding for 4 novel human EPH-like receptor protein
 CC tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively,
 CC were isolated from a human foetal brain cDNA library using a directed
 CC PCR approach with primers (see T02960-61) based on conserved regions of
 CC receptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show
 CC extensive homology to the catalytic domain of chicken EPH-like
 CC receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known
 CC EPH-like receptor. The isolated cDNAs are used for prodn. of
 CC recombinant HEKs and chimeric receptors, in hybridisation assays, and
 CC to detect abnormalities in HEK receptor genes.
 SQ Sequence 3116 BP; 859 A; 720 C; 812 G; 725 T;

Query Match 34.8%; Score 23; DB 1; Length 3116;
 Best Local Similarity 68.1%; Pred. No. 8.8;
 Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 1 gtcaacttacttgattcaaaacattcaaggagctggctgattg 47
 DB 124 GTTACTTATGTGATTCAGATCTGTTCAGGAGAACTTGCTGAT 170

RESULT 15
 T03100
 ID T03100 standard; DNA; 3348 BP.

AC T03100: 14-FEB-1996 (first entry)
 DE Protein tyrosine-kinase bptk7 gene.
 KW Protein tyrosine-kinase; PTK; bptk7; agonist; cell growth;
 KM differentiation; ss.
 OS Homo sapiens.

PH Key Location/Qualifiers
 FT cds 1..2961
 FT signal_peptide 1..57
 FT /*tag= a
 FT /*tag= b
 FT mat_peptide 58..2958
 FT /*tag= c
 PN WO9527061-A1.

PD 12-OCT-1995.
 PF 04-APR-1995; U04228.
 PR 04-APR-1994; US-22616.
 PA (GENY) GENENTECH INC.
 PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
 DR WPI: 95-366160/47.
 DR P-PSDB: R85936.

PT Agonist antibodies which activate specific protein tyrosine
 PT kinase(s) - also activate chimeric proteins of kinase extracellular
 PT domain and Ig constant domain, useful for studying, and therapeutic
 PT modulation of, cell growth and differentiation
 PS Disclosure; Page 88-92; 125pp; English.
 CC DNA probes based on protein tyrosine-kinase (PTK) sequences were used

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 11:43:02 ; Search time 1225.64 Seconds
(without alignments)
-52.384 Million cell updates/sec

Title: US-09-104-340-7
Perfect score: 66
Sequence: 1 gtcacatctactgattcaca.....tctctatcatcatcatg99 66

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba1:*
2: gb_ba2:*
3: gb_on:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pi1:*
8: gb_pi2:*
9: gb_pi3:*
10: gb_pi4:*
11: gb_pi5:*
12: gb_pi6:*
13: gb_pi7:*
14: gb_pi8:*
15: gb_pi9:*
16: gb_pi10:*
17: gb_pi11:*
18: gb_pi12:*
19: gb_pi13:*
20: gb_pi14:*
21: gb_pi15:*
22: gb_pi16:*
23: gb_pi17:*
24: gb_pi18:*
25: gb_pi19:*
26: gb_pi20:*
27: gb_pi21:*
28: gb_pi22:*
29: gb_pi23:*
30: gb_pi24:*
31: gb_pi25:*
32: gb_pi26:*
33: gb_pi27:*
34: gb_pi28:*
35: gb_pi29:*
36: gb_pi30:*
37: gb_pi31:*
38: gb_pi32:*
39: gb_pi33:*
40: gb_pi34:*
41: gb_pi35:*
42: gb_pi36:*
43: gb_pi37:*
44: gb_pi38:*

45: gb_pi39:*
46: gb_pi40:*
47: gb_pi41:*
48: gb_pi42:*
49: gb_pi43:*
50: gb_pi44:*
51: gb_pi45:*
52: gb_pi46:*
53: gb_pi47:*
54: gb_pi48:*
55: gb_pi49:*
56: gb_pi50:*
57: gb_pi51:*
58: gb_pi52:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	66	100.0	3132 5 A28003	A28003 H. sapiens H
2	66	100.0	3132 5 I68018	I68018 Sequence 9
3	66	100.0	3149 9 H0MHEK	M83941 Human recep
4	59.6	90.3	3241 4 CHCKEK4	M68514 Chicken eph
5	59.6	90.3	3254 5 I15007	I15007 Sequence 15
6	54.8	83.0	2032 12 MUSMEK4SE	M68515 Mouse eph-r
7	54.8	83.0	3197 12 MUSMEK4	M68513 Mouse eph-r
8	53.2	80.6	3077 12 RNU5278	U69278 Rattus eph-r
9	34	51.5	3162 10 HUMRPTK8	U69278 Rattus eph-r
10	34	51.5	3903 10 HSEK1	L36644 Homo sapien
11	32.4	49.1	4124 4 GCEK7B	X95425 H. sapiens m
12	32.4	49.1	4737 12 MMU72207	U03910 Gallus galli
13	32.4	49.1	160703 10 HS61A9	U72207 Mus musculu
14	31.2	47.3	4523 10 HUMRPTK	AL035703 Human DNA
15	31.2	47.3	116490 32 HSJ189K14	L36642 Homo sapien
16	31.2	47.3	143140 43 AC015609	AL121966 Homo sapi
17	30	45.5	184277 55 AC021955	AC015609 Homo sapi
18	29.8	45.2	3042 4 XLSK1	AC021955 Homo sapi
19	29.8	45.2	3193 4 XELPAGANA	X91191 X. laevis mr
20	29.2	44.2	3531 12 RNEK1	L26099 Xenopus lae
21	29.2	44.2	3906 5 AR062744	X78689 R. norvegicu
22	29.2	44.2	4165 5 AR025488	AR062744 Sequence
23	28.4	43.0	132805 41 AC009425	AR025488 Sequence
24	27.6	41.8	3943 4 GGY14271	AC009425 Homo sapi
25	27.6	41.8	139334 33 AL138846	Y14271 Gallus galli
26	27	40.9	2006 12 RNU21955	AL138846 Homo sapi
27	27	40.9	2323 12 MKKIN172	U21955 Rattus norv
28	27	40.9	2901 12 MKKIN171	U21955 Rattus norv
29	27	40.9	3208 12 RNU21954	X79084 M. musculus
30	27	40.9	3943 12 MMU58332	U21954 Rattus norv
31	27	40.9	4304 12 MKKIN1	U58332 Mus musculu
32	26.8	40.6	105210 40 AC006383	X79082 M. musculus
33	26.6	40.3	170804 40 AC009411	AC006383 Homo sapi
34	26.6	40.3	185587 43 AC009496	AC009411 Homo sapi
35	26.4	40.0	4664 4 XLAJ2493	AC009496 Homo sapi
36	26.2	39.7	4242 12 MMSEK	AJ002493 Xenopus l
37	26.2	39.7	4242 12 S57168	X65138 M. musculu
38	26.2	39.7	77484 42 AC015510	S57168 Sek-Eph-rel
39	26.2	39.7	170504 33 HSD5551D2	AC015510 Homo sapi
40	26	39.4	3600 4 CHCKEK8	AL109928 Homo sapi
41	26	39.4	4322 5 AR043381	D38174 Gallus galli
42	26	39.4	4322 5 MMU07357	AR043381 Sequence
43	26	39.1	4577 4 DEU89295	U07357 Mus musculu
44	25.8	39.1	1988 12 MMU57413	U89295 Danio rerio
45	25.8	39.1	2000 12 MMU40930	U57413 Mus musculu
				U40930 Mus musculu

ALIGNMENTS

[illegible]

REFERENCE	1 (bases 1 to 3132)
AUTHORS	Boyd,A.W., Simpson,R John,Wicks,I., Ward,L.David and Wilkinson,D.
TITLE	Method of screening for ligands to a receptor-type tyrosine kinase
JOURNAL	Patent: US 5674691 A g 07-OCT-1997;
FEATURES	Location/Qualifiers 1..3132 /source
BASE COUNT	888 a 709 c 761 g 774 t
ORIGIN	
Query Match	100.0%; Score 66; DB 5; Length 3132; Best Local Similarity 100.0%; Pred.No.2,3e-15; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DQ	1 gtcaatcctacgcggattccaanaacaatttaagagggaagcgctggtacttcatccatca 60 Db 187 gtCATCTACGATCAAAAACAATTCAAGGGAGCGTGGGTGCATCTTTATTCATCA 246
DQ	61 catggg 66 Db 247 CATGGG 252
RESULT 3	
HUMHER	3149 bp mRNA PRI 31-Dec-1994
LOCUS	Human receptor tyrosine kinase (HEK) mRNA, complete cds.
DEFINITION	M83941
VERSION	M83941.1 GI:183931
KEYWORDS	receptor protein-tyrosine kinase.
SOURCE	Homo sapiens lymphoid tumor CDNA to mRNA. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 3149) Wicks,I.P., Wilkinson,D., Salvatis,E. and Boyd,A.W. Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed by human lymphoid tumor cell lines Proc. Natl. Acad. Sci. U.S.A. 89 (5), 1611-1615 (1992)
JOURNAL MEDLINE	
FEATURES	location/Qualifiers 1..3149 /oranism="Homo sapiens" /db_xref="taxon:9606" /cell_line="LK63" /tissue_type="lymphoid tumor" 101..3052 /gene:"HEK" 101..3052 /gene:"HEK" /codon_start=1 /product="receptor protein kinase" /protein_id="PAA58633.1" /db_xref="GI:183932"
CDS	/translatio="MDQQSLILLLSCSVLDSFEGELIPDPSPNEVNLIDSTIGDELGW ISPSHGMEIISGVDEHYTP IRTYQVCNVADHSQMMLRTNVPNRNSAOKIVYLKET LRDNCSEPLVLGTCKEFTENLYMESDDDHVSDFREHQFTLDITIADESFDNDGR ILKNTEIRIEVGPKKKGFALFOVDVCAVALSVRYFKCPETVNLAHPDTGM DOSGLVEVRGSVCNKSKEEDPRMYCSTBEEMLVPICKCSNMGEERGMCOCAPRG FYKLDSNMKCARKPHSSQEDOGSMSCRENNTFRADKPSPMACTRPPSRPNYS NINETSYILDMSNPDLDTGGRKDVTFNIICKCCGNINICEPCSNVAFLEPGELINT TSVTTLDAHTNFTFEIDAANGVSELSPROFAAVSITTNOAPSFLVLIKRDTRS NSTLSIQEPDEHPNGILIDEVUYEKODETSTILLRAGTNVISLKDPTIYYO IKRTAGAAGTINSRKFEFTSPDSFSIGESSQVMATAASAAILLTIVYILIER FCRTASGADGERKHLPBGHLPGRLTYVDPTYEDPDQVAHEPAKELDATNISID KYVAGEERGESGRLKPSKETSVA IKTKLYGYTKQRDPLEGASINGODHPHI TRLGCVTKSKPMHVIYTEKENSDLSFLKHDQFTVIOVGMRRIASGMRTLSWM GYRHDIRAANLNILNSULVKCVSDFGLSRVLEDDEPEAYTTREGKIP INWTSPAIY RKFTFSADWSYSGIVLEWMSYGERPWEMSNDVIKA VDEGYRLPMPDCPALYOL MLMCOAMDNNRPFEQIVSIIDLKLINPGLSKITISAARSENLLDGSDNVIDSTER TTOGKMLPVRAHCKEIFTVGVVSSCDTIAKISTDMKKKVGVTVGPQKIISIALK FTTGKMLPVRA*

```

BASE COUNT      891 a      711 c      768 g      779 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 66; DB 9; Length 3149;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gtcacatctactgattcaaaacaattcaaggagctggctggatctcttaccatca 60
    |||||||
Db 188 gttcaatctctgattcaaaacaattcaaggagctggctggatctcttaccatca 247

Oy 61 catggg 66
    |||||
Db 248 CATGGG 253

RESULT 4
LOCUS CHRCER4 3241 bp mRNA VRT 15-FEB-1994
DEFINITION Chicken eph-related receptor tyrosine kinase (cek4) mRNA, complete cds.
ACCESSION M68514
VERSION M68514.1 GI:454809
KEYWORDS receptor tyrosine kinase.
SOURCE Gallus gallus 10 day embryo embryo cDNA to mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 3241)
AUTHORS Sajjadi, F.G., Pasquale, E.B. and Subramani, S.
TITLE Identification of a new eph-related receptor tyrosine kinase gene
from mouse and chicken that is developmentally regulated and
encodes at least two forms of the receptor
JOURNAL New Biol. 3, 769-778 (1991)
MEDLINE 92031278
COMMENT On Feb 16, 1994 this sequence version replaced gi:211446.
FEATURES
source Location/Qualifiers
    1..3241
    /organism="Gallus gallus"
    /db_xref="taxon:9031"
    /dev_stage="10 day embryo"
    /tissue_type="embryo"
    32..2983
    /gene="cek4"
    32..2983
    /gene="cek4"
    /codon_start=1
    /product="receptor tyrosine kinase"
    /protein_id="AAA48666.1"
    /db_xref="GI:211447"
    /translation="MDRRRLPLLICALGSGRISARPGNEVNILDSKTIGELGWI
    STPSHGEIISGVDEHYPIRTYQESNWDHSQNMWLRNMLPRNSAKIYELKFTL
    RDCNSIPVLVGLCKETPNLYMESDDDLAKREHOFKIDILADESTOGLDRI
    LKLTNEVEVGVSKKGFYLAQDVAGCAALVAVYEFKCFYKXNLMFDTVPM
    SOSLVEVSGVNSHKEEPPKMCSTGEEMLVPIGKLCNAGYERGAACAGSGE
    YKASAGNYKCAKCPHSSYEDASLNCCEKRYSEEDPCSDNYRFLPRQGLNNT
    INESVLIIDMSKPLDTGGRKDVTPNITCKCGSSKICEPCSDNYRFLPRQGLNNT
    VTVDLHNTITFEIDAANGVSDLSLRSKPAVASITTNQAPSPITVIRDRSRN
    SVSLSMQEPHPNGIILIDYEVYERKQDESYTILRAKSTNVTISGLKPDYVFOI
    RAKTAAKGTISRKFEFETSPSPSISSENSQVMAISAVALIILTVVYLGRF
    GYKRSKGTIDKRLHFGNGHLKPLGLRTYDPRHYEDNOAHEFAKELDASNSID
    KYVAGGEGVCSGRKLPSRKEISVALIKTLAGYTEKORDFLEASMGQFDPNT
    IRLBEVYTKSRVYVITYEMNGSIDSPFRKDAQFTYIQLGMLGSLSGKTYLSDM
    GYVHDLARNTLINSNLCKVSDFLSLRVLDDDEAVYTRGKIPLRMSPEAIAY
    RKFTSASDAMSGIYLMEVMSYGERPYEMSDYIKAVDEGRILPPDCPAAIYOL
    TADCMQKDRNNRPFQEIYSILDKLIRNPSSTKITNAARSNTLLDOSNIDISAFR
    TAGDLNGEFTRCGCKGIFGVYESSCDITAKISTDMKVKVTVVGGPKKIVTSIKTL
    EHTKNSPVV"
POLY_A_site 916 a 735 c 794 g 796 t
BASE COUNT
ORIGIN

```

```

Query Match
Best Local Similarity 90.3%; Score 59.6; DB 4; Length 3241;
Matches 62; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 gtcacatctactgattcaaaacaattcaaggagctggctggatctcttaccatca 60
    |||||||
Db 116 gttcaatctctgattcaaaacaattcaaggagctggctggatctcttaccatca 175

Oy 61 catggg 66
    |||||
Db 176 CATGGG 181

RESULT 5
LOCUS 115007 3254 bp DNA PAT 02-APR-1996
DEFINITION Sequence 15 from patent US 5457048.
ACCESSION 115007
VERSION 115007.1 GI:1249915
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 3254)
TITLE Pasquale, E.B. and Sajjadi, F.G.
Eph-related tyrosine kinases, nucleotide sequences and methods of
use
JOURNAL Patent: US 5457048-A 15 10-OC7-1995;
MEDLINE
FEATURES
source Location/Qualifiers
    1..3254
    /organism="unknown"
BASE COUNT 926 a 737 c 796 g 795 t
ORIGIN

Query Match
Best Local Similarity 93.9%; Score 59.6; DB 5; Length 3254;
Matches 62; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 gtcacatctactgattcaaaacaattcaaggagctggctggatctcttaccatca 60
    |||||||
Db 116 gttcaatctctgattcaaaacaattcaaggagctggctggatctcttaccatca 175

Oy 61 catggg 66
    |||||
Db 176 CATGGG 181

RESULT 6
LOCUS MUSMEK4SE 2032 bp mRNA ROD 15-FEB-1994
DEFINITION Mouse eph-related receptor tyrosine kinase (Mek4) secreted mRNA,
complete cds.
ACCESSION M68515
VERSION M68515.1 GI:454828
KEYWORDS receptor tyrosine kinase.
SOURCE Mus musculus (strain IRC x Swiss Webster) 11.5 day embryo embryo
cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sclurognathii; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2032)
AUTHORS Sajjadi, F.G., Pasquale, E.B. and Subramani, S.
TITLE Identification of a new eph-related receptor tyrosine kinase gene
from mouse and chicken that is developmentally regulated and
encodes at least two forms of the receptor
JOURNAL New Biol. 3, 769-778 (1991)
MEDLINE 92031278
COMMENT On Feb 16, 1994 this sequence version replaced gi:199121.
FEATURES
source Location/Qualifiers
    1..2032
    /organism="Mus musculus"

```

Query Match	83.0% ; Score 54.8 ; DB 12 ; Length 3197 ;
BASE COUNT	907 a 767 c 775 g 748 t
ORIGIN	1

OY	1	gtcaatcactgattccaataaacaaattcaaggagagctggctggatcttcatcacca	60
Db	176	GTTATCTACTTACGTAGATTCCAAAACAATTCAAGAGAGCTGGGCTGGATCTCCTACCACATCC	235
OY	61	catgag 66	
Db	236	CATGGG 241	
RESULT	8		
RNU69278			
LOCUS			
DEFINITION	RNU69278	3077 bp	mRNA
ACCESSION			ROD
VERSION			23-MAR-1998
KEYWORDS			Rattus norvegicus eph-related receptor tyrosine kinase homolog
SOURCE			(Rck4) mRNA, complete cds.
ORGANISM			U69278.1 GI:1943913
REFERENCE			Norway rat.
AUTHORS			Rattus norvegicus
TITLE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
JOURNAL			Eutheria; Rodentia; Scuriongnathi; Muridae; Murinae; Rattus.
MEDLINE			1 (bases 1 to 3077)
REFERENCE			L.Y.Y., McTierman,C.F. and Feldman,A.M.
AUTHORS			IL-1 beta alters the expression of the receptor tyrosine kinase
TITLE			gene r-EphA3 in neonatal rat cardiomyocytes
JOURNAL			Am. J. Physiol. 274 (1), H331-H341 (1998)
MEDLINE			98120505
REFERENCE			2 (bases 1 to 3077)
AUTHORS			L.Y.Y., McTierman,C.F. and Feldman,A.M.
TITLE			Direct Submission
JOURNAL			Submitted (01-SEP-1996) Cardiology, University of Pittsburgh, 200
COMMENT			Lothrop Street, Pittsburgh, PA 15213, USA
FEATURES			On Apr 18, 1997 this sequence version replaced gi:1698721.
			Location/Qualifiers

```
gene
/cell_type="cardiomyocytes"
1..3077
/gene="Rek4"
35..2989
/gene="Rek4"
/codon_start=1
/product="eph-related receptor tyrosine kinase homolog"
/protein_id="AAC06273.1"
```


[illegible]

	/db_xref="GI:551612"
	/translacion-"PASTLACTICACPPRAPPLITCLLCALRLTLASPSNEVNLIDST
	VMDLMIAPAPKNGWEIEIGEDVENTIAPFIRHYQCKWMEONQNMMLTSMVSNBSASRI
	FILFKTLTRDCNLSIPGLGICKETFFNNYIESPDONGRINKENOYIKIDITIADESEPT
	EILDGRVMKLNTEVRDVGPLSKRGFLAFOVDGACIALVSRYRYKKCSYVHLAV
	FPTLTIGADSOLLEVSGSVNSVTDPREKMCASGEMLVPFGCMKAGYEENG
	TCOVCARGPFRAAPHIOSCKCPPHSYTHEEATSCYCENDVTRERREDPYTMATRPP
	SAAKNISNVENESVELEWTPPADTGKRVOYSTYLACKNCNSHAGVCEECEGARVYLP
	ROGKLANTSYMVDLAHTNYPRFEIAVNWSPLSPARQYSVNVLTTNOAPSPTIN
	VKGSLAKNISLSMOEPDRPNGIIILEYELKHFEKOETSYYTIISKETTITAEGLRP
	ASYVFOIRARTAAQGVFSERREFETPVKAASDOSLOPIVALSVTVGVILLAYVI
	GULLSRRGCYSKAKODPEERKEFHNGHIKLJGCVRYIDPHYVEDPNQVHEAKTI
	EASCITIERTIGAGEFGEVCSGMLKPGRKELVYAIKTLLVGTTERORRPLDEASTM
	GMDHPDIHLEGDVITRSKPMVLTITEMENGSLDTLELKNDGGFYIVQLGMGRGISA
	GNMYLDMGVYHEDVDLARNTLINNSNVCYSKSDGLSLVLEDDEPAVTTGGKIPIM
	TABEAIALFRKETFASDYWSXGYIMVEVSYGERSEMNTQOVYIAVEEGYRLSPMD
	CFAALVOLMDDCKONEKRNPKRFDEIVNMLDKLI RNSSSLKTIIVMNSCRYSNLIAHS
	PDSGDARSYGEMLEAKMRRTIEIFMENKSSMDAVAQVTLIEDRLSLGTYLVGHQRK
	IANSLOBMKQVLNKMVPL"
	2977..3162
BASE COUNT	922 a 667 c 774 g 799 t
ORIGIN	/gene="HER7"
Query Match	51.5%; Score 34; DB 10; Length 3162;
Best Local Similarity	69.7%; Pred. No. 0.0075;
Matches	46; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Oy	1 gtcacatctactcggttcaaaaacaatccaaggygaagtggcgtgacctcttacccatca 60
Db	109 GTGATTATTATCGATTACGCCACCTCATGGGGACCCTGGATGATTGCTTTCCAAA 168
Oy	61 catggg 66
Db	169 AATGGC 174
RESULT 10	
LOCUS	HSEHK1 3903 bp mRNA PRI 11-AUG-1999
DEFINITION	H.sapiens mRNA for EHR-1 receptor tyrosine kinase.
ACCESSION	X95425
VERSION	X95425.1 GI:1177465
KEYWORDS	EHR-1; receptor tyrosine kinase.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS	Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 3903)
JOURNAL	Miescher,G.C., Taylor,V., Olivier,I.G., Mindermann,T., Schrock,E.
MEDLINE	Extensive splice variation and localization of the EHR-1 receptor
REFERENCE	tyrosine kinase in adult human brain and glial tumors
AUTHORS	Brain Res. Mol. Brain Res. 46 (1-2), 17-24 (1997)
TITLE	97334377
JOURNAL	2 (bases 1 to 3903)
	Miescher Constant,G.
	Direct Submission
	Submitted (26-JAN-1996) Guido C. Miescher, University Hospitals
	Basel, Department of Research, Department Forschung, Kantonspsital
	Basel, 4031 Basel, Switzerland
	Overlaps with L36642-L36645
COMMENT	Partial human EHR-1 cDNA without information on mRNA splicing
	variants has been published by Fox, G.W. et al. (1995). Oncogene
	10:897-905.
FEATURES	location/Qualifiers
SOURCE	1..3903
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="4"
	/clone_lib="lambda ZAPII #936206"
	/clone="HF8415"

	mat_peptide	RVLDDPEAAVTRGGKRPITWTAPEALAFKKFSLASQNVSYSGYIMMVMYSGERPFI ENTLDDVIYKAEEGYRIPLSPDCCPAALYLQLMLDCMKDRNSRPPDFELVSMDLRPI PSSIKTLTVNASSRVSNLLVERSPVGSGYRSRGVLEHFKGRTLETFMNGYSMSDS VAOVTLEDRLRLGLVTLVGHQKINKINSIEMOEVOLVNGMYPL"
	85..3123	
	/gene="Cek7"	
	/product="protein-tyrosine kinase precursor"	
	85..177	
	/gene="Cek7"	
	/note="predicted signal sequence"	
	join(85..1801,1868..3126)	
	/gene="Cek7"	
	/note="product of alternatively spliced mRNA lacking insertion B"	
	/codon_start=1	
	/product="receptor-type protein-tyrosine kinase"	
	/protein_id="AAB60613.1"	
	/db_xref="GI:555619"	
	/translation="MGLRGGGGRAGGPAPGTCLLCALNSLASPGSEYNLLDSRT VMGLGWLAIPKRMWEIEVDENYAPRHITQVCVKMNQNMMILTSMISNERPAPA SFEELKFTLRDNCSLPGGIGTCKEFTNMITYPSDEDGNIRENOYIKIDTIADAESF ELDLDGRMRKNTLEVRYDGPLTKKGFLYAFSDVACIALVSRYYKKCPVIRNLIAAF PPDIITGDGDSOLLSEVSGCVNHSITDPARSCSAEEMLYPIGKCICRAGEKNKN TCOCYCRGFEPKASPSPSCSKCPHSTYITLDAASISCCEHYFRRESPPIMACTRRP SAPSALSINWETSVFLEWIPPADTGKNDVSYITACKCNHSGCLCACSHVRYLE QQTDLKNTSMVVLDLAHTNYTFELEAVNGSDNPGARQPSVNVTINOAPSPVS VKRKITRKSISLSMOEDPRNGILLLEIFYPEDQESTYIIKSKRTALTADGLAK GSFAVFQRIARTTAGYGFSRRFEETSFPVAASDGOIPIIVSYGVVILLAVAYE GFLSGRRCGYSKAKODEEEKMHFNHCTILPCVRYTDPHTEDPMAVHERAKEI EASTITERVIGAGEPFQVCGSKRLKLOKRFPATKLTAKYTTEKQRDLGERASTI GOPHPNIHLEGVYTKSPMIYVETEENESLDTFELKNDGFVLIOLVGMLGIAA GMKTLSDMGVYHRDLAANNILNSNLVCKVSDFGLSRYLEDPEAAYTTNRGKLPIRM TAPALIYRFKFTSADWSYGIIVMWESYGEERPWTNDVIAVEEGYRIPLSPML CPALAIYOLMLDCMQDKRNSRKPDEIYMCLKLIRPESLKTIVNASRVSNNLYEHSH PVSGAYRSVGENMELEIKMGXYTELFMENGSSMDSVAQVTLIEDLRGLVTLVGHQK INLSLQEKVQLVNGMPPL"	
	642	
variation	/gene="Cek7"	
	/note="polymorphism in third position of the codon which does not alter the amino acid sequence"	
	/replace="t"	
variation	771	
	/gene="Cek7"	
	/note="polymorphism in third position of the codon which does not alter the amino acid sequence"	
	/replace="a"	
variation	879	
	/gene="Cek7"	
	/note="polymorphism in third position of the codon which does not alter the amino acid sequence"	
	/replace="t"	
variation	882	
	/gene="Cek7"	
	/note="polymorphism in third position of the codon which does not alter the amino acid sequence"	
	/replace="g"	
misc_feature	1726..1797	
	/gene="Cek7"	
	/note="hydrophobic region characteristic of a transmembrane domain"	
	3127..4124	
3'UTR	4124	
polya_site	917 c	1060 g 1044 t
BASE COUNT	1103 a	
ORIGIN		
Query Match	49.1%; Score 32.4; DB 4; Length 4124;	
Best Local Similarity	68.2%; Pred. No. 0.033;	
Matches 45; Conservative 0; Mismatches 21; Indels 0; Gaps 0;		
1 gtcacatctactcagatcatcaaaaacaattcaaggggagcgcyggtcgtgatctcttatccatca 60		
193 gggaattttacttgacctgcacgcacagttaattgggggcatcttagagattgcatacccttacccaana 252		

QY	61	catggg	66		
Db	253	AATGGG	258		
RESULT	12				
LOCUS	MMU72207	4737 bp	mRNA	ROD	23-DEC-1996
DEFINITION	Mus musculus	Eph- and Elk-related kinase (eek)	mRNA, complete cds.		
ACCESSION	U72207				
KEYWORDS	U72207.1	GI:1750258			
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 4737)				
TITLE	The Eek receptor, a member of the Eph family of tyrosine protein kinases, can be activated by three different Eph family ligands				
JOURNAL	Oncogene (1996) In press				
REFERENCE	2 (bases 1 to 4737)				
AUTHORS	Park, S.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-SEP-1996) Molecular Oncology, Bristol-Myers Squibb, P.O. Box 4000, Princeton, NJ 08543, USA				
FEATURES	location/Qualifiers				
SOURCE	1..4737				
gene	/organism="Mus musculus"				
CDS	/db_xref="taxon:10090"				
	79..3093				
	/gene="eek"				
	79..3093				
	/gene="eek"				
	/note="Eek"				
	/codon_start=1				
	/product="Eph- and Elk-related kinase"				
	/protein_id="AAB39218.1"				
	/db_xref="GI:1750259"				
	/translation="MAPKARLSPALWVYTAANAATCVSAGREYVNLIDSTIHQDWKWLTPYPAHQWDSINEVDSEFRPIHTYOVCAWNSPQNMNLRITNWPDRDARVYAEIKKTLIRCNCSIPGVLTGCKETKFFNLHYLESRDLSAQSEOFILIDTIADESTFADLGATLRKLNTEVREGVGLSKRGFYLAODIGACLAIIISLRYYKCPAMVNLAFSEAVNGADSSILVEYVGCVRHSEEDPTKMTCSAGEMLVPGKVCVCSAGYEBRDACMACLGFKTSAPGDOGLCARCPPHSATSATPAACOTCCDLSYTRALADPPSACTRPPSAFVNLISVNGSVLTLEMAPLPDPPGGRSDITYNAVCRCPMAWLSHCEAGSGTRFVPOQTSLGQASLLVNLALAHMYSEWIEAVNVNSLSPERSAAVNTTNOAAPQVAVIROERERISGATSVLMOPEQPNGLILEYEIKYEEKDEMOSYSLKAVTTATVSGLKGRTYRFOVATRSAGCGGRFSQMAVEYETGKPRPRYDRTITVMTCTLTITGLIVALLILICKRRRCYGRKAFODSDSEKMHYONGCAPPPVPLPLNHPGKFPETQFSAPNRTIEEPGRGRRTFRTIESRRIITEKTIIGSGEGEYCYGLQVPGRDVPAVIAKALKAGTTEKRODFLSEALMAGOFDPHNIIIRLEGVYTRGLAMVLYTMKSGSLDAFLRTHDGFYVQALGMIRGVAGAGFYLSLDLGYIHRDLAARVNLVDGRLVCVSGFGLSRALEDDEAAYTTAGAMIPIMWTAPLEAIAFTFSASDVMSFEGVNVMLVAGSEPPYNNMTNODYISSVEGYYRIPAPGCPRALHQLDCMHWRAQRAPRAHYVSVLDALVHSPESLRATATVSRCPPPAFARCPDLRAGSGSGNDLTVDWLDSTIMKGYRDPHFAGAGYSSLGMYLRMAQDVRAIGTILMGHOKTLISIQTRRAQLSSIQGRRLH"				
BASE COUNT	971 a	1504 c	1381 g	881 t	
ORIGIN					
Query Match	49.1%	Score 32.4;	DB 12;	Length 4737;	
Best Local Similarity	68.2%;	Pred. No. 0.033;			
Matches	45;	Conservative 0;	Mismatches 21;	Indels 0;	Gaps 0;
QY	61	catggg	66		
Db	169	GIGAACTCTGTGGATACATCAACATCCATGAGACTGGGGCTGCGCTACAGTATCCCGCT	228		
QY	61	catggg	66		
Db	229	CATGGG	234		

RESULT 13
HS61A9/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

HS61A9 160703 bp DNA PRI 22-NOV-1999
Human DNA sequence from clone RPI-61A9 on chromosome 1p35.2-36.13,
complete sequence.
AL035703
AL035703.20 GI:6434643
HTG.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 160703)
Wilson, S.
Direct Submission
Submitted (22-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Nov 15, 1999 this sequence version replaced gi:6114770.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPeP; Information
on the WormPeP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone configs of human
Chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RPI-61A9 is from the library RPCI-1 constructed at the Roswell Park
Cancer Institute by the group of Plier de Jong. For further
details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
This sequence is the entire insert of clone RPI-61A9.

FEATURES
Source
1..160703
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="p35.2-36.13"
/clone="RPI-61A9"
/clone_1lb="RPCI-1"
complement(939..1245)
/note="match: GSS: Em:AQ134928"
9482..9888
/note="match: GSS: Em:AQ010082"
25683..25889
/note="match: GSS: Em:AQ594605.1"
29241..29448
/note="Weak Data"
29451..29575
/note="Single clone region"
41090..41437
/note="match: GSS: Em:AQ816982.1"
complement(51292)
/note="Random repeat. Forced join. Gap sized by
restriction digest to be 1200-1500bp"
/note="match: GSS: Em:AQ750654.1"
complement(82496..82871)
misc-feature

misc-feature
/note="match: GSS: Em:AQ816014.1"
82591..82878
/note="match: STS: Em:HS4048YH1"
86392..86712
/note="match: GSS: Em:AQ670525.1"
118067..118469
/note="match: GSS: Em:AQ210441"
complement(121941..12454)
/note="match: STS: Em:HSPE55G06"
126813..127149
/note="match: GSS: Em:AQ260557"
126867..127465
/note="match: GSS: Em:AQ419366"
126892..127225
/note="match: GSS: Em:AQ264734"
130356..130685
/note="match: GSS: Em:AQ766010.1"
130356..130674
/note="match: GSS: Em:AQ332261 Em:AQ332293"
130376..130747
/note="match: GSS: Em:AQ530794.1"
130586..131194
/note="match: GSS: Em:AQ746639.1"
complement(138395..138703)
/note="match: GSS: Em:AQ214151"
complement(138397..138766)
/note="match: GSS: Em:AQ429746.1"
complement(138397..138744)
/note="match: GSS: Em:AQ504997.1"
complement(138398..138763)
/note="match: GSS: Em:AQ718784.1"
138773..139200
/note="match: GSS: Em:AQ118462"
138774..139225
/note="match: GSS: Em:AQ700467.1"
139230..139556
/note="match: GSS: Em:AQ876817.1"
139243..139556
/note="match: GSS: Em:AQ602397.1"
147098..147635
/note="match: GSS: Em:AQ479682.1"
complement(152202..152820)
/note="match: STS: Em:G58359.1; match: GSS: Em:AQ347856.1"
BASE COUNT 41742 a 40589 c 39795 g 38577 t
ORIGIN

Query Match 49.1%; Score 32.4; DB 10; Length 160703;
Best Local Similarity 68.2%; Pred. No. 0.044;
Matches 45; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 gtcattctctcgtgattcaaaacattcaagggagcggtggtatctatcatca 60
|||||
DB 59996 gtcattttctctgacacgctccacatccaggagctgctgctacgtatccgct 59997
|||||

QY 61 catggg 66
|||||
DB 59936 catggg 59931

RESULT 14
HUMRPRK
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

HUMRPRK 4523 bp mRNA PRI 10-AUG-1995
Homo sapiens receptor protein-tyrosine kinase (HEK11) mRNA,
complete cds.
L36642
L36642.1. GI:551607
EPR-like receptor PRK; receptor protein-tyrosine kinase.
Homo sapiens female fetus, 17-18 weeks gestation brain cDNA to
mRNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.

```

REFERENCE 1 (bases 1 to 4523)
AUTHORS Fox,G.M., Holst,P.L., Chute,H.T., Lindberg,R.A., Janssen,A.M.,
          Basu,R. and Welcher,A.A.
TITLE     cDNA cloning and tissue distribution of five human Eph-like
          receptor protein-tyrosine kinases
JOURNAL   Oncogene 10 (5), 897-905 (1995)
MEDLINE   95206782
FEATURES
Source    1..4523
           /organism="Homo sapiens"
           /db_xref="taxon:9606"
           /dev_stage="Fetus, 17-18 weeks gestation"
           /sex="female"
           /clone="Stratagene premade library, cat #936206"
           /tissue_type="Brain"
mRNA      1..4523
           /gene="HEK11"
           /product="receptor protein-tyrosine kinase"
gene       1..4523
           /gene="HEK11"
           /product="receptor protein-tyrosine kinase"
5'UTR     1..185
           /gene="HEK11"
           /codon_start=1
           /product="receptor protein-tyrosine kinase"
           /protein_id="AA074243.1"
           /db_xref="GI:551608"
CDS        186..3182
           /gene="HEK11"
           /translation="VFQTRPSPVITLITWLRPAHTGEAQAKEYLLDSKAQTE
           LEWISSPPNGWEISGIDENYTPRTYOVCOMEPNQNWLNTNWSGNORFVEL
           KFTLDNCSLPGVLGTCKETENLYETDYDGNIRENLRYKIDTIADESFTGDL
           GERKMLNTEVEIGELPSKRGFLAFODVAGCALVAYKYKKMSIENIAFIDPT
           VTGSEFSSILVEVRGTCVSAEEEAENAPRMHSAEGLVPGKICAGAOQKDDC
           EPGCGEYKSSSODLCRCPHSDSKEGSSRCCEGYYRAEDPPYVACTRPSA
           PONLIFNINQTVSLEMSPPADNGRNQVYTRILKRCWEDECVPGSGNQTWPQ
           TGLDNYTVVDLHANVTEVEAVNVSQSLRSQRLFAAVSITTGQAAPSOVSGM
           KERYLQSRVELSMOPEHPNGVITEYEIKYEKIDQERTYSVTYKTSASINMLKPG
           TVYVQIRAFPAIAGYAGNSPRLDVALEATGKMEATVASEONPVIIINAVAGT
           IILVWVGFIIGRRHCGYSKADODELIVFHFPEGTKTYTIDETEDPRAVHOF
           AKELDASCITKIERVIGAGEPGEVCGSRKLKGRKRVAAITLKYTEKORDFICE
           ASIMGQPHPNVHLEGYVTRKRPVATIEFENGALDAFLKHGQFTVIOVGLR
           GIAGMRYLADMGVYHRDLAARNILVNSNLVCKSDFLSRVIDEDDPVAYTTGKI
           PVRWAPPAIORYKFTSADVWSYGIWMEVWASGEERFMSNDYIKALIEGYRLP
           APDCPPALHOLDCMOEKERAEKRFEOIYGIIDKMIKRNPSLTKPIGTGSRPSPL
           LDONPDFTFCVSGVELOATIKERYKDNFTPAAGYNSLESVARNITIEDVMSGITLVG
           HOKRMSSTQTRKRAOMLHKGIOY"
           /gene="HEK11"
3'UTR     3183..4523
           /gene="HEK11"
BASE COUNT 1447 a 833 c 999 g 1244 t
ORIGIN
Query Match 47.3%; Score 31.2; DB 10; Length 4523;
Best Local Similarity 70.0%; Pred. No. 0.097;
Matches 42; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Oy 7 ctactggattcaaaaacattcaaggagcgctggctgattctctatcatcactgg 66
    11111111111111111111111111111111111111111111111111111
Db 288 CTGCTGGATTCTTAAGCACACACAGAGTTGAGTGGATTCTCTCCACCAATGGG 347

RESULT 15
LOCUS     HSJ189K14 116490 bp DNA HTG 23-NOV-1999
DEFINITION Homo sapiens chromosome 6 clone RPI-189K14, *** SEQUENCING IN
PROGRESS ***, 6 unordered pieces.
ACCESSION AL121966
VERSION    AL121966.1 GI:6981849
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

```

REFERENCE 1 (bases 1 to 116490)
AUTHORS Sims,S.
TITLE     Direct Submission
JOURNAL   Submitted (16-OCT-1999) Wellcome Trust Genome Campus, Hinxton,
          Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
          humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
          On Feb 16, 2000 this sequence version replaced gi:6066105.
          IMPORTANT: This sequence is unfinished and does not necessarily
          represent the correct sequence. Work on the sequence is in progress
          and the release of this data is based on the understanding that the
          sequence may change as work continues. The sequence may be
          contaminated with foreign sequence from E.coli, yeast, vector,
          phage etc. Order of segments is not known; 800 n's separate
          segments. Unfinished: dj189K14 Contig_ID: 00239 acc=AL121966
          Length: 4081 bp Unfinished: dj189K14 Contig_ID: 00235
          acc=AL121966 Length: 19639 bp Unfinished: dj189K14 Contig_ID:
          00870 acc=AL121966 Length: 26994 bp Unfinished:
          Contig_ID: 00919 acc=AL121966 Length: 31021 bp Unfinished:
          dj189K14 Contig_ID: 01165 acc=AL121966 Length: 29139 bp
          Unfinished: dj189K14 Contig_ID: 01338 acc=AL121966 Length: 1616
          bp.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 4081: contig of 4081 bp in length
* 4082 4881: gap of 800 bp
* 4882 24520: contig of 19639 bp in length
* 24521 25320: gap of 800 bp
* 25321 52314: contig of 26994 bp in length
* 52315 53114: gap of 800 bp
* 53115 84135: contig of 31021 bp in length
* 84136 84935: gap of 800 bp
* 84936 114074: contig of 29139 bp in length
* 114075 114874: gap of 800 bp
* 114875 116490: contig of 1616 bp in length.
FEATURES
Source    1..116490
           /organism="Homo sapiens"
           /db_xref="taxon:9606"
           /chromosome="6"
           /clone="RPI-189K14"
           /clone_1b="RPCI-1"
BASE COUNT 37770 a 18571 c 20111 g 36038 t 4000 others
ORIGIN
Query Match 47.3%; Score 31.2; DB 32; Length 116490;
Best Local Similarity 70.0%; Pred. No. 0.13;
Matches 42; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Oy 7 ctactggattcaaaaacattcaaggagcgctggctgattctctatcatcactgg 66
    11111111111111111111111111111111111111111111111111111
Db 15905 CTGCTGGATTCTTAAGCACACACAGAGTTGAGTGGATTCTCTCCACCAATGGG 15964

```

Search completed: May 15, 2000, 11:43:14
Job time: 18621 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 11:20:19 ; Search time 1358.94 Seconds
(without alignments)
1368.540 Million cell updates/sec

Title: US-09-104-340-8

Perfect score: 660

Sequence: 1 tgggaagagatcagtggtgt.....aaagaggtttatgtgcca 660

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 202661650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*

45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_est45:*
80: gb_est46:*
81: gb_est47:*
82: gb_gss1:*
83: gb_gss2:*
84: gb_gss3:*
85: gb_gss4:*
86: em_gss1:*
87: em_gss2:*
88: em_gss3:*
89: em_gss4:*
90: gb_gss5:*
91: gb_gss6:*
92: gb_gss7:*
93: gb_gss8:*
94: gb_gss9:*
95: em_gss5:*
96: em_gss6:*
97: em_gss7:*
98: em_gss8:*
99: em_gss9:*
100: em_gss10:*
101: em_gss11:*
102: gb_gss10:*
103: gb_gss11:*
104: em_gss12:*
105: gb_gss12:*
106: gb_gss13:*
107: gb_gss14:*
108: gb_gss15:*
109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

Qy 596 g 596
Db 816 g 816

RESULT 2

H38363

LOCUS

DEFINITION

H38363 435 bp mRNA EST 16-AUG-1995
yp50q04.r1 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:190902 5', similar to gb:M83841 TYROSINE-PROTEIN KINASE
RECEPTOR HEK PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION H38363
VERSION H38363.1 GI:907862
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 435)
Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT On May 5, 1995 this sequence version replaced gi:797807.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
Insert Size: 2663
High quality sequence stops: 276
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 2663 Std Error: 0.00
Seq primer: M13Rev
High quality sequence stop: 276.
Location/Qualifiers

FEATURES

source

1..435
/organism="Homo sapiens"
/db_xref="GDB:3847311"
/db_xref="taxon:9606"
/clone="IMAGE:190902"
/clone_11b="Soares retina N2b4HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACATGTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted into
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 109 a 108 c 103 g 109 t 6 others
ORIGIN

Query Match 30.4%; Score 200.6; DB 23; Length 435;
Best Local Similarity 96.7%; Pred. No. 1.3e-48;
Matches 203; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 tgggaagatcatggtgtgtgataacattacacacccatcaagatccaggtgtgc 60
Db 220 TGGGAAGATCATGCTGTGTGTGATGACATTTACACACCCATGAGCTTACCAAGTGTGC 279
Qy 61 aatgtcatgacacacagtcataaacaattgctgtgagaacaactgggtcccaagaaacta 120
Db 280 AATGTCATGACACACAGTCATATAACATTTGCTGTAGAACAACTGGGTCCCAAGAACTCA 339
Qy 121 gcttcgaagaattatgtgtgagctcaagttcattctcaagcagactgtcaatgtcattcatg 180
Db 340 GCTCGAAGAAATTATGTGTGAGCTCAAGTTCACCTCTACGAGACTGCATAATGATTCATTN 399
Qy 181 gtttagaactgtcaagagacattcaac 210
Db 400 GTTTTAGNACTTNCAGGCGACATTAAAC 429

RESULT 3

AM175051

LOCUS

DEFINITION

AM175051 572 bp mRNA EST 16-NOV-1999
f131902.y1 Sugano Kawakami zebrafish DRB Dario rerio cDNA clone
2639282 5' similar to SW:EP44_CHICK Q07496 EPHRIN TYPE-A RECEPTOR 4
PRECURSOR ;, mRNA sequence.

ACCESSION AM175051
VERSION AM175051.1 GI:6441079
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Dario rerio

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
AUTHORS Eukaryota; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinidae; Rasbora; Dario.
1 (bases 1 to 572)
Sugano, S., Kawakami, K., Johnson, S., Li, F., Marra, M., Eddy, S.,
Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T.,
Martin, J., Page, D., Page, D., Steptoe, M., Underwood, K., Theising, B.,
Ritter, E., Bowers, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1999
Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189572.
Other ESTs: f131902.x1
Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
sequencing by: Washington University Genome Sequencing Center
Seq primer: T3 EF from Amersham
High quality sequence stop: 485.
Location/Qualifiers

FEATURES

source

1..572
/organism="Dario rerio"
/strain="AB"
/db_xref="taxon:7955"
/clone="2639282"
/clone_11b="Sugano Kawakami zebrafish DRB"
/sex="mixed (one male and one female, including
unfertilized eggs)"
/dev_stage="adult"
/lab_host="DH10B (phage resistant)"
/note="Vector: pHE18-F13; Site_1: DraIII (CACTGTG);
Site_2: DraIII (CACCATG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCCTTTTCTTTTCTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTGGCCCTGCTG], digested and cloned into distinct DraIII
sites of the pHE18-F13 vector (5' site CACTGTG, 3' site
CACCATG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science) and
kindly donated by Dr. Koichi Kawakami. Custom primers for
sequencing: 5' end primer CTTCGCTCTTAAGCTGCG and 3' end

BASE COUNT 169 a 136 c 160 g 104 t 3 others
 ORIGIN

Query Match 27.9%; Score 184.2; DB 74; Length 572;
 Best Local Similarity 70.8%; Pred. No. 9.4e-44;
 Matches 257; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

QY 1 tgggaagaagatcagtggtgtgtgagatgaacattacaccaccatca-ggacctaccaggtgtg 59
 |||||
 Db 196 TGGGAAGAGCTGAGCATCATGATGAGAGAAATACGCCAATCAGGGACGTCGCCANGTGTG 255
 QY 60 caatgtcatcagaccacagtcacaaacaaattgtgtgagaaacaaatgggtccccaaggaaatc 119
 |||||
 Db 256 CAACGTAATGGAACCCAGCAGCAACACTGGCTCCGAACGAGACTGGATCCCGCTGGCGG 315
 QY 120 agctcagaagaattatgtgtgagctcaagttcactctcagagagctgcaatgacattcatt 179
 |||||
 Db 316 AGCTACCGGGGTCTACATCGAGATCAAAATTCACCTCGTGACAGCAACGCCCTGGCAGG 375
 QY 180 ggttttagaagactcgaaggagacattcaacctgtactacatgagatctgattgtatca 239
 |||||
 Db 376 AGCATATGGAACTCGCAAGAGACCTTTAATCTTTACTATTATGAGTCCACAATGACAA 435
 QY 240 tgggtgtgaaatttcgagaagcatcagtttacaagaattgacacattgcaagctgtgaaag 299
 |||||
 Db 436 AGAGCGATACATCCGAAACAGATTACACAAATCGACATCGACATGATGTAAG 495
 QY 300 ttccactcaaatgagatctgtggagcgtatcttgaagctcaacacgtgagattgagaagt 359
 |||||
 Db 496 CTTCACGAGGTGACATAGAGACCCGATCATGAACTGAAACNGAGGTGAGGATGT 555
 QY 360 aag 362
 ||
 Db 556 GGG 558

RESULT 4
 B36983 LOCUS 424 bp DNA GSS 17-OCT-1997
 DEFINITION HS-1042-A2-F05-MR.abl C17 Human Genomic Sperm Library C Homo
 sapiens genomic clone Plate=CT 824 Col=10 Row=K, genomic survey
 sequence.
 ACCESSION B36983
 VERSION B36983.1 GI:2536352
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 424)
 Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
 Traicoff,R., Abajlan,C., Blanchard,A., West,A. and Hood,L.E.
 Construction of a Characterized Clone Resource for Genomic
 Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
 Tagged Connectors
 Unpublished (1997)
 JOURNAL Contact: Mahairas GG, Zackrone KD, Hood L
 COMMENT University of Washington
 Seattle, WA 98195, USA
 Tel: (206) 616-8744
 Fax: (206) 685-7301
 Email: kzackrone@u.washington.edu
 Sequence Tagged Connector
 Plate: CT 824 row: K column: 10
 Class: BAC ends
 High quality sequence stop: 424.

FEATURES

source
 1.424
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=CT 824 Col=10 Row=K"

/clone_1lb="C17 Human Genomic Sperm Library C"
 /sex="M"
 /note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
 E-Coli DH10B"
 BASE COUNT 123 a 77 c 101 g 122 t 1 others
 ORIGIN

Query Match 21.7%; Score 143.4; DB 84; Length 424;
 Best Local Similarity 67.7%; Pred. No. 8.9e-32;
 Matches 233; Conservative 0; Mismatches 102; Indels 9; Gaps 2;

QY 326 gtaattcgaagctcaacactgagattagagaagtaagctctgtcaacaagaaggattctt 385
 |||||
 Db 2 GNAATACCAAGCTTAACTACACTGAGAGTGAAGATGTGACCTTGTCCAAAAGGATTC 61
 QY 386 atttgacattcaagatgt 445
 |||||
 Db 62 ATCTGCTTTCAAGAGATGAGGCGCTTGCAATGCTTGGTTGTTCAAAGTGTACTACA 121
 QY 446 aaaaagcccatctacagtgagaagatcgtgctatgtttccagacaggtacc---catgg 502
 |||||
 Db 122 AGAAGTCTGCTGCATTTATGAGAACTTACTTCTTCCAGATACAGTACTGTTGAC 181
 QY 503 actccagctccctgtgtgagaggttagaggtctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 556
 |||||
 Db 182 AATTTCTCTTTAGTCGAGAGTTCGAGGACATGTGTACACATGACAGAGAGAAAGCGG 241
 QY 557 aagatctcgaagatgtagttagtgcagtagcagaagagcgaatgctgtgtaccattggcaagt 616
 |||||
 Db 242 AAAACGCCCCAGAGATGCTGCAAGTGCAGAAAGAGAAAGTGTAGTGTGATTCGAAAT 301
 QY 617 gtctctcaatgctgtgtatgaaagaaggttttattgtgtccaa 660
 |||||
 Db 302 GTATCTCAAGACGAGCTTACCAGCAAAAAGACAGCACTTGTGA 345

RESULT 5
 A1011631 LOCUS 474 bp mRNA EST 31-JAN-1999
 DEFINITION EST206082 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
 ROVA55.3' end, mRNA sequence.
 ACCESSION A1011631
 VERSION A1011631.1 GI:3225463
 KEYWORDS EST.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 474)
 Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
 Kerlavage,A.R. and Adams,M.D.
 Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat
 Gene Index
 Unpublished (1998)
 JOURNAL On Jan 19, 1998 this sequence version replaced gi:2153373.
 COMMENT Contact: Lee, NH
 ATCC

The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 Seq primer: M13-21.

FEATURES

source
 1.474
 /organism="Rattus sp."
 /db_xref="ATCC (inhost):2021827"
 /db_xref="taxon:10118"
 /clone="ROVA55"
 /clone_1lb="Normalized rat ovary, Bento Soares"
 /note="Organ: ovary; Vector: pTVT3Pac; Site_1: EcoRI;
 Site_2: NotI"

QY 364 ccctcaacaagaaggttatttgcattcaagaatgttgcttgcttg 423
 |||||
 Db 311 CCTGTGTCCTCCAGCGGCTTACTGCTTACTGTAACGGGAGCGAGTGGCTG 370
 QY 424 gtgtc 428
 |||||
 Db 371 GTGCC 375

RESULT 13
 AI967980/c
 LOCUS
 DEFINITION
 AI967980 418 bp mRNA EST 25-AUG-1999
 w111f04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516671 3'
 similar to SW:EPF8_MOUSE 009127 EPHRIN TYPE-A RECEPTOR 8 PRECURSOR
 ; mRNA sequence.

ACCESSION
 VERSION
 SOURCE
 ORGANISM
 AI967980.1 GI:5764798
 EST.
 human.
 Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 On Jun 5, 1998 this sequence version replaced gi:3189146.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html

FEATURES
 Source
 Seq primer: -400p from G1bco.
 Location/Qualifiers

1. 418
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2516671"
 /clone_1lb="NCI_CGAP_GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10b"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Plasmid DNA from the normalized library
 NCI_CGAP_GC4 was prepared and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from a pool of 5,000 clones made
 from the same library (clonoids 1257096-1258631,
 1469064-1470983, and 1475592-1476743). Subtraction by
 Bento Soares and M. Fatima Bonaldo."

BASE COUNT
 ORIGIN
 73 a 152 c 116 g 77 t

Query Match 13.4% Score 88.2; DB 63; Length 418;
 Best Local Similarity 62.9%; Pred. No. 1.6e-15;
 Matches 15; Conservative 0; Mismatches 88; Indels 3; Gaps 1;

QY 400 gatgttgctgtgtgtccttggtgtgtgtgagatatactcaaaagtgccattt 459
 |||||
 Db 417 GACATAGTGGCTCCCTGCGCATCTCTCGCATCTACTATTAAGAAAGTCCCTGCC 358
 |||||
 QY 460 acagatgaagaatctgcttatgttccagacaggttaaccatgagctccagctcc---ctg 516
 |||||

Db 357 ATGTGGCGCATTCGCTGCTTCTCGAGAGCACTGACGGGGCGACTGCTCTCACTG 298
 QY 517 gtgaggttaagggtctgtgtcaacaattctaagagaagaatcctccaagatgtac 576
 |||||
 Db 297 GTGAGGTGAGGGCCCATGTGCTGCGCACTACAGAGAGCGGACACACCAATGATGAC 238
 QY 577 tgcagtaacaagaagcgaatgctgtgtacccattgtgcaagtgttcctgcaatgctgctat 636
 |||||
 Db 237 TCGAGCGGGAGAGGGCGATGTGCTGCTGCCCATTCGGCAATGCGTGTGACAGTCCGGCTAC 178
 QY 637 gaaga 641
 |||||
 Db 177 GAGGA 173

RESULT 14
 AW366937/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 AW366937 344 bp mRNA EST 04-FEB-2000
 IL0-HT0156-251099-132-a12 HT0156 Homo sapiens cDNA, mRNA sequence.
 AW366937
 EST.
 human.
 Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 HCGP http://www.ludwig.org.br/ONESTES.
 The PAPSP/LICR Human Cancer Genome Project
 Unpublished (1999)
 On Mar 16, 1998 this sequence version replaced gi:2961824.
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?IL0&t2=IL0-HT0156-
 251099-132-a12&t3=1999-10-25&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 30
 High quality sequence stop: 343.
 Location/Qualifiers

FEATURES
 Source
 High quality sequence start: 30
 High quality sequence stop: 343.

1. 344
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1lb="HT0156"
 /dev_stage="Adult"
 /note="Organ: head,neck; Vector: puc18; site.1: SmaI;
 site.2: SmaI; A mini-library was made by cloning products
 derived from ONESTES PCR (U.S. Letters Patent application
 No. 196 716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue RNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT
 ORIGIN
 73 a 98 c 95 g 78 t

Query Match 13.0% Score 86; DB 80; Length 344;
 Best Local Similarity 60.1%; Pred. No. 6.6e-15;
 Matches 14; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 29 attacacacatcaggaactacaggtgtgcaatgcatgagaccacagcacaacatt 88
 |||||
 Db 268 ATGACATGCGGATCTACTGACTCCGTGTGCAACGTGATGTCTGGGACAGCAACT 209
 |||||
 QY 89 ggcgtgaacaactgggtcccccaggaactcagctcagaagattatgtgagctcaagt 148
 |||||

Db 208 GGGCGGCGACCACTGGTGTGTCACGAGAGAGAGCTGACGCTATCTTCATTGAGCTCAACT 149
QY 149 tcacttcaagactgcaatagcatccattggttttaggaacttgcaagagacatca 208
Db 148 TTAGCTAGCTGACGACCACTTCCCTGTGGCGGCGACCTCCCTCAAGAGACTTCA 89
QY 209 accttactactgagcttgatgatgatacatgagggatgaatttgagagcatcaagt 266
Db 88 ACCTTACTATGCGGAGTCAAGACCTGAGTACGCGCTCCAAATTCAGAGCGCCTGT 31

RESULT 15

AM045268 314 bp mRNA EST 18-SEP-1999
LOCUS UI-M-BH1-ekn-b-03-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone
DEFINITION UI-M-BH1-ekn-b-03-0-UI 3', mRNA sequence.
ACCESSION AM045268
VERSION AM045268.1 GI:5905797
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 314)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
On Jun 5, 1998 this sequence version replaced g1:3187490.
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov

JOURNAL
MEDLINE
COMMENT
REFERENCE
AUTHORS
TITLE
Normalizaton and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
On Jun 5, 1998 this sequence version replaced g1:3187490.
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov

Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLY-A-No.

FEATURES
source

Location/Qualifiers
1..314
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH1-ekn-b-03-0-UI"
/clone_lib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73p-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S2 library is a subtracted library derived from
NIH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_LIB=NIH_BMAP_M_S2
TAG_TISSUE=olfactory-bulbs
TAG_SEQ=CATGG"

BASE COUNT 72 a 84 c 96 g 61 t 1 others
ORIGIN

Query Match 11.5%; Score 75.6; DB 64; Length 314;
Best Local Similarity 62.6%; Pred. No. 7.4e-12;
Matches 117; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 32 acacacccatcagagacttaccagagtggtgcaatgataatgagaccacgctcaaaatgagc 91
Db 124 ACATGCTATCTACATGTCGTGTCGACGTCGATTCGCGGACGACGACCACTGGC 183
QY 92 tgaagacaaactgggtccccaagaaactcagctcaagaatattatgtgagctcaagtcca 151
Db 184 TCCGACCACTAGGTTGATACCGGAGAGGCGGACGATCTTATGAGCTCAAGTTCA 243
QY 152 cctcagagactgcaatagcatcattcattggttttaggaacttgcaagagacatccaac 211
Db 244 CGGTGCGAGACTGTAAACAGCTTCCCGGGTGGCCGACGCTCATGACAGACCTTCAAC 303
QY 212 tgtacta 218
Db 304 TCTACTA 310

Search completed: May 15, 2000, 11:20:21
Job time: 19144 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 12:05:06 ; Search time 102.62 Seconds
(without alignments)
816.623 Million cell updates/sec

Title: US-09-104-340-8

Perfect score: 660
1 tgggaagagatcagtggtgtt.....aaagaagtttatgtgccaa 660

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 226296 seqs, 63486255 residues

Total number of hits satisfying chosen parameters: 452592

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Issued Patents, NA.*
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/1na/5C.COMB.seq:*
4: /cgn2_6/ptodata/2/1na/5D.COMB.seq:*
5: /cgn2_6/ptodata/2/1na/6.COMB.seq:*
6: /cgn2_6/ptodata/2/1na/PTUS.COMB.seq:*
7: /cgn2_6/ptodata/2/1na/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	660	100.0	3132	1 US-08-167-919A-9	Sequence 9, Appl
2	660	100.0	3132	5 US-08-715-106-9	Sequence 9, Appl
3	463.2	70.2	3254	1 US-08-162-809-15	Sequence 15, Appl
4	327	49.5	3116	4 US-08-449-645A-14	Sequence 14, Appl
5	327	49.5	3116	4 US-08-702-367A-14	Sequence 14, Appl
6	327	49.5	3116	6 PCT-US95-04681-14	Sequence 14, Appl
7	327	49.5	3348	1 US-08-222-616-34	Sequence 14, Appl
8	327	49.5	3348	6 PCT-US95-04228-34	Sequence 34, Appl
9	321.2	48.7	3592	3 US-08-469-537A-100	Sequence 100, App
10	317.4	48.1	3906	3 US-08-469-537A-102	Sequence 102, App
11	317.4	48.1	4165	2 US-08-442-248-1	Sequence 1, Appl
12	317.4	48.1	4165	2 US-08-442-815-1	Sequence 1, Appl
13	317.4	48.1	4322	2 US-08-673-789-1	Sequence 1, Appl
14	303	45.9	3162	4 US-08-449-645A-12	Sequence 12, Appl
15	303	45.9	3162	4 US-08-702-367A-12	Sequence 12, Appl
16	303	45.9	3162	6 PCT-US95-04681-12	Sequence 12, Appl
17	303	45.9	4529	4 US-08-449-645A-16	Sequence 16, Appl
18	303	45.9	4529	4 US-08-702-367A-16	Sequence 16, Appl
19	303	45.9	4529	6 PCT-US95-04681-16	Sequence 16, Appl
20	298.2	45.2	2323	6 PCT-US96-00419-6	Sequence 6, Appl
21	298.2	45.2	2901	6 PCT-US96-00419-4	Sequence 6, Appl
22	298.2	45.2	4304	6 PCT-US96-00419-1	Sequence 1, Appl
23	245.2	37.2	3056	1 US-08-162-809-21	Sequence 21, Appl
24	245.2	37.2	3059	1 US-08-162-809-3	Sequence 3, Appl
25	245.2	37.2	3125	1 US-08-162-809-19	Sequence 19, Appl
26	219.6	33.3	2820	1 US-08-162-809-5	Sequence 5, Appl
27	186.8	28.3	4049	1 US-08-162-809-17	Sequence 17, Appl

28	186.8	28.3	4097	1 US-08-162-809-11	Sequence 11, Appl
29	168	25.5	2962	4 US-08-449-645A-10	Sequence 10, Appl
30	168	25.5	2962	4 US-08-702-367A-10	Sequence 10, Appl
31	168	25.5	2962	6 PCT-US95-04681-10	Sequence 10, Appl
32	138.4	21.0	3546	1 US-08-162-809-9	Sequence 9, Appl
33	138.4	21.0	3591	1 US-08-162-809-13	Sequence 13, Appl
34	119.8	18.2	3776	1 US-08-162-809-7	Sequence 7, Appl
35	117.6	17.8	2982	1 US-08-348-143-2	Sequence 2, Appl
36	117.6	17.8	2982	2 US-08-571-785-2	Sequence 2, Appl
37	117.6	17.8	4027	1 US-08-348-143-3	Sequence 3, Appl
38	117.6	17.8	4027	1 US-08-348-143-4	Sequence 4, Appl
39	117.6	17.8	4027	2 US-08-571-785-3	Sequence 3, Appl
40	117.6	17.8	4027	2 US-08-571-785-4	Sequence 4, Appl
41	98	14.8	3133	1 US-08-162-809-1	Sequence 1, Appl
42	79.8	12.1	3969	1 US-08-436-044-5	Sequence 5, Appl
43	79.8	12.1	3969	1 US-08-222-616-23	Sequence 23, Appl
44	79.8	12.1	3969	3 US-08-436-054-5	Sequence 5, Appl
45	79.8	12.1	3969	6 PCT-US95-04228-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-167-919A-9
: Sequence 9, Application US/08167919A
: Patent No. 5674691
: GENERAL INFORMATION:
: APPLICANT: Boyd, Andrew W.
: APPLICANT: Simpson, Richard J.
: APPLICANT: Wicks, Ian
: APPLICANT: Ward, Larry D.
: APPLICANT: Wilkinson, David
: TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
: NUMBER OF INVENTION: AND USE THEREOF
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Scully, Scott, Murphy & Presser
: STREET: 400 Garden City Plaza
: CITY: Garden City
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 11530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/167, 919A
: FILING DATE: 18-APR-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PK6841 (AU)
: FILING DATE: 21-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PK8992 (AU)
: FILING DATE: 12-DEC-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/AU92/00294
: FILING DATE: 19-JUN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Digiglio, Frank S.
: REGISTRATION NUMBER: 31,346
: REFERENCE/DOCKET NUMBER: 9159
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (516) 742-4343
: TELEFAX: (516) 742-4366
: TELEX: 230 901 SANS UR
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3132 base pairs
: TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..3048
US-08-167-919A-9

Query Match 100.0%; Score 660; DB 1; Length 3132;
Best Local Similarity 100.0%; Pred. No. 8.7e-208;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgggaagagatcagtggtgtgtgatacattacacccatcaggacttaccagtggtgc 60
DB 253 TGGGAAGAGATCAGTGTGTGTGATGATACACCCATCAGAGCTTACAGAGTGTGC 312
QY 61 aatgtcattgaccacagtcataaacaattgctgagagaacaattgggtccccaaggactca 120
DB 313 AATGTCATGTGACACAGTCAAAACAAATTGGTGAAGAACAACTGGGTCCCGAGAACTCA 372
QY 121 gctcagaagattatgtgtgagctcaagttcactctacgagactgacatagattccattg 180
DB 373 GCTCAGAAGATTATGTGTGAGCTCAAGTTCACTCTACGAGACTGCAGATTCATTG 432
QY 181 gtttagaactctgcaaggagacattcaaccctgtactacatgagtcgtatgatacat 240
DB 433 GTTTTAGAAGACTTGCAGAGACATTCACCTGTACTACATGAGTGTGATGATCAT 492
QY 241 ggggtgaaatttcgagagatcagtttacaagaattgacacattcgaactatgaagaat 300
DB 493 GGGGTGAAATTTTCGAGAGCATGATTACAAAGATTGACACCACTGATGAAAGT 552
QY 301 ttcactcaaatgactcttgaggagccgtattctgaagctcaacactgagattagaagta 360
DB 553 TTCACCTCAATGATTTGGGAGCCGTATTCTGAACCTCAACCTGAGATTAGAGAGTA 612
QY 361 ggtcctgtcaacaagaaggatttatttggcaattcaagatgtgtgtgtgtgtgc 420
DB 613 GGTCCGTCAACAAGAGGAGATTATTGTGGCAATTCAAGATGTTGCTGTGTGTGC 672
QY 421 ttgggtgtcgtgagagatatacttcaaaaagtgcccaattacagtgtaagaatcgtgata 480
DB 673 TTGGGTGTCTGTGAGATATACTTCAAAAAGTGCCATTACAGATGAAGATCTGCTAAG 732
QY 481 ttccagaacggtaccatctgagctccagtcctcgtgtgaggttagaggtctgtgc 540
DB 733 TTTCAGAGACGATNCCATGAGCTCCAGTCCCTGTGTGAGGTTAGAGGCTTTGTGTC 792
QY 541 aacaattctaaggaggaagatccctcaagatgtactgacgtacagaaggcgaatgctt 600
DB 793 AACAAATTCAAGAGGAGAGATCCTCCAGAGATGACTGCAGTACAGAAAGCGAATGCT 852
QY 601 gtaaccattggcagatgttctcctgcaatgtgtgtatgagaagaagatttattgtccaa 660
DB 853 GTACCCATTGGCAAGTCTCTGCAATGCTGCTATGAGAAAGAGGTTTATGTGCCAA 912

RESULT 2

US-08-715-106-9
Sequence 9, Application US/08715106
Patent No. 6020306
GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Plesser

STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..3048
US-08-715-106-9

Query Match 100.0%; Score 660; DB 5; Length 3132;
Best Local Similarity 100.0%; Pred. No. 8.7e-208;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgggaagagatcagtggtgtgtgatacattacacccatcaggacttaccagtggtgc 60
DB 253 TGGGAAGAGATCAGTGTGTGTGATGATACACCCATCAGAGCTTACAGAGTGTGC 312
QY 61 aatgtcattgaccacagtcataaacaattgctgagagaacaattgggtccccaaggactca 120
DB 313 AATGTCATGTGACACAGTCAAAACAAATTGGTGAAGAACAACTGGGTCCCGAGAACTCA 372
QY 121 gctcagaagattatgtgtgagctcaagttcactctacgagactgacatagattccattg 180
DB 373 GCTCAGAAGATTATGTGTGAGCTCAAGTTCACTCTACGAGACTGCAGATTCATTG 432
QY 181 gtttagaactctgcaaggagacattcaaccctgtactacatgagtcgtatgatacat 240
DB 433 GTTTTAGAAGACTTGCAGAGACATTCACCTGTACTACATGAGTGTGATGATCAT 492
QY 241 ggggtgaaatttcgagagatcagtttacaagaattgacacattgcaagctgtatgaagaat 300
DB 493 GGGGTGAAATTTTCGAGAGCATGATTACAAAGATTGACACCATTCGAGCTGATGAAAGT 552
QY 301 ttcactcaaatgactcttgaggagccgtattctgaagctcaacactgagattagaagaat 360
DB 553 TTCACCTCAATGATTTGGGAGCCGTATTCTGAAAGCTCAACCTGAGATTAGAGAGTA 612

OY	361	ggtcctgtcaacaagaagagtttattcttgcatctcaaatgtgtgtcttctgtgc	420
Db	613	ggtcctgtcaacaagaagagtttattcttgcatctcaaatgtgtgtcttctgtgc	672
OY	421	tttgtgtctgtgagatatacttcaaaaagtgtccattcaagtgaagaatctgtcagt	480
Db	673	tttgtgtctgtgagatatacttcaaaaagtgtccattcaagtgaagaatctgtcagt	732
OY	481	tttcagacaaggtgaccatgacatgacatcccaagtcctgtgtgaggtttaagaagtcctgtgc	540
Db	733	tttcagacaaggtgaccatgacatgacatcccaagtcctgtgtgaggtttaagaagtcctgtgc	792
OY	541	aacaatcttaagsgagaagatcctccaagaagtgtactgcgttacagaagaagtcgaatggtc	600
Db	793	aacaatcttaagsgagaagatcctccaagaaggtgtactgcgttacagaagaagtcgaatggtc	852
OY	601	gtaccacattgacaagtattctcgtcaatgtcgtgcataaagaagaagtttatagtgtcaa	660
Db	853	gtaccacattgacaagtattctcgtcaatgtcgtgcataaagaagaagtttatagtgtcaa	912

RESULT 3
US-08-162-809-15
; Sequence 15, Application US/08162809
; Patent No. 5457048

1. APPLICANT: pasquale, Elena B.
 2. APPLICANT: Sajjadi, Fereydoon G.
 3. TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
 4. TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
 5. NUMBER OF SEQUENCES: 26
 6. CORRESPONDENCE ADDRESS:

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92130

```

: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: Patentin Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/162,809
:
: FILING DATE:
:

```

? CLASSIFICATION: 514
 ?
 ? ATTORNEY/AGENT INFORMATION:
 ?
 ? NAME: Campbell, Cathryn A.
 ?
 ? REGISTRATION NUMBER: 31,815
 ?
 ? REFERENCE/DOCKET NUMBER: P-LJ 9503
 ?
 ? TELECOMMUNICATION INFORMATION:
 ?

TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 3254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
;
FEATURE:

```

```

;      NAME/KEY:  CDS
;      LOCATION:  32..2980
US-08-162-809-15

```

Query Match	70.2%	Score 463.2	DB 1	Length 3254
Best Local Similarity	81.4%	Pred. No. 6.3e-143		
Matches 537	Conservative 0	Mismatches 123	Indels 0	Gaps 0
1	tgggagagatcagcggcgtgtgaacttcacacccatcaggactaccaggtg	60		

Db	182	TGGGAAAGGATTAGNGGTGTGATGAGCATTTATACCTCAATCAGAACTTACCAAGAGAGC	241
Qy	61	aatgtcactgagccaccacatgtccaacaatlttgctgtgagaaccaactggygtccccaagaaetca	120
Db	242	AATGTATATGGATTCACAGCCAAACAAATTTGGCTGGGAACCAACTGGATTTCCACGCCAATTC	301
Qy	121	gctcgaagaatttatgttgagctcaagtctcactctacgaagctgcaatagcatctcatg	180
Db	302	GCGCAGAAGATATATGTGTGAGCTCAAGTTTACCTTGTAGGGGACTTCGAATATATATCCCTCTA	361
Qy	181	gltttaggaacttgcnaagagacatccaacctgtactactatgtagtctgtatgtatcat	240
Db	362	GTTCTGGGCACTTGCACAAAGAACCTTTCATCTGTATTTACATGTGAGATCCGATGTAGACCAT	421
Qy	241	gggtgtgaaatttcagagacatcagttctacaagaagtcttcaaccatctgactgtatgaagt	300
Db	422	TTGGCAAAAGTTTCAGAGACACCAATTTTACGAAAGTTTACACCAATGCGGCTGTATGAAGC	481
Qy	301	ttcactcaaatlgatctcttggagaccgfatcttgaagcttcaacactgtagatctaagaagta	360
Db	482	TTTCACCCAGATGGATCTTGGGGACCGGATTTCTCAAGCTGAATACCGAAGTCCCGAGAGTG	541
Qy	361	ggtcctgtccaacaaagaaggatlttatlttgcacatccaagaagtgttggtctgtgtgcc	420
Db	542	GGACCTGTTACTAGAGAGGGCTTTTACTTGCTTCCAAATGTAGAGTGCATGTGTTGCC	601
Qy	421	tttgtgtctgtgagaagataactttaaaagaagggccacttttcagtggaagaatctgycatg	480
Db	602	TTAGTCTGGGTGCGAGGTACTTTCAAGAGGGCCCTTTCACCTGTCCAAGAACTTCGCCATG	661
Qy	481	tttcagaacaaagtaccatgtgactcccaagtcccttggctggaagtttaagaggtctgtgc	540
Db	662	TTTCCAGATACAGTTCCATGTGATCCCAAGTCCCTGGTGGAGGTGCGGGTTCTTGTGTC	721
Qy	541	aacacttctaagsgaagaatctctccaagaagtactgcagttacacagaaggcgaatggtc	600
Db	722	AATCATTTCCAAGGAGAGAGACCCCAACCAAGATGTACTGCAGCACGAGAGAGAAATGGCTA	781
Qy	601	gtaccacattgcagaagtgtctctgcaaatgtctgagctatgaagaagaagttttagtggcaa	660
Db	782	GTCGCCATAGGGAAGTGCTTTGTGTAAATGCTGGCTATATAGAGAGAGGCTTGTGGTGGCAA	841

RESULT 4
US-08-449-645A-14
; Sequence 14, Application US/08449645A
; Patent No. 5981245

```

? GENERAL INFORMATION:
?
? APPLICANT: Fox, Gary M.
?
? TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
?
? TITLE OF INVENTION: Kinases
?
? NUMBER OF SEQUENCES: 43
?
? CORRESPONDENCE ADDRESS:
?

```

;; ADDRESSEE: Amgen Patent Operations/RBWA
;; STREET: 1840 Dehavilland Drive
;; CITY: Thousand Oaks

```

; STATE: Calif
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READAB
; MEDIUM TYPE:
; COMPUTER. TR

```

```
;
; CURRENT APPLICATION DATA:
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; OPERATING SYSTEM: PC-DOS/MS-DOS
; HARDWARE: IBM PC compatible
```

```

?
? FILING DATE:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Winter, Robert B.
? REFERENCE/DOCKET NUMBER: A-287
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:

```

LENGTH: 3116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 34..2994
US-08-449-645A-14

Query Match 49.5%; Score 327; DB 4; Length 3116;
Best Local Similarity 69.4%; Pred. No. 4.7e-98;
Matches 460; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 1 tgggaagagatcagtggtgtgataacattacacacccatcagagcagtggtgc 60
DB 193 TGGGAGGAGAGTGTATCATGTATGATAAATAATACCCATCCGAACTCCAGAGTGTGC 252
QY 61 aatgtcaatgagccacagtcataaacaatgtgtcgtgagaacaactgggtcccaagaactca 120
DB 253 AATGTGATGGAACCCAGCCAGATTAACCTGGCTACGAACTGATGGATCACCCGAGAAAGG 312
QY 121 gctcagaagaattatgtagtgatcaagtctcaactctacagatgagatggaattcattcatg 180
DB 313 GCTCAGAGGGGTATATATGATTAATTCACCTTGAGGGAGCTGCATAATGCTTCGGGCG 372
QY 181 gtttaagaactctgaagaagagacatccaactctactacatgagtgctgatgatcat 240
DB 373 GTCATGGGGGACTTGCAGAGAGAGCGTTTACCTGTACTACTATGATGATCAACAGCAAA 432
QY 241 ggggtgaaattcagagagatcagatttacaagaattgacacatgagcagtgatgaaagt 300
DB 433 GAGCGTTTCATCAGAGAGAGAACCAAGTTTGTCAAAATTGACACCATGCTCTGATGAGAGC 492
QY 301 ttcactcaaatgagatctgtggagccgattctgaagctcaacactgagattagagaagta 360
DB 493 TTCACCCCAAGTGGACATTGGTGTACAGAAATCATGAACTGAACACCGAGATCCGGGATGTA 552
QY 361 ggtcctgtcaacaagaaggatcttattatgtgcatctcaagatgtgtgtctgtgtgc 420
DB 553 GGGCCATTAAAGCAAAAGGGGTTTAACTGCGCTTTTCAAGAGTGGGGGCGTCGATCGGC 612
QY 421 ttgtgtctgtgtagagatatactcaaaaagtgcccaattcaagtgagaagaattgtgctatg 480
DB 613 CTGGATATCATGCTCCGTGTCTTATTAATAAAGTGTCCACTCACAGTCCGCAATGTGGCCAG 672
QY 481 ttccagagacaggtaccatg---gactccagagtcctgtgtgaggttagaggtcttgt 537
DB 673 TTTCCTGACACATCATCAGAGGGCTGATACGCTTCCCTGTGGAAATTCGAGGCTCTGT 732
QY 538 gtcaacaattctaaggaaggagatccctccaagatgtactgtcagtaagaagaagcgaaatg 597
DB 733 GTCAACAATCTAGAAAGAGAAAGATGTGCCAAAATGTACTGTGGGCAATGTGATATG 792
QY 598 ctgtgacccatgtggcaagtgtctcctgcaatgctgtgctatgaaagaaggttttatgtgc 657
DB 793 CTGGTATCACCATTGGCAAACTGCTATGCAACGCTGGGCAAGAGGAGCGGAGATGC 852
QY 658 caa 660
DB 853 CAA 855

RESULT 5
US-08-702-367A-14
Sequence 14; Application US/08702367A
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
Kinases
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702.367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 34..2994
US-08-702-367A-14

Query Match 49.5%; Score 327; DB 4; Length 3116;
Best Local Similarity 69.4%; Pred. No. 4.7e-98;
Matches 460; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 1 tgggaagagatcagtggtgtgataacattacacacccatcagagcagtggtgc 60
DB 193 TGGGAGGAGAGTGTATCATGTATGATAAATAATACCCATCCGAACTCCAGAGTGTGC 252
QY 61 aatgtcaatgagccacagtcataaacaatgtgtcgtgagaacaactgggtcccaagaactca 120
DB 253 AATGTGATGGAACCCAGCCAGATTAACCTGGCTACGAACTGATGGATCAACCGAGAAAGG 312
QY 121 gctcagaagaattatgtagtgatcaagtctcaactctacagatgagatggaattcattcatg 180
DB 313 GCTCAGAGGGGTATATATGATTAATTCACCTTGAGGGAGCTGCATAATGCTTCGGGCG 372
QY 181 gtttaagaactctgaagaagagacatccaactctactacatgagtgctgatgatcat 240
DB 373 GTCATGGGGGACTTGCAGAGAGAGCGTTTAACTGTACTACTATGATGATCAACAGCAAA 432
QY 241 ggggtgaaattcagagagatcagatttacaagaattgacacatgagcagtgatgaaagt 300
DB 433 GAGCGTTTCATCAGAGAGAGAACCAAGTTTGTCAAAATTGACACCATGCTCTGATGAGAGC 492
QY 301 ttcactcaaatgagatctgtggagccgattctgaagctcaacactgagattagagaagta 360
DB 493 TTCACCCCAAGTGGACATTGGTGTACAGAAATCATGAACTGAACACCGAGATCCGGGATGTA 552
QY 421 ttgtgtctgtgtagagatatactcaaaaagtgcccaattcaagtgagaagaattgtgctatg 480
DB 613 CTGGTATCACCATTGGCAAACTGCTATGCAACGCTGGGCAAGAGGAGCGGAGATGC 672
QY 481 ttccagagacaggtaccatg---gactccagagtcctgtgtgaggttagaggtcttgt 537
DB 673 TTTCCTGACACATCATCAGAGGGCTGATACGCTTCCCTGTGGAAATTCGAGGCTCTGT 732
QY 538 gtcaacaattctaaggaaggagatccctccaagatgtactgtcagtaagaagaagcgaaatg 597

```

Db      723  GTCAACAACATCAGAGAGAAAGATGTGCCAAAAAAGTACTGTGGGGCAGCATGTGATATGC 792
        ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      598  ctgtaccatctggcgaagtgttcctgcacatgctgcatgaaagaagagtttatgtgc 657
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      793  CTGTACCCATTGGCAACGTGCTTATGCAACGCTGGGCGATGAGGACGCGAGCAATGC 852
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      658  caa 660
        |||||
Db      853  CAA 855

RESULT      6
PCT-US95-04681-14
: Sequence 14, Application PC/TUS9504681
: GENERAL INFORMATION:
: APPLICANT: Fox, Gary M.
: TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
: TITLE OF INVENTION: Kinases
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Amgen Patent Operations/RBW
: STREET: 1840 Dehaviiland Drive
: CITY: Thousand Oaks
: STATE: California
: COUNTRY: USA
: ZIP: 91320
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/04681
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Winter, Robert B.
: REFERENCE/DOCKET NUMBER: A-287
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3116 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 34..2994
: PCT-US95-04681-14

Query Match      49.5%; Score 327; DB 6; Length 3116;
Best Local Similarity 69.4%; Pred. No. 4.7e-98;
Matches 460; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

Oy      1  tgggaagagatcagtggtgtgtatgaacatcacacccataaggacttaccagtggtgc 60
Db      193  TGGGAGGAAGTAGATATCATGTGATGAAAAAATAACCCCAATCGGAACCTACCAAGTGTC 252
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      61  aatgcatacggaccacagtcacaaacaattgctgtgagaacaactgggtcccgaaactca 120
Db      253  AATGATATGGAAACCCAGCCAGATACTGGCTACGCACTGATGGATCCCGAAGAGG 312
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      121  gctcgaagattatgtgtgagctcaagttcaactctcagcagagattgtaattgcatatcg 180
Db      313  GCTCAGAGGCTATATATTGAGATTAAATTACCTTGAGGAGGACTGCATATGCTTCCGGGC 372
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      181  gtttaaggaaacttgcagaaggagacattcaacctgtactacatgagtgatgatgatcat 240
Db      373  GTCATGGGAGCTTGAAGAGAGAGCGTTTAACTCCTGTACTACTATGANTCANACAGCAAAA 432
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      241  ggggtggaatttcgagagcatcagtttaccaaagattgacacattcagcgtatgaagt 300

```

```

Db 433 GAGCGTTTCATCAGAGAGGAACCAATTGTCAAAATTGACACCATTGCTGATGAGAGC 492
Qy 301 ttccctcaaatgagctcttggagaccggtatcttgaaagctcaacactgagattagaagta 360
Db 493 TTCAACCAAGTGAGCATTGGTGAGCAGAATCATGAGCTGAAACACCGAGATCGGGATGTA 552
Qy 361 ggtcctgtcaacaagaaggaatttatcttgacattccaagaattgtgtgtctgtgtcc 420
Db 553 GGGGCATTTAACCAAAAAGGGGTTTACTGCTTTCAGAGATGTGGGGGCTTCATCGCC 612
Qy 421 ttgtgtctgtgagagatatacttcaaaaagtgccattcaatgaagaatctggtctatg 480
Db 613 CTGGATATAGTCCGTGTGTCTTATATAAAAGTGCACCTACAGTCGCAATCTGGCCAG 672
Qy 481 ttccagacaagggagaccatg---gactcccaagtcacctgtgtgaggttaagggcttgt 537
Db 673 TTTCCTGACACACATCAGAGGGGCGTGATAGCTCTTCCCTGCTGGAAGTTCAGGCTCCTG 732
Qy 538 gtcaacaatttcaagsgaagaatcctccaagaagtactgacgtacagaagcgaaatgg 557
Db 733 GTCAACAACCTAGAGAGAGAAAGATGTGCCAAAATGATCTGTGGGCGAGATGATGATGG 792
Qy 598 ctgtaccatctggcaagtgcttctgtcaagctcggctatgaagaagagtttattgtgc 657
Db 793 CTGTGACCCATTGGCAACTGCTTATGCAACGCTGGGCGATGAGAGCGGACGAGATGTC 852
Qy 658 caa 660
Db 853 CAA 855

RESULT 7
US-08-222-616-34
: Sequence 34, Application US/08222616
: Patent No. 5635177
: GENERAL INFORMATION:
: APPLICANT: Bennett, Brian D.
: APPLICANT: Goeddel, David
: APPLICANT: Lee, James M.
: APPLICANT: Matthews, William
: APPLICANT: Tsai, Siao Ping
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/222,616
: FILING DATE: 4-APR-1994
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/00586
: FILING DATE: 22-JAN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/826935
: FILING DATE: 22-JAN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER:
: REFERENCE/DOCKET NUMBER: 821P2
: TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3348 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-222-616-34

Query Match 49.5%; Score 327; DB 1; Length 3348;
 Best Local Similarity 69.4%; Pred. No. 4.9e-98;

Matches 460; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

```

QY 1 tgggaagagatcagtggtgtgtgagatgaacattacacacccatcaggacttaccaggtgtgc 60
   ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
DB 160 TGGGAGGAGAGTGTATGATGATGAAAAAATACCAATCCGAACTTCCAAAGTGTGC 219
QY 61 aatgcatggaccacagctcaaaaacattggctgagaacaaactgggtccccaagaaactca 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 220 AATGTATGGAACCCAGCCAGATACTGGCTAGAACTGATTGGATCACCAGAAAGGG 279
QY 121 gctcaagaattatgtgtgggtcccaagttcaactctcaagagactgcgaatcgaattccatg 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 280 GCTCAAGAGGTGTATGTGATTAATTCACCTTGAGGAGCTGCATATGTTCTCCGGGC 339
QY 181 gttttaggaactctgcaagagagacattcaacctgtactacatggagttgtatgtatcat 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 340 GTATGAGGAGCTTGCAAGAGAGAGCTTTAAGCTTACTACTACTATGATACAAAGCAAA 399
QY 241 ggggtgaatttcgagaagacatcagtttacaagaattgacacattgcagctgtatgaagt 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 400 GAGCGTTTTCATCAGAGAGACAGTGTTCAAAATTGCACACATTCGCTGATGAGAGC 459
QY 301 ttacatcaaatgtatcttggggaccgtatcttgaagctcaacactgagattagaagaagta 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 460 TTACCCCAAGTGGACATGGTGTACAGATATCATGATGAGTGAACCGAGATCCGGGATGTA 519
QY 361 ggtcctgtcaacaagaaggattttatttggaatttcaagaatttggtgtgtgtgtgc 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 520 GGGCCATTAAAGCAAAAAGGGGTTTACTGCTTTTCAGATGTGGGGGCTTCGATCGCC 579
QY 421 ttgtgtctgtgtgagatatacttcaaaaagtgcacattacagttgaagaattctgtgtatg 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 580 CTGTATCACTCGTGTGTCTATTAATAAGTGTCACTACAGTCCGCAATCTGGCCAG 639
QY 481 ttcccaagacaggtaccatg---gaetcccaagtcctgtgtgaggttagaggtcttgt 537
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 640 TTTCTGTACACCATCATCAGAGGGGTGATACCTTCCTCGTGGAAAGTTCGAGGCTCTCTGT 699
QY 538 gtcaacaattctaagagagagatccctcaagagatgtacgtcagttacagaagaaggcgaatg 597
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 700 GTCAACAACCTCAGAAAGAAAGATGTGCCAAAATGTACTGTGGGCAAGATGGTGAATGG 759
QY 598 ctgtatcccaattgtgcaaggtttcctgtcaatgtgtcgtatgaagaagaaggttttattgtg 657
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 760 CTGTATCCCAATGTGGCAACTGCTATGCACAGCTGGGCAATGAGAGCGGACGGAATGC 819
QY 658 caa 660
   |||
DB 820 CAA 822

```

RESULT 8

PCT-US95-04228-34

Sequence 34, Application PC/TUS9504228

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Bennett, Brian D.

APPLICANT: Goeddel, David

APPLICANT: Lee, James M.

```

APPLICANT: Matthews, William
APPLICANT: Tsai, Shao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: path (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3348 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-04228-34

```

Query Match 49.5%; Score 327; DB 6; Length 3348;

Best Local Similarity 69.4%; Pred. No. 4.9e-98;

Matches 460; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

```

QY 1 tgggaagagatcagtggtgtgtgagatgaacattacacacccatcaggacttaccaggtgtgc 60
   ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
DB 160 TGGGAGGAGAGTGTATGATGATGAAAAAATACCAATCCGAACTTCCAAAGTGTGC 219
QY 61 aatgcatggaccacagctcaaaaacattggctgagaacaaactgggtccccaagaaactca 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 220 AATGTATGGAACCCAGCCAGATACTGGCTAGAACTGATTGGATCACCAGAAAGGG 279
QY 121 gctcaagaattatgtgtgggtcccaagttcaactctcagagactgcgaatcgaattccatg 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 280 GCTCAAGAGGTGTATGTGATTAATTCACCTTGAGGAGCTGCATATGTTCTCCGGGC 339
QY 181 gttttaggaactctgcaagagagacattcaacctgtactacatggagttgtatgtatgtatcat 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 340 GTATGAGGAGCTTGCAAGAGAGAGCTTTAAGCTTACTACTATGATACAAAGCAAA 399
QY 241 ggggtgaatttcgagaagacatcagtttacaagaattgacacattgcagctgatgaagt 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 400 GAGCGTTTTCATCAGAGAGACAGTGTTCAAAATTGCACACATTCGCTGATGAGAGC 459
QY 301 ttacatcaaatgtatcttggggaccgtatcttgaagctcaacacatcagattagaagaagta 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 460 TTACCCCAAGTGGACATGGTGTACAGATATCATGATGAGTGAACCGAGATCCGGGATGTA 519
QY 361 ggtcctgtcaacaagaaggattttatttggaatttcaagaatttggtgtgtgtgtgtgc 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 520 GGGCCATTAAAGCAAAAAGGGGTTTACTGCTTTTCAGATGTGGGGGCTTCGATCGCC 579

```

```

Oy 421 ttgggtctgtgaaaggttacttcaaaaagtgccattcaagtgaaagaaatctgcatg 480
Db 580 CTGGTATGAGTCCTGCTGTCTTTATTAATAAAGTGTCCACTCAAGTCCGCAATCTGGCCAG 639
Oy 481 ttccacaacacggtatcccatg---gactccagtcacctggtgaggttaagggtcttgt 537
Db 640 TTCTCTGACACATCACAAGGGGCGATGATACGCTTCCTCGTGGAGAAAGTTCAGAGCTCTGT 699
Oy 538 gtcaacaattctaaggaggaagatcctccaaagatgactgacgtacagaagaagcgaaatg 597
Db 700 GTCAACAACATCAGAAAGAAAGATGTGCCAATAATGTACTGTGGGGCAGATGGGAATGG 759
Oy 598 ctgtgaccattggcaagtgctctgtcaatgctgcatgaagaagaagtttatgtgc 657
Db 760 CTGGTACCATTTGGCAACTGCTTATGCAACGCTGGGATGAGGAGCGAGCGAGAAATGC 819
Oy 658 caa 660
Db 820 CAA 822

RESULT 9
US-08-469-537A-100
: Sequence 100, Application US/08469537A
: Patent No. 5843749
:
: GENERAL INFORMATION:
: APPLICANT: Maisondier, et al.
: TITLE OF INVENTION: KINASES
: TITLE OF INVENTION: RHAS
: NUMBER OF SEQUENCES: 107
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Regeneron Pharmaceuticals, Inc.
: STREET: 777 Old Saw Mill River Road
: CITY: Tarrytown
: STATE: NY
: COUNTRY: U.S.A.
: ZIP: 10591
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/469,537A
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/406,247
: FILING DATE: 17-MAR-1995
: APPLICATION NUMBER: USSN 08/144,992
: FILING DATE: 28-OCT-1993
: APPLICATION NUMBER: USSN 07/736,559
: FILING DATE: 26-JUL-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Kempster, Ph.D., Gail M
: REGISTRATION NUMBER: 32,143
: REFERENCE/DOCKET NUMBER: REG 070C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 914-345-7400
: TELEFAX: 914-345-7721
: TELEX:
:
: INFORMATION FOR SEQ ID NO: 100:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3592 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 598..3444
: FEATURE:
: NAME/KEY: modified_base

```

```

; LOCATION: 56 /mod_base- OTHER
; OTHER INFORMATION: /label= N
; OTHER INFORMATION: /note= "where N = G, A, C or T"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 3538
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /label= N
; OTHER INFORMATION: /note= "where N = G, A, C or T"
US-08-469-537A-100

Query Match 48.7%: Score 321.2; DB 3; Length 3592;
Best Local Similarity 68.9%: Pred. No. 4.1e-96;
Matches 456; Conservative 0; Mismatches 203; Indels 3; Gaps 1;

QY 1 tgggaagagatgaagtggtgtgtgataaacctcacacccatgaaggactacaggttggc 60
DB 763 TGGGATGCCATTACTGGAATGATGATGACCAACAGGCCCATCATACATACCGATATGC 822
QY 61 aatgcatgagccacagtlcaaaaacatttgctctgagacaacactgggtccccaagactca 120
DB 822 AATGTCATGGAACCAACACGAGAACACAGTGGCTCTACTCAATGGATGATCTCTGTATGT 882
QY 121 gctcagaagattatgtgtgagctcaagttactactctaagctgaagactgcaataagcat 180
DB 883 GCTCGAATAATTAAGTGTGAATGAGAGTTCACTTAGAGATTGTACAGCATCCCATGG 942
QY 181 gtttagagacttgtaagagagacatcaacctgctctacatgtagtctgatatcat 240
DB 943 GCTTGTGGCACTGTAAAGAAACATTCTCTGTATTTATTGAATCTGACCAATCCAC 1002
QY 241 ggggtgaaattcgcagagagcatcagtttcaaaagattgacaccattgcagctgatgaag 300
DB 1003 GGAATAAATTCAACGCCAAGCCAAATATTAAGATTGACACAAATTGCTGGGATGAGACT 1062
QY 301 ttcaactcaatgagatcttggggaccgtaattctgaagctcaacactgagattagaagta 360
DB 1063 TTACTTCAGATGATTTGGGTGATGSCATCCTTTAACTCAACACAGAGTTCGTGAGTGG 1122
QY 361 ggtctgtcaacaagaagagatttaatttgagatttcaagaatggttggtgtgtgcc 420
DB 1123 GGGCCAAATGAAGAAGAAAGATTCTATTGGCTTTTCAAGATTGGAGCATGATGCT 1182
QY 421 ttgggtctgtgagagatatacttcaaaaagtgccattacagtgagaatctggtctatg 480
DB 1183 CTGGTCTCAGTCCGTGTGTCTTACAAAANAATGCCCTTCACTGTCCGGAACTGGCTATG 1242
QY 481 ttccaagacaggttacc--tgagctcccaagtcctccggttgtagagttagaagtcgtg 537
DB 1243 TTTCGGAAATACATCCCAAGGGTGTACTCTTCTCTTTGGTGAAGTGGGGGCTCATGCG 1302
QY 538 gtcaacaattctaagagaggaagatcctccaagatgtactgacagtcagagaaggcaatgg 597
DB 1303 GTGAAGAGATTGAGAGAGGAGATACTCTTAAACTCTATGTGGAGCTCATGGAACATGG 1362
QY 598 ctgtgacccattgggaagatggtctcgcgaatgtgctctatgagaagaagggttttatgtgc 657
DB 1363 CTCGTCCCTCTTGGAAAGGTATCTGTGACACTACAGGGATGAAGAATGAGGGTCTTGTGC 1422
QY 658 ca 659
DB 1423 CA 1424

RESULT 10
US-08-469-537A-102
; Sequence 102, Application US/08469537A
; Patent No. 5843749
; GENERAL INFORMATION:
; APPLICANT: Maisonnepierre, et al.
; TITLE OF INVENTION: EHR AND FOR TYROSINE

```


Db 1453 CNA 1455

RESULT 13
US-08-673-789-1
: Sequence 1, Application US/08673789
: Patent No. 5814479
: GENERAL INFORMATION:
: APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
: APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WODDE,
: APPLICANT: GEORGE, F.
: TITLE OF INVENTION: BSK RECEPTOR LIKE
: TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
: TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
: METHODS
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORGAN & FINNEGAN
: STREET: 345 PARK AVENUE
: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: USA
: ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4322
TYPE: NUCLEOTIDE
STRANDEDNESS: DOUBLE
TOPOLOGY: UNKNOWN
US-08-673-789-1

Query Match 48.1%; Score 317.4; DB 2; Length 4322;
Best Local Similarity 68.5%; Pred. No. 8,1e-95;
Matches 454; Conservative 0; Mismatches 206; Indels 3; Gaps 1;

QY 1 tgggaagaagatcagtggtggaatgaacattacacacccatcaggactaccagggtgagc 60
|||||
Db 670 TGGGAAGAGATTGTGATGATGAAGAACTATGCCCCATCCACACATACCAAGTGTGC 729
|||||

QY 61 aatgcataagacacagacaacaaattggtcgtgagaacaaattggtcccgagaactca 120
|||||
Db 730 AAAGTTATGGAACAAGATCGAATATGCGTGTGACCAAGTTGATCTTAACGAGGT 789
|||||

QY 121 gctcagaagatttaagtggaagctcaagttcactcagcagactgcaatagcatcctcatg 180
|||||
Db 790 GCTTCAGAAATCTTATTCAGACTCAAGTTTACTTTAAGGAGATCGAACAGCCTTCTCTGA 849
|||||

QY 181 gtttaagaacttgaagaagacatcaaccctgtactacatgagtgctgatatgatcat 240
|||||
Db 850 GGACTGGGGACTTGTAAAGAGACATTTAAATGATTTATTTGAATCAGATGATGAAAT 909
|||||

QY 241 ggggtgaaatttcgagagacatcagtttacaaagattgaacacattgcagctgataaagt 300
|||||

Db 910 GGGAGAAATATCAAGAGACCAATACATCAAGATTGATACCTGTCAGATGAGAC 969
|||||

QY 301 ttcactcaaatgagatcttgggagccgttatctgaagctcaacactgagatagaagaatga 360
|||||

Db 970 TTCACAGAACTTGATCTTGGTGACCCGTGTGATGAAGTGAATACAGAGATGATGC 1029
|||||

QY 361 ggtcctgtcaacaagaagaatttatattggaatttcaagaatgtgtgtctgtgtcc 420
|||||

Db 1030 GGACCTTGAGCAAAAGAGATTTTATCTTGCTTCCAAAGATGCGGCTTGATCTCT 1089
|||||

QY 421 ttgtgtctgtgagagatctactcaaaaatgcccattcaagtgagaatcctgtctatg 480
|||||

Db 1090 CTGGTTTGTGCTCGTGTACTATATAAGTGTCTCTGTAGTAAAGACTTGGCTATC 1149
|||||

QY 481 ttccagacaggtac---atgagccccaagtcctccggtggaggttaagggtctgt 537
|||||

Db 1150 TTCCTGACACTATCTACTGAGCAGATTCATCACAGTTGTTAGAGTGTCCAGGCTCTGC 1209
|||||

QY 538 gtcaacaattctaaggagaaatctcccaaggaatgactgacagacagaagcgaaatgg 597
|||||

Db 1210 GTCAACCAATTTCTGTACAGATGATCTCTCCAAAGATGATTCAGATGCGTGAAGGGAGTGC 1269
|||||

QY 598 ctgtacccattgcaagtgcttctgcaatgctgctatgagaagaaggtttatgtgc 657
|||||

Db 1270 CTGGTTCCCATTTGGGAATGATGTGCAAGGCTGTGATGAAGAAAAAATGTAAGTCTGC 1329
|||||

QY 658 caa 660
|||

Db 1330 CNA 1332

RESULT 14
US-08-449-645A-12
: Sequence 12, Application US/08449645A
: Patent No. 5981245
: GENERAL INFORMATION:
: APPLICANT: Fox, Gary M.
: TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
: Kinases
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Amgen Patent Operations/RBW
: STREET: 1840 Dehaven Drive
: CITY: Thousand Oaks
: STATE: California
: COUNTRY: USA
: ZIP: 91320

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2976
US-08-449-645A-12

```

Query Match      45.9%; Score 303; DB 4; Length 3162;
Best Local Similarity 67.1%; Pred. No. 3.8e-90;
Matches 445; Conservative 0; Mismatches 215; Indels 3; Gaps 1;

OY 1 tgggaagatcagtggtggtgatacattacacccatcaggtaccaggtgtgc 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 175 tgggaagatcagtggtggtgatacattacacccatcaggtaccaggtgtgc 234
OY 61 aatgcatgagcacagtcacaaacattgctgagacaaactgggtcccggaacta 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 AAGATGATGACAGATACAGATACAGATACAGATACAGATACAGATACAGAT 294
OY 121 gctcagaagattatggtgagctcaagtcactcactcagagactgacatgcat 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 GCTTCAGAACTTGTATAGAACTCAAAATTTACCTCGGAGACTGCAGACGCTTCTGGA 354
OY 181 gtttagaactctgcaagagacattcaaccgtactcaatgagtcgtatgatcat 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 355 GAGCTGGGACCTGTAGAGAAACCTTATATGTATTTAGTGTAGTATGATGATGATGAT 414
OY 241 ggggtgaatttcgagagatcagttacaaagattgacacattgacagctgagaa 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 415 GGGAGAAACATCAAGGAAACCAATACATCAATCAATCAATCAATCAATCAATCAAT 474
OY 301 ttactcaaatgagatcttgggagccgtatctgaagctcaacactgagattagaga 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 475 TTTACAGAACTTGATCTGTGAGCGGTGTATGAAACTGAATACAGAGGTCAAGATGTA 534
OY 361 ggtcctgcacaagaagagatttattcttggcattcaagatggtgtgtgtgtgc 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 535 GGAACCTTAAGGAAAGGATTTATCTGCTTTCAAGATGTGGTCTTGCAATTCGT 594
OY 421 ttggtctgtgagagatatactcaaaaagtgccattcaagtgagaaatttggtat 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 595 CGGTTTCGTGCTGTATACATTAATAAATGCCCCCTTCTGTGTAGCAACTTGGCTGTC 654
OY 481 ttccagacacggtaccatgagctccagtc---tggtagaggttagagaggtctgt 537
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 655 TTCCCTGACACCATCACTGAGACTGATCTCTCCCAATTCGTGAGAGTGTGGGCTCTGT 714
OY 538 gtcacacattcgaagagagaaagatctcgaagatgtagtcagtcagaagagcgaatg 597
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 715 GTCACACCATCTGTGACCGATGACCTCCCAAAATGCACTGACGCGCCAGAGGAGTGG 774
OY 598 ctgtgacattggaagaggttccctgcgaatgctggtcgtatgagaagagaggttttatg 657
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 775 CTGGTCCCATGGGAAATGCAATGTGCAAGGCAAGATATGAAGAGAAATGGCACTGT 834
OY 658 caa 660
   |||
DB 835 CAA 837

```

```

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2976
US-08-702-367A-12

```

```

Query Match      45.9%; Score 303; DB 4; Length 3162;
Best Local Similarity 67.1%; Pred. No. 3.8e-90;
Matches 445; Conservative 0; Mismatches 215; Indels 3; Gaps 1;

OY 1 tgggaagatcagtggtggtgatacattacacccatcaggtaccaggtgtgc 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 175 tgggaagatcagtggtggtgatacattacacccatcaggtaccaggtgtgc 234
OY 61 aatgcatgagcacagtcacaaacattgctgagacaaactgggtcccggaacta 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 AAGATGATGACAGATACAGATACAGATACAGATACAGATACAGATACAGAT 294
OY 121 gctcagaagattatggtgagctcaagtcactcactcagagactgacatgcat 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 GCTTCAGAACTTGTATAGAACTCAAAATTTACCTCGGAGACTGCAGACGCTTCTGGA 354
OY 181 gtttagaactctgcaagagacattcaaccgtactcaatgagtcgtatgatcat 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 355 GAGCTGGGACCTGTAGAGAAACCTTATATGTATTTAGTGTAGTATGATGATGAT 414
OY 241 ggggtgaatttcgagagatcagttacaaagattgacacattgacagctgagaa 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 415 GGGAGAAACATCAAGGAAACCAATACATCAATCAATCAATCAATCAATCAATCAAT 474
OY 301 ttactcaaatgagatcttgggagccgtatctgaagctcaacactgagattagaga 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 475 TTTACAGAACTTGATCTGTGAGCGGTGTATGAAACTGAATACAGAGGTCAAGATGTA 534
OY 361 ggtcctgcacaagaagagatttattcttggcattcaagatggtgtgtgtgtgc 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 535 GGAACCTTAAGGAAAGGATTTATCTGCTTTCAAGATGTGGTCTTGCAATTCGT 594
OY 421 ttggtctgtgagagatatactcaaaaagtgccattcaagtgagaaatttggtat 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 595 CGGTTTCGTGCTGTATACATTAATAAATGCCCCCTTCTGTGTAGCAACTTGGCTGTC 654
OY 481 ttccagacacggtaccatgagctccagtc---tggtagaggttagagaggtctgt 537
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 655 TTCCCTGACACCATCACTGAGACTGATCTCTCCCAATTCGTGAGAGTGTGGGCTCTGT 714
OY 538 gtcacacattcgaagagagaaagatctcgaagatgtagtcagtcagaagagcgaatg 597
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 715 GTCACACCATCTGTGACCGATGACCTCCCAAAATGCACTGACGCGCCAGAGGAGTGG 774
OY 598 ctgtgacattggaagaggttccctgcgaatgctggtcgtatgagaagagaggttttatg 657
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 775 CTGGTCCCATGGGAAATGCAATGTGCAAGGCAAGATATGAAGAGAAATGGCACTGT 834
OY 658 caa 660
   |||
DB 835 CAA 837

```

Wed May 17 09:45:58 2000

us-09-104-340-8.rni

Page 12

Search completed: May 15, 2000, 12:05:24
Job time: 4443 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OK nucleic - nucleic search, using sw model

Run on: May 15, 2000, 12:08:32 ; Search time 111.14 Seconds
(without alignments)
1485.755 Million cell updates/sec

Title: US-09-104-340-8
Perfect score: 660
Sequence: 1 tgggaagagatcagtggtgtt.....aaagaggtttatgtgcca 660

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues
Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	660	100.0	3132	1 034513	HEK coding sequenc
2	463.2	70.2	3254	1 090659	Eph-related PTK Ce
3	327	49.5	3116	1 T02948	Eph-1-like receptor
4	327	49.5	3348	1 T03100	Protein tyrosine-k
5	321.2	48.7	3592	1 V70208	Rat receptor tyros
6	317.4	48.1	3906	1 V70207	Rat receptor tyros
7	317.4	48.1	4165	1 T18893	Rat REX7 CDNA. AL-
8	317.4	48.1	4322	1 V58192	Mouse BSK receptor
9	303	45.9	3162	1 T02947	Eph-1-like receptor
10	303	45.9	4529	1 T02949	Eph-1-like receptor
11	298.2	45.2	2323	1 T32962	Mouse developmenta
12	298.2	45.2	2901	1 T32961	Mouse developmenta
13	298.2	45.2	4304	1 T32960	Mouse developmenta
14	245.2	37.2	3056	1 090662	Eph-related PTK Ce
15	245.2	37.2	3059	1 090663	Eph-related PTK Ce
16	245.2	37.2	3125	1 090661	Eph-related PTK Ce
17	219.6	33.3	2820	1 090654	Eph-related PTK Ce
18	202.2	30.6	4281	1 053471	elk CDNA. Expressi
19	192	29.1	3105	1 T07308	Receptor tyrosine
20	192	29.1	3105	1 T84528	Mouse Nuk tyrosine
21	186.8	28.3	4049	1 090660	Eph-related PTK Ce
22	186.8	28.3	4097	1 090657	Eph-related PTK Ce
23	168	25.5	2962	1 T02946	Eph-1-like receptor
24	138.4	21.0	3546	1 090656	Eph-related PTK Ce
25	138.4	21.0	3591	1 090658	Eph-related PTK Ce
26	119.8	18.2	3776	1 090655	Human embryonal ki
27	119.2	18.1	3751	1 062461	Human embryonal ki
28	117.6	17.8	2982	1 090971	Protein p140 CDNA
29	117.6	17.8	4027	1 090972	Protein p140 CDNA
30	115.2	17.5	3663	1 T72320	Embryonic stem cel
31	115.2	17.5	3663	1 T72320	Eph-related tyrosi
32	98	14.8	3133	1 090652	PTK gene HPTK5. Ne
33	80.6	12.2	3969	1 049757	Protein tyrosine-k
34	79.8	12.1	3969	1 T03099	

35	79.8	12.1	4290	1 092641	Human non-differen
36	79.8	12.1	4290	1 T18394	Receptor type tyro
37	79.8	12.1	4290	1 T42593	Coding sequence fo
38	79.8	12.1	4290	1 T51235	Receptor-type tyro
39	48.8	7.4	450	1 V90061	EST clone CM960. N
40	48.8	7.4	3673	1 V33697	Human thymus recep
41	48.8	7.4	4022	1 V62177	Human receptor typ
42	37.4	5.7	324	1 061342	Human brain expres
43	31.4	4.8	4822	1 V04445	Sequence used in d
44	31.2	4.7	786	1 V43665	Non-inducible immu
45	31.2	4.7	786	1 V46279	A. Chailana NIM-1

ALIGNMENTS

RESULT 1	
034513	Q34513 standard; DNA; 3132 BP.
ID	Q34513;
AC	Q34513;
DE	24-MAY-1993 (first entry)
DR	HEK coding sequence.
DT	HEK coding sequence.
KM	Primer: expression vector; extracellular domain; human; HEK;
KM	eph/elk-like; kinase; pre-B; cell; T; tumour; lymphoid; LK63;
KM	Lila-1; JM; epithelial; Hela; receptor-type; tyrosine kinase;
KM	TK; ligand; B;cellular response; growth; differentiation; ss.
OS	Synthetic.
PH	Key
FT	Location/Qualifiers
FT	5'utr
FT	1..99
FT	/*tag= a
FT	cds
FT	100..3051
FT	/*tag= b
FT	3'utr
FT	3052..3132
FT	/*tag= c
FT	signal_peptide
FT	100..159
FT	/*tag= d
FT	misc_feature
FT	1723..1795
FT	/*tag= e
FT	mat_peptide
FT	160..216
FT	/*tag= f
FT	/*note= "Purified HEK protein #1"
FT	2617..2679
FT	/*tag= g
FT	/*note= "Purified HEK protein #2"
PD	W03300425-A.
PD	07-JAN-1993.
PD	AU0294.
PR	19-JUN-1992; AU-006841.
PR	21-JUN-1991; AU-006841.
PR	12-DEC-1991; AU-009992.
PA	(HALL-) HALL INSR MEDICAL RES WALTER & ELIHA.
PI	Boyd AD, Simpson R, Ward LD, Wicks I, Wilkinson D;
DR	P-PSDB; R31466.
DR	WPI; 93-036373/04.
PT	Receptor-type tyrosine kinase reactive with monoclonal antibody
PT	IRI-A4 - is Eph-Elk-like kinase, useful for phosphorylating
PT	proteins in modulating pre-B, B and T cell function, in cancer
PT	therapy etc.
PS	Claim 6; Fig 1; 58pp; English.
CC	This sequence encodes human eph/elk-like kinase (HEK). HEK is
CC	expressed in both pre-B cells and T cell lines and in a number of
CC	tumours of human origin, eg. lymphoid tumours LK63, Lila-1 and JM,
CC	and the epithelial tumour Hela. This receptor-type thymidine kinase
CC	(TK) and/or its ligands are useful as agents in modulation of the
CC	production and/or function of pre-B, B and T cells. The TK and its
CC	analogues have activity in transducing signals or in stimulating
CC	cellular responses such as growth and/or differentiation.
SQ	Sequence 3132 BP; 888 A; 711 C; 759 G; 774 T;

Query Match 100.0%; Score 660; DB 1; Length 3132;
Best local Similarity 100.0%; Pred. No. 1.4e-209;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgggaagagatcagtggtgtggtgatacattacacacccatcaggaacttaccaggtgtgc 60
DB 253 TGGGAAGAGATCAGTGTGTGTGATGAACATTAACACCCATCAGACTTAACGAGGTGCG 312
QY 61 aatgtcatgaccacagctcaaaaacattgtctgagaaacaactgggtcccccaggaactca 120
DB 313 AATGTCATGACACAGCTAAAAACAATTGGCTGAGAACAAACGGGTCCCGAGAACTCA 372
QY 121 gttcagaagattatgttgagagctcaagttcactctcagagactcgaataagattcattcg 180
DB 373 GCTCAGAAATTTATGTGAGAGCTCAAGTTCACCTTACGAGACTGCAATATGCAATTCAT 432
QY 181 gtttaggaactctgcaagagagacattcaacctgtactacattgagttcgtatgatacat 240
DB 433 GTTTTAGAACTTGCAGAGAGACATTCACCTGTACTACTAGAGCTGATGATGATCAT 492
QY 241 ggggtgaattctcgagagacatcagtttacaagaattgacacacatctgagctgaataagt 300
DB 493 GGGGTGAATTTTCGAGAGCATGATTACAAAGATTGACACCATTCACCTGATGAAAGT 552
QY 301 ttoactcaaatgagatcttgaggacgtattctgaaagctcaacacatgagattagaagta 360
DB 553 TTCACCTCAATGATCTTGGGAGCCGTATTCTGAACCTCAACCTGAGATTAGAGAACTA 612
QY 361 ggtcctgtcaacaagaaggagatttatttggcaattcagaagattgtgtctgtgtgc 420
DB 613 GGCTCGTCAACAAAGAGGATTTATTGGCAATTCAAGATGTGTGTGTGTGC 672
QY 421 ttggtgtctgtgagagatatacttcaaaaagtgccatttcaagtgagaatctgctatg 480
DB 673 TTGGTGTCTGTGAGATATACCTTCAAAAAGTGCCTTTACATGAGAAATCTGGCTATG 732
QY 481 ttccagaacaggttaccatctgagctccagtcctgtgtgaggttgaaggtctgtgtgc 540
DB 733 TTTCAGAACAGGTATCCATGAGACTCCAGTCCCTGTGTGAGGTTTGAAGGTTTGTGTC 792
QY 541 aacaattctaaaggaggaagatcctccaagatgtactgcagtaacagaaggcgaaatgctt 600
DB 793 AACAAATTCAAGAGGAGAAATCCTCCAGAGATGACTGCAGTACAGAAAGCGAATGGCTT 852
QY 601 gtaaccattggcaagtgcttcctgcaatgtcgtgataagaagaaggtttatgtgtcca 660
DB 853 GTACCCATTGGCAAGTGTCTGCAATGCTGCTATGAAGAAAGAGGTTTATGTGCCAA 912

RESULT 2
QY 090659 standard; DNA; 3254 BP.
AC 090659;
DT 11-NOV-1995 (first entry)
DE EPH-related PTK Cdk4.
KW Cdk4; EPH; protein tyrosine-kinase; PTK; cancer; diagnosis;
OS Gallus sp.
FH Key
FT cds Location/Qualifiers
AC 32..2980 /*tag= a
FT MO9515375-A.
PN 08-JUN-1995.
PF 07-SEP-1994; U10140.
PR 03-DEC-1993; US-162809.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PI Paquale EB, Sajjadi FG;
DR WPI: 95-215256/28.
P-PSDB: R75711.
PT EPH-related protein tyrosine kinase(s) - for monitoring and diagnosing cancer.
PS Disclosure; Page 85-89; 129pp; English.
CC Probes derived from the EPH-related PTKs Cdk4 (090659) and Cdk5 (090660) were used to isolate novel cDNA clones (090652-58).
CC 090661-62) from chicken embryo and embryonic brain libraries.
CC Cdk4 is highly expressed in the chicken developing brain and

CC embryonic tissues, as well as in the adult brain and retina.
SQ Sequence 3254 BP; 926 A; 737 C; 796 G; 795 T;
Query Match 70.2%; Score 463.2; DB 1; Length 3254;
Best Local Similarity 81.4%; Pred. No. 4.4e-144;
Matches 537; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
QY 1 tgggaagagatcagtggtgtggtgatacattacacacccatcaggaacttaccaggtgtgc 60
DB 182 TGGGAAGAGATCAGTGTGTGTGATGAACATTAACACCCATCAGACTTAACGAGGTGCG 241
QY 61 aatgtcatgaccacagctcaaaaacattgtctgagaaacaactgggtcccccaggaactca 120
DB 242 AATGTCATGACACAGCTAAAAACAATTGGCTGAGAACAAACGGGTCCCGAGAACTCA 301
QY 121 gttcagaagattatgttgagagctcaagttcactctcagagactcgaataagattcattcg 180
DB 302 GGCAGAAAGATATATGTGAGAGCTCAAGTTCACCTTGAAGGAGCTGCAATATGATCCCTCTA 361
QY 181 gtttaggaactctgcaagagagacattcaacctgtactacattgagttcgtatgatacat 240
DB 362 GTTTCGGCACTTGCAGAAAGACATTTCAATCTGTTATGATGAGATCCGATATGACCAT 421
QY 241 ggggtgaattctcgagagacatcagtttacaagaattgacacacatctgagctgaataagt 300
DB 422 TTGGCAAAAGTTCAAGAGACCAATTTAGAGATTGACACCATTCGCGCTGATGAGAC 481
QY 301 ttoactcaaatgagatcttgaggacgtattctgaaagctcaacacatgagattagaagta 360
DB 482 TTCACCCAGATGATCTTGGGAGCCGTATTCTGAACCTCAACCTGAGATTAGAGAACT 541
QY 361 ggtcctgtcaacaagaaggagatttatttggcaattcagaagattgtgtctgtgtgc 420
DB 542 GGACCTGTAGTAAAGAGGCGTTTACTTGCTTCCAGATGAGTGCATGATGTGTGC 601
QY 421 ttggtgtctgtgagagatatacttcaaaaagtgccatttcaagtgagaatctgctatg 480
DB 602 TTAGTCTCGTGCAGATGTATCAAGAGTGCCTTTCACTGTCAGTCAAGAACTCGCCCAT 661
QY 481 ttccagaacaggttaccatctgagctccagtcctgtgtgaggttgaaggtctgtgtgc 540
DB 662 TTTCAGATACAGTTCCTATGAGACTCCAGTCCCTGTGTGAGGTTTGTGTGTC 721
QY 541 aacaattctaaaggaggaagatcctccaagatgtactgcagtaacagaaggcgaaatgctt 600
DB 722 AATCATTCAGAGGAGAAAGCCACCCAGATGATGACAGCAGAGAAAGATATGCTTA 781
QY 601 gtaaccattggcaagtgcttcctgcaatgtcgtgataagaagaaggtttatgtgtcca 660
DB 782 GTGCCCATGAGGAAAGCTGTGTATGCTGCTATGAAGAGAGAGGCTTTCGTGCCAA 841

RESULT 3
QY T02948 standard; CDNA; 3116 BP.
AC T02948;
DT 16-APR-1996 (first entry)
DE EPH-like receptor protein tyrosine kinase HEK8 cDNA.
KW EPH-like receptor protein tyrosine kinase; PTK; HEK8;
KW human eph-like kinase; therapy; diagnosis; antibody; vector; ss.
OS Homo sapiens.
FH Key
FT cds Location/Qualifiers
AC 34..2994 /*tag= a
FT MO9528484-A1.
PN 26-OCT-1995.
PD 14-APR-1995; U04681.
PF 15-APR-1994; US-229509.
PR (AMGE-) AMGEN INC.
PI Fox GM, Jing S, Welcher AA;
DR WPI: 95-373799/48.
P-PSDB: R85091.

PT New nucleic acid encoding Eph-like receptor tyrosine kinase(s) -
PT and related vectors, host cells, proteins, antibodies etc., used
PT diagnostically and therapeutically to modulate receptor activation
PT or prodn.

Query Match	49.5%	Score 327;	DB 1;	Length 3116;
Best Local Similarity	69.48;	Pred. No. 9.2e-99;		
Matches 460; Conservative	0;	Mismatches 200;	Indels 3;	Gaps 1

QY	1	ttggaaagagatcagtgctgtgtgtgtgaacattacaccaccttcgaacttaccagtgctg	60
Db	193	TGGGGGAGAGTGAATATCATATGGAAGAAAAAATACCAATCCGAACTCTCCAAAGTGTGC	252
QY	61	aatgcatacagccacagtcacaacaatttggcttgagaaacaactggtgtccccagaactca	120
Db	253	AATGTGATGGAAACCCACGCAAAATAACTGGCTACGAACCTGTTGGATACCCGAGAAAGG	312
QY	121	gtccagaagaattatgtgagagctcaagttcaactctcagagactgcaatagcatlccatg	180
Db	313	GCTCAGAGGGGTATATATGAAATTAATTCACCTTTGAGGGGACTGCATATGCTTCCGGGC	372
QY	181	gttttaggaacttgcaaggagagacttcaacctgtacactacatgtgagtcctgatgatcat	240
Db	373	GTCAATGGGGACTTTCAGAGGAGACCTTTAACTGTACACATGATGATAGCAACGACAAA	432
QY	241	ggggtgaaatttcgagagcacctcagtttacaagaattacaccacttgtagctgtagaagt	300
Db	433	GAGGGTTTCATCAGAGAGAACCACTTTGTCAAATTTACACCACTTGTCTGTATGAGGC	492
QY	301	ttcactcaaatggaatcttgyggaccgtaattctgaagctcaacactgagatlaagaagta	360
Db	493	TTCAACCCAAAGTGACATTTGGTACAGATCATGAAAGCTGAACCCGAGATCCGGAGTGA	552
QY	361	ggtccctgcacaagaaggagatttatttggcatlccaagatgtgtgtgtgtgtcc	420
Db	553	GGGGCATTTAAACCAAAAGGGGCTTTTACTGGCTTTTCAGAGATGGGGGCTCTCATCGCC	612
QY	421	tttgtgtctgtgagagatatacttcaaaaagtgccacttcaagtgaaagaatctgcatg	480
Db	613	CTGGTATACAGTCCGTGTGTTTATATAAAGATGTCACTACAGTCCGCAATCTGGGCCAG	672
QY	481	tttccagaacagtgtaacctgt---gactccaggtccctgtgtgaggttgaaggtctgt	537
Db	673	TTTCTGTGACACATACACAGGGGGCTGATACGCTCTCCCTGGGTGAAGTTCCAGGCTCCTG	732
QY	538	gtcaacaatttaagaggaagaagatcctccaaagatgtactgtcagltacagaagtcgaatg	597
Db	733	GTCAACAACATCAGAAAGAGAAAGATGTGCAAAAATATGATCTGTGGGGCAGATGGGAATGG	792
QY	598	ctgttaccacattgccaagtgtctctgaaatgtgtgcatgaagaagaagtttattgtgc	657
Db	793	CTGTGATCCCATTTGGCAACTGCTTATGCAACGCTGGCATAGAGCCGACCGAGAGATGC	852
QY	658	caa 660	
Db	853	CAA 855	
RESULT	4		
703100			

ID T03100 standard; DNA; 3348 bp.
AC T03100:
DT 14-FEB-1996 (first entry)
DE Protein tyrosine-kinase PTK7 gene.
KW Protein tyrosine-kinase; PTK; ptk7; agonist; cell growth;
OS differential; ss.
KW Homo sapiens.

FH	Key	location/Qualifiers
FT	cds	1..2961
FT		/*tag= a
FT	signal_peptide	1..57
FT		/*tag= b
FT	mat_peptide	58..2958
FT		/*tag= c
PN	W09527061-A1.	
PD	12-OCT-1995.	
PF	04-APR-1995; U04228.	
PR	04-APR-1994; US-222616.	
PA	(GETH) GENENTECH INC.	
PI	Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP,	
PI	Wood WI,	
DR	WPI; 95-366160/47.	

PR Agonist antibodies which activate specific protein tyrosine
PR kinases) - also activate chimeric proteins of kinase extracellular
PR domain and Ig constant domain, useful for studying, and therapeutic
PR modulation of, cell growth and differentiation
PS Disclosure; Page 88-92; 125pp; English.

CC DNA probes based on protein tyrosine-kinase (PTK) sequences were used
CC to screen cDNA libraries to identify novel ptk genes. The bptks,
CC bptp1, bptk2, bptk3, bptk4, bptk5 and bptk6 (R85924-28 and R85933,
CC respectively) are expressed in human brain tissue and show homology
CC to known PTKs. A full-length sequence for the bptk7 gene (T03100)
CC was obtained. This gene may be used to design new drugs, peptides and
CC antisense constructs that modulate ptk activity.
SQ Sequence 3348 BP; 924 A; 769 C; 855 G; 800 T;

Query Match	49.58;	Score 327;	DB 1;	Length 3348;
Best Local Similarity	69.48;	Pred. No. 9.6e-99;		
Matches 460; Conservative	0;	Mismatches 200;	Indels 3;	Gaps 1.

QY	1	tggsaagagcatcagtggtgtgtatgaacattacaccaccatcagacttaccagtgctg	60
Db	160	tggggggaagtagatgATCATGGAATGAAAAAATATACCAATCCAACTTACCAAGTGTGC	219
QY	61	aatgcacatgagccacagctcaacaacattgctgtgaacaacactggtgcccaagaaactca	120
Db	220	AATGATGATGGAACCCAGCCCAATATACGCGTTACGAACTGATTGGATCTACCCGGAAGGG	279
QY	121	gtctgaagaatttatgtgagctcaagttcactctacagagctgcaataagcatctcatg	180
Db	280	GCTCAGAGGGGTATATATGAAATTAAATTCACCTTGAGGGGACTGCATATGCTTCCGGGC	339
QY	181	gttttaggaactltgcaagagaacattcaacctgacacatagatggtctgtatgatcat	240
Db	340	GTCATGGGGACTTGCAGAGGAACGCTTTTAACTGTACTATCTATGATATGACAAACGACAAA	399
QY	241	ggggtgaaatttcgaagagcatcagtttacaagaattacacacatctgacatgtatgaagt	300
Db	400	GAGCGTTTCATCAGAGGAACACAGTTGTCAAATATGCACCATGTGCTGATGAAAGC	459
QY	301	ttcactcaaatgagatcttggggaccgtattcttgaagctcaacactgagatagaagaatga	360
Db	460	TTCAACCCAAAGTGGAATTGTGACAGATCTGGAAGCTGAACACCGAGATCCGGGAGTGA	519
QY	361	ggctctgcacaagaaggaatttatattgctcatccaagatggtgtgtcttgtgtgc	420
Db	520	GGGCGCATTTAACCAGAAAAGGGTTTAACTGGCTTTTGAAGATGTGGGGCCCTGCATCGCC	579
QY	421	ttgtgtctctgtgagagatacttcaaaaagtgtccacttaccagltgaagaatctgtgcatg	480
Db	580	GTGGATATAGTCCGTGTCTTTATATAAAGTGTCCACTCAGTCCGCATCTGGGCCAG	639

```

QY 481 ttccagacaggtaccatg---gactccagtccttggtgaggttagaggtcttct 537
DB 640 TTTCCGATCACCATCACAGGGCGCTGTACGTCTTCCCTGGTGAATGAGGCTCTGT 699
QY 538 gtcaacaattcgaaggaggaagatcctcgaagatgtactgcagtcgtcagaagcgatgg 557
DB 700 gtcaacaactcgaagaggaagatgtgccaataatgtactgtggcagatggtgaatgg 759
QY 598 ctgtacccatgtgcaagtgctcctcgaatgtctgctatgaagaagagtttattgtgc 657
DB 760 CTGCTACCATTTGGCAACGTCCTATGCAACGCTGGCATTGAGAGAGCGGAGCGAATGC 819
QY 658 caa 660
DB 820 CAA 822

RESULT 5
V70208
ID V70208 standard; DNA; 3592 BP.
AC V70208;
DR 11-FEB-1999 (first entry)
DE Rat receptor tyrosine kinase Ehk-2 encoding DNA.
KW Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection;
KW neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
KW binding protein; BDNF; NT-3; diagnosis; ss.
OS Rattus sp.
FH Key Location/Qualifiers
FT CDS 598..3444
FT FT /tag= a
FN US5843749-A.
PD 01-DEC-1998.
PF 06-JUN-1995; 469537.
PR 17-MAR-1995; US-406247.
PR 26-JUL-1991; US-736559.
PR 28-OCT-1993; US-144992.
PR 06-JUN-1995; US-469537.
PA (REG-) REGENERON PHARM INC.
PI Maisondier PC, Maslakowski P, Yancopoulos GD;
DR WPI: 99-044584/04.
DR P-PSDB: W83148.
PT DNA encoding receptor tyrosine kinase proteins - and corresponding
PT proteins
PS Claim 7; Fig 21; 194pp; English.
CC The present invention describes nucleic acid molecules for ror-1,
CC ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins:
CC Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor
CC tyrosine kinases. The present sequence encodes rat Ehk-2.
SQ Sequence 3592 BP; 946 A; 916 C; 894 G; 834 T;

Query Match 48.7%; Score 321.2; DB 1; Length 3592;
Best Local Similarity 68.9%; Pred. No. 8.5e-97;
Matches 456; Conservative 0; Mismatches 203; Indels 3; Gaps 1;

```

```

DB 1003 GGAACTAAATTCAGCCCAAGCCAAATATATAAGATTGACACAAATTCGCGATGAGACT 1062
QY 301 ttactcaatgtgacttgggacgctatctgaagctcaaacctgagattagaaagta 360
DB 1063 TTTACTCAATGATGATTTGGGTGATCCATCTTAACTAACTACTGTGAGCTGATGAGACTGG 1122
QY 361 gttcctgtcaacaagaaggaatttatttgcattcgaagatgtgtgttctgttgc 420
DB 1123 GGCCCAATGAAAGAAAGGATTCATTTGGCTTTTCAAGATATTGGACATGACATTCGT 1182
QY 421 ttggtctgtgtagagatatacttcaaaaagtgcattcaagtgtagaagatctgtatg 480
DB 1183 CTGCTCAGTCCGTGTCTTACAAAATAATCCCTTCATCTGTGGGAACTGGCTATG 1242
QY 481 ttccagacaggtaccga---tgactccagtcctcgttggtgaggttagaggtcttct 537
DB 1243 TTTCCGATCACCATCCCAAGGTTGACTTCTCTTGGTGAATGCGGGCTCATGC 1302
QY 538 gtcaacaattcgaaggaggaagatcctcgaagatgtactgcagtagcagaagcgatgg 597
DB 1303 GTGAAGATTTCTGAGAGGAGGAGATCTCTTAACCTACTGTGAGCTGATGAGACTGG 1362
QY 598 ctgtacccatgtgcaagtgctcctcgaatgtctgctatgaagaagagtttattgtgc 657
DB 1363 CTGCTCCTCTTGGAAAGGTGATCTGCTACACAGGCTATGAAGAAATCGAGGTTCTTGC 1422
QY 658 ca 659
DB 1423 CA 1424

```

```

RESULT 6
V70207
ID V70207 standard; DNA; 3906 BP.
AC V70207;
DR 11-FEB-1999 (first entry)
DE Rat receptor tyrosine kinase Ehk-1 encoding DNA.
KW Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection;
KW neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
KW binding protein; BDNF; NT-3; diagnosis; ss.
OS Rattus sp.
FH Key Location/Qualifiers
FT CDS 476..3493
FT FT /tag= a
FN US5843749-A.
PD 01-DEC-1998.
PF 06-JUN-1995; 469537.
PR 17-MAR-1995; US-406247.
PR 26-JUL-1991; US-736559.
PR 28-OCT-1993; US-144992.
PR 06-JUN-1995; US-469537.
PA (REG-) REGENERON PHARM INC.
PI Maisondier PC, Maslakowski P, Yancopoulos GD;
DR WPI: 99-044584/04.
DR P-PSDB: W83147.
PT DNA encoding receptor tyrosine kinase proteins - and corresponding
PT proteins
PS Claim 5; Fig 22; 194pp; English.
CC The present invention describes nucleic acid molecules for ror-1,
CC ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins:
CC Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor
CC tyrosine kinases. The present sequence encodes rat Ehk-1.
SQ Sequence 3906 BP; 1097 A; 876 C; 990 G; 943 T;

Query Match 48.1%; Score 317.4; DB 1; Length 3906;
Best Local Similarity 68.5%; Pred. No. 1.6e-95;
Matches 454; Conservative 0; Mismatches 206; Indels 3; Gaps 1;

```



```
OY 61 aatgcatgaccacagtcacaaacaattggtctgagacaacattggtccccagactca 120
DB 788 AAGATTATGGAACAAATACAGATATATGGCTGTGACCAGTGGATCTCTACAGAGT 847
OY 121 gctcagaagaatttatgtgagagctcaagttcactctacagagactgcaataagatccattg 180
DB 848 GCTTCCAAATTTTATGAACTCAAGTTACTGTAGAGGATTGCAACAGCCTTCTCGA 907
OY 181 gtttaggaacttggaagaagacattcaaccgtctactacatggaatctgatatcatat 240
DB 908 GGACTGGGAGCTTGCAAGAGAGCTTTTAACATGATTTATTTTGAATCCGATCATAGAT 967
OY 241 ggggtgaattctcagagacatcattcaagaagattgacacagctgagcagctgaagat 300
DB 968 GGGAGAAATATCAAGAACACAGTACATCAAGATCGATACCTGCTGCTGATAGAGC 1027
OY 301 ttcactcaaatggaatcttggggagccgtatcttgaagctcaacactgagattagaagta 360
DB 1028 TTCAACCGAACTTGACCTTGAGAGCCGGGTGATGAGCTGAATACGAGGTGATGATGA 1087
OY 361 ggtcctgcacaaagaagagtttatttattgcatctcaagaatggtgctgtgtgc 420
DB 1088 GGACCTCTGACGAAAGAGGATTTATCTTGTTCCTCAAGATGTGAGCTTGATCGCT 1147
OY 421 ttggtgtctgagaggtatacttcaaaaagtgccattacagtgtagaatctgctatg 480
DB 1148 CTGGTTTGTGTCGCTGTACTATATAAAATTCCTTCTGTGATTAGACATTTGGCTGTT 1207
OY 481 ttccaagaacaggtacccatggaactccagtc--tggtagaggttagaaggtctgt 537
DB 1208 TTCCCTGACAGATCAGAGACAGATTTCTTCCAGTTGCTAGAGGTGTCAGAGCTCGGC 1267
OY 538 gtcaacaattctaaaggagagatcctccaagagatgtaactgtagtgcagaagggcaatgg 597
DB 1268 GTCAACCAATCTGTGACAGAGATCTCCCAAAATGCAATTCGAGTGCAGAGGGAGTGG 1327
OY 598 ctgtgaccattggaagtgttccctgcaatgctggtctatgaaagaagaggtttatgtgc 657
DB 1328 CTGGTTCCCATCGGAATGCAATGTGCAGAGCCGATATGAGAGAAAAATGTTACCTGT 1387
OY 658 caa 660
DB 1388 CAA 1390

RESULT 7
T1893 T1893 standard; cDNA; 4165 BP.
AC T1893;
DN 05-JAN-1997 (first entry)
DE Rat REK7 cDNA.
KW REK7; eph-related tyrosine kinase receptor; AL-1; ligand;
KW neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis;
KW Rattus sp.
FH Key Location/Qualifiers
FT cds 541..3327
FT signal_peptide 541..711
FT mat_peptide 712..3324
FT /*tag= b
FT /*tag= c
PN MO9613518-A1.
PD 09-MAY-1996; U14016.
PE 26-OCT-1995; U14016.
PR 27-OCT-1994; US-330128.
PR 07-JUN-1995; US-486449.
PA (GETH ) GENENTECH INC.
PI Caras IM Winslow JM;
DR WPI: 96-239448/24.
DR P-PSDB: R97853.
PT AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in
```

```
PT treatment and diagnosis of neuronal disorders and
PR angiogenesis-related conditions.
PS Example 1: Page 47-49; 75pp; English.
CC A cDNA clone (T1893) codes for rat REK7 (R97853), an eph-related
CC tyrosine kinase receptor, for which AL-1 (see also W97854) is a
CC ligand. It was isolated using degenerate receptor tyrosine kinase
CC primers (T1894-96) to amplify cDNAs of an adult mouse hippocampal
CC cDNA library. A PCR fragment was used as a probe to isolate the
CC full-length REK7 cDNA from a rat hippocampal cDNA library. An
CC REK-igg fusion was used to screen cultured cell lines for surface
CC expression of REK7-binding activity. Primers based on isolated
CC ligands were used to amplify human breast carcinoma B720 cell
CC cDNA, and an amplified fragment was used to screen a human foetal
CC brain cDNA library, leading to the isolation of AL-1 cDNA (T18997).
SQ Sequence 4165 BP; 1157 A; 907 C; 1035 G; 1066 T;

Query Match 48.1%; Score 317.4; DB 1; Length 4165;
Best Local Similarity 68.5%; Pred. No. 1,7e-95;
Matches 454; Conservative 0; Mismatches 206; Indels 3; Gaps 1;

OY 1 tgggaagagatcagtggtgtagatgacattacacaccatcagacttaccaggtgctc 60
DB 793 TGGGAAGAGATTGGTGAAGTGAAGAAATATCCCCCATCCACACTATCAAGTGTGC 852
OY 61 aatgcatgaccacagtcacaaacaattggtctgagacaacattggtccccagactca 120
DB 853 AAGATTATGGAACAAATACAGATATATGGCTGTGACCAGTGGATCTCTACAGAGT 912
OY 121 gctcagaagaatttatgtgagagctcaagttcactctacagagctgcaataagatccattg 180
DB 913 GCTTCCAAATTTTATGAACTCAAGTTTACTGTAGAGGATTGCAACAGCCTTCTCGA 972
OY 181 gtttaggaacttggaagaagacattcaaccgtctactacatggaatctgatatcatat 240
DB 973 GGACTGGGAGCTTGCAAGAGAGCTTTTAACATGATTTTATTTGAGTCCGATGATGAGAT 1032
OY 241 ggggtgaattctcagagacatcagtttcaagaagattgacacatgcaagctgtagaagt 300
DB 1033 GGGAGAAATATCAAGAACACAGTACATCAAGATCGATTACATGCTGCTGATGAGAGC 1092
OY 301 ttcactcaaatggaatcttggggagccgtatcttgaagctcaacactgagattagaagta 360
DB 1093 TTCAACCGAACTTGACCTTGAGAGCCGGGTGATGAGCTGAATACGAGGTGATGATGA 1152
OY 361 ggtcctgcacaaagaagagtttatttattgcatctcaagaatggtgctgtgtgc 420
DB 1153 GGACCTCTGACGAAAGAGGATTTATCTTGTTCCTCAAGATGTGCGTTCGATGCT 1212
OY 421 ttggtgtctgagaggtatacttcaaaaagtgccattacagtgtagaatctgctatg 480
DB 1213 CTGGTTTGTGTCGCTGTACTATATAAAATGTCCTTCTGTGATTGACATTTGGCTGT 1272
OY 481 ttccaagaacaggtacccatggaactccagtc--tggtagaggttagaaggtctgt 537
DB 1273 TTCCCTGACAGATCAGTGGAGCAGATTTCTTCCAGTTGCTAGAGGTCTAGGCTCCGTC 1332
OY 538 gtcaacaattctaaaggagagatcctccaagagatgtaactgtagtgcagaagggcaatgg 597
DB 1333 GTCAACCAATCTGTGACAGAGATCCTCCAAATGCAATTCGAGTGCAGAGGGAGTGG 1392
OY 598 ctgtgaccattggaagtgttccctgcaatgctggtctatgaaagaagaggtttatgtgc 657
DB 1393 CTGGTTCCCATCGGAATGCAATGTGCAGAGCCGATATGAGAGAAAAATGTTACCTGT 1452
OY 658 caa 660
DB 1453 CAA 1455

RESULT 8
V58192 V58192 standard; cDNA; 4322 BP.
```

AC	VS8192; (first entry)
DT	25-NOV-1998
DE	Mouse Bsk receptor-like tyrosine kinase cDNA clone.
KW	Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neoplasm;
KW	neurodegenerative disease; limbic system neuron regeneration;
KW	chromosomal abnormality; degenerative growth; development disorder;
KW	viral infection; bacterial infection; Alzheimer's disease; epilepsy;
KW	schizophrenia; stroke; cerebral ischemia; ds.
OS	Mus sp.
FT	Key
FT	Location/Qualifiers
FT	418..3051
FT	/tag= a
FT	/product= "Bsk"
FT	/note= "receptor-like tyrosine kinase"
FN	US814479-A.
PD	29-SEP-1998.
PR	11-JUN-1996; 673789.
PR	04-JAN-1994; US-177812.
PR	11-JUN-1996; US-673789.
PA	(KROM/) KROMER L F.
PA	(SCHU/) SCHULZ N T.
PA	(WOUD/) WOUDÉ G F V.
PA	(ZHOU/) ZHOU R.
PI	Kromer LF, Schulz NT, Woudé GFV, Zhou R;
DR	WPI: 98-541751/46.
DR	P-PSDB: W71628.
PT	Isolated nucleic acid sequence encoding protein - used in Bsk
PT	nucleic acid probes, used in detecting alterations in level of Bsk
PT	messenger-RNA in biological samples isolated from mammal afflicted
PT	with disease
PS	Claim 2: Fig 2: 72pp: English.
CC	The present sequence encodes mouse Bsk, which is a receptor-like
CC	tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in
CC	Bsk nucleic acid probes, which can be used in detecting alterations in
CC	the level of Bsk messenger-RNA (mRNA) in biological samples isolated
CC	from a mammal afflicted with a disease, such as neurodegenerative
CC	diseases or disorders and neoplasms. The nucleic acid sequence can also
CC	be delivered into the limbic system of patients with limbic system
CC	neurodegenerative disease, disorder or injury, to promote or enhance
CC	limbic system neuron regeneration or growth. Such neurodegenerative
CC	diseases include, chromosomal abnormalities, degenerative growth and
CC	development disorders, viral infections, bacterial infections, brain
CC	injuries, neoplastic conditions, Alzheimer's disease, epilepsy,
CC	schizophrenia, or stroke and cerebral ischaemia.
SO	Sequence 4322 BP; 1260 A; 887 C; 1055 G; 1120 T;

D	b970	TTCACGAAGACTTGATCTGTGGTGCACCCTGTCATCGAATCAAGAATCAGAACAGTCCAGCATGCC		1029
Oy	361	ggtccctgcacaacaaaggagatttactttggcattccaagaatglttgtagtcgtcgcc		420
D	b1030	GGACCTGTGACGAAATAAGGATTATTTATCTTCTGCCAAGATGTGSGTCTGCATCTGCT		1089
Oy	421	ttagtgtcttggaagtatacttaaccaaaaagygcccatttacagtygaagaatctggcatg		480
D	b1090	CTGGTTTTGTCTCCGCTGTACTACTATTAATAAAGTGTCCCCTGTGTAAGACACTGGCTATCC		1149
OY	481	tttccagaacacgytatccc--calgatccccagtcgccctggtaggtttaaggatcctgt		537
D	b1150	TTCCTGTGACACTATACCTGGAGCACAGATTCATCACAGTTGTTTAGAGTGTCCAGGCTCTCC		1209
OY	538	gtcaacaattctaaggagaaagatcctccaaggatgtaactgcagtaacagaaagcgatatg		597
D	b1210	GTCACACCATTTCTGTACAGATGATCTCTCCAAGATGATGATTCGACAGTGAAGGAGNGTGC		1269
OY	598	ccttgaccaccttgagcaagtgcttcctgcacaatgctgcatatgaagaagaaggtttatgyc		657
D	b1270	CTGTGTTCCCCATTGGGAATATGCATGTGCACAAGCCTGTGATATGAAGAGAAAAATGTACTGCC		1329
OY	658	caa 660 D b 1330 CNA 1332		
R	E S U L T	9		
I D	T02947			
A C	T02947:	standard; cDNA; 3162 bp.		
D T	16-APR-1996	(first entry)		
K W	EPH-like receptor protein tyrosine kinase HEK7 cDNA.			
D E	EPH-like receptor protein tyrosine kinase; PTK; HEK7;			
K W	human eph-like kinase; therapy; diagnosis; vector; antibody; ss.			
O S	Homo sapiens.			
F H	Key	Location/Qualifiers		
F T	cds	1..2976		
F T		/tag= a		
P N	M095284B-A1.			
P D	26-OCT-1995.			
B F	14-APR-1995; U04681.			
P R	15-APR-1994; US-229509.			
P A	(AMGE-) AMGEN INC.			
P I	Fox GM, Jing S, Welcher AA;			
D R	WPI: 95-373799/48. P-PSD8: R85090.			
P T	New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -			
P T	and related vectors, host cells, proteins, antibodies etc., used			
P T	diagnostically and therapeutically to modulate receptor activation			
P T	or Prodn.			
P S	Claim 1: Page 49-54; 133pp; English.			
C C	CDNAs (T02946-49) coding for 4 novel human EPH-like receptor protein			
C C	tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively,			
C C	were isolated from a human foetal brain CDNA library using a directed			
C C	PCR approach with primers (see T02960-61) based on conserved regions of			
C C	receptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show			
C C	extensive homology to the catalytic domain of chicken EPH-like			
C C	receptors CeK5, CeK7 and CeK8. HEK1 shows no homology to any known			
C C	EPH-like receptor. The isolated cDNAs are used for Prodn. of			
C C	recombinant HEKs and chimeric receptors, in hybridisation assays, and			
C C	to detect abnormalities in HEK receptor genes.			
S O	Sequence 3162 BP; 921 A; 667 C; 775 G; 799 T;			
Q	Uery Match	45.9%; Score 303; DB 1; Length 3162;		
	Best Local Similarity	67.1%.; Pred. No. ge-91;		
	Matches 445; Conservative 0; Mismatches 215; Indels 3; Gaps 1.			
O Y	1 tgggaagagatcacgtggtgtgtgataaacatcacaccatcataagacttaccaggtlgtgc			60
D b	175 TGCGAAGAGATTTGTGGAAGTGGATGAATAATTTATGCCCCCTATCCACACATACCAATGATATGC			234


```

FH Key Location/Qualifiers
FT cds 233..2113
FT /tag= a
FT signal_peptide 233..316
FT /tag= b
FT mat_peptide 317..2110
FT /tag= c
FT /tag= d
FT misc_feature 2017..2113
FT /note= "divergent sequence due to alternative
FT splicing"
PV W09621013-A1.
PD 11-JUL-1996.
PE 03-JAN-1996; U00419.
PR 03-JAN-1995; US-368776.
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (SUGEN ) SUGEN INC.
PI Closssek T, Millauer B, Ullrich A;
DR WPI: 96-333988/33.
DR P-PSDB: W03423.
PT New mouse development kinase 1 gene - used for developing prods. for
PT diagnosis and treatment of abnormalities in signal transduction
PT pathways
PS Example 1: Page 115-116, 128pp; English.
CC cDNA cloning using adult mouse brains and Northern blotting
CC identified 2 clones, MDK1 T1 (T32961) and MDK1 T2 (T32962), that
CC coded for truncated versions (W03422 and W03423, respectively) of
CC the novel mouse developmental kinase 1 (MDK1) (see also T32960), a
CC new member of the eck/eph family of receptor tyrosine kinases.
CC MDK T1 and T2 each possess the entire ectodomain, the transmembrane
CC domain and part of the juxtamembrane region of MDK1 (see also W03421),
CC but lack the catalytic tyrosine kinase domain. They may have a
CC modulatory function. The cDNA clones can be used to produce MDK1
CC T1 and T2, which are useful for screening potential agents for
CC treatment of diseases characterised by abnormal signal transduction.
SQ Sequence 2323 BP; 680 A; 497 C; 609 G; 537 T;

```

```

Query Match 45.2%; Score 298.2; DB 1; Length 2323;
Best Local Similarity 67.6%; Pred. No. 3.1e-89;
Matches 452; Conservative 0; Mismatches 208; Indels 9; Gaps 2;

```

```

OY 1 tgggaagagatcagtggtgtgataacattacacccatcagagcttaccaggtgtgc 60
DB 395 TGGGAAGAAATATGAGTGTGATGAGACTACACTCCATAGAAACATACAGGTGTGC 454
OY 61 aatgtcatgtaccacagtcataaaatgtgtgagagacaaatgtgtcccggaactca 120
DB 455 CAGGTCATGTGAGCCCAACCAAGAACTGGCTGCGACTGAGTTCTTAAAGCAAC 514
OY 121 gctcagaagattatgtgagctcaagttcactctacgagactgcataagctcatcgt 180
DB 515 GCACAAAGAGTTTGTGTAATAATTGAATTCACCTTGAGGAGTTGTATGTCTCCGGA 574
OY 181 gtttcaggaacttcagagagacatacaactgtactacatgagtgatcgtatgcatc 240
DB 575 GTCCTGGGAGCTTGCAGAGAAAGCTTTAATTGTACTATTATGAACAACACACGACACC 634
OY 241 gggtgaaattcgcagagagatcagtttacaaagatgagacatgcatgcatgaagt 300
DB 635 GGCAGGAATATCGAGAAAACCTTTATGTTAAATATGACACCAATGCTCTCAATGAAT 694
OY 301 ttactcaaatgagatcttggggaccgtatctgaagctcaacactagatgtagagaagta 360
DB 695 TTCACAGCAAGTGAGCTTGTTGAAGAAAGATGAAGCTACACACTAGAGTGAGAGATT 754
OY 361 ggtcctgtcaacaagaaggatttattcgtgcaattcaagatgttggtgtgtgtgcc 420
DB 755 GGAACCTTTGTCAGAAAAGGAGATTCTATCTTGCTTTCAGAGATGAGGGCTTCATAGCA 814
OY 421 ttggtgtctgtgagagtaactcaaaagtgtcccatctacagtgtagaatctgtgtatg 480
DB 815 TTGGTTTCTGTCAAAAGTGTACTACAAAGAGTGCTGACCACTTGTGTAGAACTTACGCTGTC 874

```

```

OY 481 ttccagacacgtacc---catgactcccaagtcctcgtgtggaaggttagaggtctgt 537
DB 875 TTTCAGATACAGTGACACGCTTCGCAATTTTCTCTTACTAGTCGAGCTCCGTGGGACATGT 934
OY 538 gtcaacaattctaagga-----ggaagatcctccaagatgtactcagtaacagaagc 591
DB 935 GTCACAGTGTCCGAGAGAGAGCAAGAAATTCCTCCCAAGATGCATTGCGACGACAGAGA 994
OY 592 gaatgctgtgacccatggtgcaagtgctcctgcgaatgtgtgctatgaaagaaggtttc 651
DB 995 GAGTGCTAGTACCCATTGGAATGATCTGCAGAAAGCGCTATACACAAAAGGGAGC 1054
OY 652 atgtgcaa 660
DB 1055 ACTTGCGAA 1063

```

```

RESULT 12
ID T32961 standard; cDNA; 2901 BP.
AC T32961.
DT 11-NOV-1996 (first entry)
DE Mouse developmental kinase 1 MDK1 T1 clone.
KW RTK; signal transduction; probe; diagnosis; gene therapy;
KW neurodegeneration; neuroproliferation; cancer; ss.
OS Mus sp.

```

```

FH Key Location/Qualifiers
FT cds 233..2065
FT /tag= a
FT signal_peptide 233..316
FT /tag= b
FT mat_peptide 317..2062
FT /tag= c
FT misc_feature 2031..2065
FT /tag= d
FT /note= "divergent sequence due to alternative
FT splicing"
FT polyA_signal 2839..2843
FT /tag= e

```

```

PV W09621013-A1.
PD 11-JUL-1996.
PE 03-JAN-1996; U00419.
PR 03-JAN-1995; US-368776.
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (SUGEN ) SUGEN INC.
PI Closssek T, Millauer B, Ullrich A;
DR WPI: 96-333988/33.
DR P-PSDB: W03422.
PT New mouse development kinase 1 gene - used for developing prods. for
PT diagnosis and treatment of abnormalities in signal transduction
PT pathways
PS Example 1: Page 111-12, 128pp; English.
CC cDNA cloning using adult mouse brains and Northern blotting
CC identified 2 clones, MDK1 T1 (T32961) and MDK1 T2 (T32962), that
CC coded for truncated versions (W03422 and W03423, respectively) of
CC the novel mouse developmental kinase 1 (MDK1) (see also T32960), a
CC new member of the eck/eph family of receptor tyrosine kinases.
CC MDK T1 and T2 each possess the entire ectodomain, the transmembrane
CC domain and part of the juxtamembrane region of MDK1 (see also W03421),
CC but lack the catalytic tyrosine kinase domain. They may have a
CC modulatory function. The cDNA clones can be used to produce MDK1
CC T1 and T2, which are useful for screening potential agents for
CC treatment of diseases characterised by abnormal signal transduction.
SQ Sequence 2901 BP; 890 A; 578 C; 650 G; 783 T;

```

```

Query Match 45.2%; Score 298.2; DB 1; Length 2901;
Best Local Similarity 67.6%; Pred. No. 3.4e-89;
Matches 452; Conservative 0; Mismatches 208; Indels 9; Gaps 2;

```

```

OY 1 tgggaagagatcagtggtgtgataacattacacccatcagagcttaccaggtgtgc 60

```

```

Db      395 TGGGAAAGAAATAGTGGTTGGATGAGAACTACCTCCGATFAGAAACATACAGAGTGTC 454
Oy      61 aatgtcatgagccacagcacaacacatggtcgtgagaaacactggtcccaagaaacca 120
Db      455 CAGGTCATGAGGCCACACCAAGAACATGGCTGCGACTAATGATTTCTTAAAGGCAAC 514
Oy      121 gctcagaagaattatgtgagactcaagttcacctcaagactcgaatgaatgactcatg 180
Db      515 GCACAAAGATTTTGTGTAATGAAATTCACCTTGAGAGGATGTAAATAGTCTTCCCGA 574
Oy      181 gtttaagaaacttcaagagagacattcaacctgtactacatgagctgcatgatatcat 240
Db      575 GTCTGGGAACCTTGCAAGAAACGTTTAAATTTGTACTATTTGAAACAGACTACACACC 634
Oy      241 ggggtgaatttcgagagacatcagtttacaagatgacacattgcaagctgataagtc 300
Db      635 GGCAGGAATATACGAGAAACCTTTATGTATAAATGACACCATTTGCTGCAGATGAAAGT 694
Oy      301 ttcaactcaaatgagatcttgggagaccgtatcttgaagctcaacaactgagattagaagta 360
Db      695 TTCAACACAAAGTGACCTTGCTGGAAGAAAGATGAAGCTGAAACCTGAGGTAGAGAGATT 754
Oy      361 ggtccgtcacaagaagaggaatttatttggcatttcaagatgttggctgtgtgtgccc 420
Db      755 GGACCTTTGTCAAAAGGAAATTTATCTTGCTTGACAGATGTAGGGGCTTGATAGCA 814
Oy      421 ttggtgtctgtgagagatctacttcaaaaagtgccatttaccagtgaaagatcgtctatg 480
Db      815 TTGGTTTCTGTCAAGTGTACTTACAAAGAGTGCTGGACCATTTGTTGAACCTTACTCTGC 874
Oy      481 ttccaagacaggtacc---catggaactcccaagctccctgtgagaggttagaggtctgt 537
Db      875 TTTCACAGATACAGTACGCTGCTTGGAAATTTTCCTTCTTATGTCGAGGCTCCGTGGACATGT 934
Oy      538 gtcaacaattcaagga-----ggaagatcctccaagatgtagtctgacagagaagc 591
Db      935 GTCAAGCACTGCGCAGAGAGAGGAGCAAAATTCGCCAGAAATGCAATTCGACGTGCAAGAGA 994
Oy      592 gaatggtctgacaccatgtgcaagtggtcctcgtcaatgctgctatgaaagaaggtttt 651
Db      995 GAGTGGCTAGTACCATTTGAAATGCAATCTGCAAAAGCAGCTATACGCAAAAAGGGGAC 1054
Oy      652 atgtgccaa 660
Db      1055 ACTTGCAGAA 1063

```

```

RESULT 13
ID T32960 standard: cDNA; 4304 BP.
AC T32960:
DT 11-NOV-1996 (first entry)
DE Mouse developmental kinase 1 cDNA.
KW Mouse developmental kinase 1; MDK1; receptor tyrosine kinase; RTK;
  signal transduction; probe; diagnosis; gene therapy;
  neurodegeneration; neuroproliferation; cancer; ss.
OS Mus sp.
PH Key
FT cds Location/Qualifiers
FT 233..3229
FT /*tag- a
FT signal_peptide 233..316
FT /*tag- b
FT mat_peptide 317..3226
FT /*tag- c
FT 3'utr 3230..3628
FT /*tag- d
FT 3568..3573
FT poly_a_signal
FT /*tag- e
FT 3627..4304
FT /*tag- f
FT /*note- "alternative 3'-untranslated region,
  found in one isolated clone"

```

```

PN      M09621013-A1.
PD      11-JUL-1996.
PE      03-JAN-1996; U00419.
PR      03-JAN-1995; US-368776.
PA      (PIAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PI      (SUG-) SUGEN INC.
PI      Closek T, Millauner B, Ullrich A;
DR      WPI: 96-333988/33.
DR      P-PSDB: M03421.
PT      New mouse development kinase 1 gene - used for developing prods. for
PT      diagnosis and treatment of abnormalities in signal transduction
PT      pathways
PS      Example 1: Page 103-105; 128pp; English.
CC      A cDNA clone (T32960) codes for mouse developmental kinase 1 (MDK1)
CC      (W03421), a new member of the eck/epn family of receptor tyrosine
CC      kinases (RTKs). To isolate the clone, cDNA from mouse embryos was
CC      subjected to PCR amplification with primers based on conserved
CC      motifs (see also W03426-27) of RTKs. An amplified fragment was used
CC      to screen an 11.5-day-old mouse embryo and an adult mouse brain cDNA
CC      library to obtain the MDK1 clone. 4 Sequence variants (see also
CC      T32961-62 and W03422-23) of MDK1 were also identified. MDK1 nucleic
CC      acids can be used for the recombinant prodn. of MDK1, as probes to
CC      detect MDK1, and for the gene therapy of diseases involving
CC      abnormalities in signal transduction, such as neurodegenerative and
CC      neuroproliferative disorders and cancer.
SQ      Sequence 4304 BP; 1297 A; 875 C; 1043 G; 1089 T;

```

```

Query Match 45.2%; Score 298.2; DB 1; Length 4304;
Best Local Similarity 67.6%; Pred. No. 4.2e-89;
Matches 452; Conservative 0; Mismatches 208; Indels 9; Gaps 2;

```

```

Oy      1 tgggaagagatcagtggtgtgtagaacattacaacaccatcagacttaccaggtgtgc 60
Db      395 TGGGAAAGAAATAGTGGTTGGATGAGAACTACCTCCGATFAGAAACATACAGAGTGTC 454
Oy      61 aatgtcatgagccacagcacaacacatggtcgtgagaaacactggtcccaagaaacca 120
Db      455 CAGGTCATGAGGCCACACCAAGAACATGGCTGCGACTAATGATTTCTTAAAGGCAAC 514
Oy      121 gctcagaagaattatgtgagactcaagttcacctcaagactcgaatgaatgactcatg 180
Db      515 GCACAAAGATTTTGTGTAATGAAATTCACCTTGAGAGGATGTAAATAGTCTTCCCGA 574
Oy      181 gtttaagaaacttcaagagagacattcaacctgtactacatgagctgcatgatatcat 240
Db      575 GTCTGGGAACCTTGCAAGAAACGTTTAAATTTGTACTATTTGAAACAGACTACACACC 634
Oy      241 ggggtgaatttcgagagacatcagtttacaagatgacacattgcaagctgataagtc 300
Db      635 GGCAGGAATATACGAGAAACCTTTATGTATAAATGACACCATTTGCTGCAGATGAAAGT 694
Oy      301 ttcaactcaaatgagatcttgggagaccgtatcttgaagctcaacaactgagattagaagta 360
Db      695 TTCAACACAAAGTGACCTTGCTGGAAGAAAGATGAAGCTGAAACCTGAGGTAGAGAGATT 754
Oy      361 ggtccgtcacaagaagaggaatttatttggcatttcaagatgttggctgtgtgtgccc 420
Db      755 GGACCTTTGTCAAAAGGAAATTTATCTTGCTTGACAGATGTAGGGGCTTGATAGCA 814
Oy      421 ttggtgtctgtgagagatctacttcaaaaagtgccatttaccagtgaaagatcgtctatg 480
Db      815 TTGGTTTCTGTCAAGTGTACTTACAAAGAGTGCTGGACCATTTGTTGAACCTTACTCTGC 874
Oy      481 ttccaagacaggtacc---catggaactcccaagctccctgtgagaggttagaggtctgt 537
Db      875 TTTCACAGATACAGTACGCTGCTTGGAAATTTTCCTTCTTATGTCGAGGCTCCGTGGACATGT 934
Oy      538 gtcaacaattcaagga-----ggaagatcctccaagatgtagtctgacagagaagc 591
Db      935 GTCAAGCACTGCGCAGAGAGAGGAGCAAAATTCGCCAGAAATGCAATTCGACGTGCAAGAGA 994
Oy      592 gaatggtctgacaccatgtgcaagtggtcctcgtcaatgctgctatgaaagaaggtttt 651

```


This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2000, 11:43:14 ; Search time 1225.64 Seconds
(without alignments)
-523.843 Million cell updates/sec

Title: US-09-104-340-8
Perfect score: 660
Sequence: 1 tgggaagagatcagtggtgt.....aaagaggtttatgtgcca 660

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_ph:*
6: gb_pi1:*
7: gb_pi2:*
8: gb_pi3:*
9: gb_pi4:*
10: gb_pi5:*
11: gb_pi6:*
12: gb_pi7:*
13: gb_pi8:*
14: gb_pi9:*
15: gb_pi10:*
16: gb_pi11:*
17: gb_pi12:*
18: gb_pi13:*
19: gb_pi14:*
20: gb_pi15:*
21: gb_pi16:*
22: gb_pi17:*
23: gb_pi18:*
24: gb_pi19:*
25: gb_pi20:*
26: gb_pi21:*
27: gb_pi22:*
28: gb_pi23:*
29: gb_pi24:*
30: gb_pi25:*
31: gb_pi26:*
32: gb_pi27:*
33: gb_pi28:*
34: gb_pi29:*
35: gb_pi30:*
36: gb_pi31:*
37: gb_pi32:*
38: gb_pi33:*
39: gb_pi34:*
40: gb_pi35:*
41: gb_pi36:*
42: gb_pi37:*
43: gb_pi38:*
44: gb_pi39:*

45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_htg4:*
50: gb_pi13:*
51: gb_pi14:*
52: gb_pi15:*
53: gb_pi16:*
54: gb_pi17:*
55: gb_pi18:*
56: gb_pi19:*
57: gb_pi20:*
58: gb_pi21:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	660	100.0	3132	5 A28003	A28003 H. sapiens H
2	660	100.0	3132	5 I68018	I68018 Sequence 9
3	660	100.0	3149	9 HUMHER	M83941 Human recep
4	564	85.5	3077	12 RN069278	U69278 Rattus norv
5	544.8	82.5	2032	12 MUSMEK4SE	M68515 Mouse eph-r
6	544.8	82.5	3197	12 MUSMEK4	M68513 Mouse eph-r
7	464.8	70.4	3241	4 CHCKEK4	M68514 Chicken eph
8	463.2	70.2	3254	5 I15007	I15007 Sequence 15
9	339.8	51.5	3600	4 CHCKEK8	D38174 Gallus gall
10	330.2	50.0	4242	12 MMSER	X65138 M. musculus
11	330.2	50.0	4242	12 S57168	S57168 Sex-eph-rel
12	327.6	49.6	3943	12 MM058332	U58332 Mus musculu
13	327.6	49.6	77197	11 U90093	U90093 Human Chrom
14	327	49.5	3107	10 HUMRPTK	I36645 Homo sapien
15	327	49.5	3348	5 I44522	I44522 Sequence 34
16	321.2	48.7	3592	5 AR062743	AR062743 Sequence
17	318.2	48.2	76022	45 AC021499	AC021499 Homo sapi
18	317.4	48.1	3531	12 RNEHK1	X78689 R. norvegicu
19	317.4	48.1	3906	5 AR062744	AR062744 Sequence
20	317.4	48.1	4165	5 AR025488	AR025488 Sequence
21	317.4	48.1	4322	5 AR043381	AR043381 Sequence
22	317.4	48.1	4322	12 MM007357	MM007357 Mus musculu
23	316	47.9	3042	4 XLESEK1	X91191 X. laevis mr
24	316	47.9	3193	4 XELPAGAA	L26099 Xenopus lae
25	304.6	46.2	3162	10 HUMRPTK	L36644 Homo sapien
26	304.6	46.2	3903	10 HSEK1	X95425 H. sapiens m
27	304.6	46.2	132805	41 AC009425	AC009425 Homo sapi
28	303	45.9	4523	10 HUMRPTK	L36642 Homo sapien
29	303	45.9	116490	32 HSJ189K14	AL121966 Homo sapi
30	298.2	45.2	2323	12 MKKIN1T2	X79084 M. musculus
31	298.2	45.2	2901	12 MKKIN1T1	X79083 M. musculus
32	298.2	45.2	4304	12 MKKIN1	X79082 M. musculus
33	297.2	45.0	2640	4 DRAJ5030	AJ005030 Danio rer
34	295	44.7	2006	12 RN021955	U21955 Rattus norv
35	295	44.7	3208	12 RN021954	U21954 Rattus norv
36	295	44.7	3943	4 GGY14271	Y14271 Gallus galli
37	291.8	44.2	4124	4 GGCEK7B	U03910 Gallus galli
38	280.8	42.5	4737	12 MMU72207	U72207 Mus musculu
39	273	41.4	4577	4 DR08295	U89295 Danio rerio
40	269.6	40.8	160703	10 HS61A9	AL035703 Human DNA
41	245.2	37.2	3056	5 I15010	I15010 Sequence 21
42	245.2	37.2	3059	5 I15001	I15001 Sequence 3
43	245.2	37.2	3125	5 I15009	I15009 Sequence 19
44	230.2	34.9	63166	55 AC023783	AC023783 Homo sapi
45	219.6	33.3	2820	4 GGCEK8A	Z19059 G. gallus Ce

ALIGNMENTS

RESULT 1
A28003 3132 bp DNA PAT 25-SEP-1995
LOCUS H.sapiens HEK gene.
DEFINITION A28003
ACCESSION A28003.1 GI:1247486
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 3132)
REFERENCE
AUTHORS
TITLE A NOVEL RECEPTOR-TYPE TYROSINE KINASE AND USE THEREOF
JOURNAL Patent: WO 9300425-A 7 07-JAN-1993;
FEATURES
source location/Qualifiers
1..3132
/organism="Homo sapiens"
/db_xref="taxon:9606"
/gene="HEK"
/gene="HEK"
100..3051
/codon_start=1
/protein_id="CAA01906.1"
/db_xref="GI:1247487"
/translation="MDCOLSTLLSLGSLVDSFGLIPDPSNEVNLSTKLTGELG
ISYSHGWEETSGVDEHETPIRTYOVCAVMDHSONNNIRTNKPNVNSQKIYELKPT
LRDCNSIPVLGTCETFNLYMESDDHGVKFRHOPTKIDTIADESFTOMDGDRI
ILKLTETEIREGVPVKKGYLAFOVGAVALVSRVYFKCPFTVKMLAFPDVPM
DSOSLVEVSGSVNNSKEDDEPRMTCSTEGEWLVPIGCSNAGAEERFGQACRPG
FYKALDGNMKCAKCPHSSSTODGSMNCENRYRADKPSNACTPSPSRNVIS
NINETSVLDSMPLDTGKRQDVTENIICKGGMNICKCEPCSPVRPLPPOGLTNT
TATVLDLAHNTPEIDAVNVSVLSPPRPRAVSTTNOAPSPLYLTIKDNTSR
NSISLSMOPHPNGLIIDYEKYTEKQDEQSTYTLARGINVITSLKPDPTIVLO
IRARTAAGYGTNSRFEETSPDSFSISGESSQVMAISAVALILTLYIVLIGR
FCGYKSHGADGKRLHFGNGLKPLGLTYDPPHYEDPTQVHEFAELDNTSID
KVYAGGEFVCSGRKLPSKKEISVALIKTLVGYTERORDFLEASIMGOFDHNT
IRLEGVTVKSRVMIIVTEYMENGLSDSLFRKDAQFTYIOLIGMRGIAISGMYSDM
GYVHRDLAARLINSNVACYRSDGSLRVLEDDEAAYTTGKPIRMTSPKAIAT
RKFTASDVWSTGIVLWEMVSYGERPIWMSQDVIKAVDSIRLPPMDCPALYOL
MLDCKQDRNNRPKEQIVSLDKLIRNPGSLKITSAAARPSNLLDQSNVDISTFR
TTGDLNGLVRIAHCKEIFTGVEYSSCDTIKISTDMKRVGVTVVGPQKIIISIKAL
ETQSKNGEVPV"

BASE COUNT 888 a 709 c 761 g 774 t
ORIGIN
Query Match 100.0%; Score 660; DB 5; Length 3132;
Best Local Similarity 100.0%; Pred. No. 4.7e-190;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tgggaagaatacagtggtgtgtgataacattacacccatcaggactaccagtggtgc 60
|||||
DB 253 tgggaagaatacagtggtgtgtgataacattacacccatcaggactaccagtggtgc 312
QY 61 aatgtcatgacacagtcacaaacaaatggctgagaaacaaactgggtcccccaggaaacta 120
|||||
DB 313 aatgtcatgacacagtcacaaacaaatggctgagaaacaaactgggtcccccaggaaacta 372
QY 121 gctcagaagaattatgttgagagtcacagtcactcagagactcagagactcagatccatc 180
|||||
DB 373 gctcagaagaattatgttgagagtcacagtcactcagagactcagagactcagatccatc 432
QY 181 gttttaggaacttgcaagaagacattcaacccgttactacatggagctcgtatgatcat 240
|||||
DB 433 gttttaggaacttgcaagaagacattcaacccgttactacatggagctcgtatgatcat 492
QY 241 ggggtgaatttcgagagagatcagtttacaagaattgaaacattcagctggtgaagt 300
|||||
DB 493 ggggtgaatttcgagagagatcagtttacaagaattgaaacattcagctggtgaagt 552

QY 301 ttcactcaaatgatccttggggaccgtatctcgaagctcacaactcagagatagagaagta 360
|||||
DB 553 ttcactcaaatgatccttggggaccgtatctcgaagctcacaactcagagatagagaagta 612
QY 361 ggtcctgtcacaagaaggagatttattcgttgacattcaagaatgtgtgtgtgtgcc 420
|||||
DB 613 ggtcctgtcacaagaaggagatttattcgttgacattcaagaatgtgtgtgtgtgcc 672
QY 421 ttggtctcgtgagagatctactcacaagaatgtcccatctacagtgagaatcgtgtgtg 480
|||||
DB 673 ttggtctcgtgagagatctactcacaagaatgtcccatctacagtgagaatcgtgtgtg 732
QY 481 ttccagaacaggtacccatgagctccagctccctcgtgtgagagttagaaggtctgtgtc 540
|||||
DB 733 ttccagaacaggtacccatgagctccagctccctcgtgtgagagttagaaggtctgtgtc 792
QY 541 aacaattctaaggaggaagatccccaaggatgtactgcagtagacagaaggcgaatgctt 600
|||||
DB 793 AACCAATTCTAAGGAGGAGATCTCCAAAGGATGTACTGCAGTACAGAAAGCGAATGCGCTT 852
QY 601 gtaccatgtggaagtgttcctcgaatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
|||||
DB 853 gtaccatgtggaagtgttcctcgaatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 912

RESULT 2
168018 3132 bp DNA PAT 04-FEB-1998
LOCUS Sequence 9 from patent US 5674691.
DEFINITION
ACCESSION 168018
VERSION 168018.1 GI:2830140
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3132)
AUTHORS Boyd,A.W., Simpson,R.John, Wicks,I., Ward,L.David and Wilkinson,D.
TITLE Method of screening for ligands to a receptor-type tyrosine kinase
JOURNAL Patent: US 5674691-A 9 07-OCT-1997;
FEATURES
source location/Qualifiers
1..3132
/organism="unknown"

BASE COUNT 888 a 709 c 761 g 774 t
ORIGIN
Query Match 100.0%; Score 660; DB 5; Length 3132;
Best Local Similarity 100.0%; Pred. No. 4.7e-190;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tgggaagaatacagtggtgtgtgataacattacacccatcaggactaccagtggtgc 60
|||||
DB 253 tgggaagaatacagtggtgtgtgataacattacacccatcaggactaccagtggtgc 312
QY 61 aatgtcatgacacagtcacaaacaaatggctgagaaacaaactgggtcccccaggaaacta 120
|||||
DB 313 aatgtcatgacacagtcacaaacaaatggctgagaaacaaactgggtcccccaggaaacta 372
QY 121 gctcagaagaattatgttgagagtcacagtcactcagagactcagagactcagatccatc 180
|||||
DB 373 gctcagaagaattatgttgagagtcacagtcactcagagactcagagactcagatccatc 432
QY 181 gttttaggaacttgcaagaagacattcaacccgttactacatggagctcgtatgatcat 240
|||||
DB 433 gttttaggaacttgcaagaagacattcaacccgttactacatggagctcgtatgatcat 492
QY 241 ggggtgaatttcgagagagatcagtttacaagaattgaaacattcagctggtgaagt 300
|||||
DB 493 ggggtgaatttcgagagagatcagtttacaagaattgaaacattcagctggtgaagt 552
QY 301 ttcactcaaatgatccttggggaccgtatctcgaagctcacaactcagagatagagaagta 360
|||||

Db	553	TTCACTCAAAATGGAATCTTTGGGAGCCAGCATTTCTGAAGCTCAACACTGAGATTAAAGAAGTA	612
Qy	361	ggccctcgtcaacaagaagggatttatttctgtgacattcaagaatgtctgtgtctgtgtgcc	420
Db	613	GGTCTCTGCAACAAAGAAGGGCATTTTATTGTGCATTTCAAGATGTGGTGGCTGTGTGCC	672
Qy	421	cttgtgtctgtgtgagatatacttcaaaaatgtgccatttcagtgaaagatctggatg	480
Db	673	TTGGGTGCTGTGAAGATATACCTTAAAGGCCCATTTTACAGTGAAGATCTGGCTATG	732
Qy	481	tttccagaacacgtaaccatgagctccagtccectgtgtgaagtttagaaggtcttgatc	540
Db	733	TTTCCAGACAGCGATACCATGATCTCCAGTCCTCGTGTGAGGTTGAGCGGTCTTGTGTC	792
Qy	541	aacaattctaaaggagagaagatccctccaaagatgtacgcgcagtaacagaaggcgaatgctt	600
Db	793	AACATTTCTAAGGAGGAAGATCCTCCAAAGATGTACGATACGATACAGAAGCGAATGGCTT	852
Qy	601	gtaccacattgycgaagtcttccctgcaatgcttggctatgataagaagaaggttttatgtgccaa	660
Db	853	GTACCCATTTGGCAAGATGCTCTCGCAATAGCTGGCATATGAAGAAAGAGGTTTATGTGCCAA	912

RESULT	3
LOCUS	HUMHEK 3149 bp mRNA PRI 31-DEC-1994
DEFINITION	Human receptor tyrosine kinase (HEK) mRNA, complete cds.
ACCESSION	M83941
VERSION	M83941.1 GI:183931
KEYWORDS	receptor protein-tyrosine kinase.
SOURCE	Homo sapiens lymphoid tumor cDNA to mRNA.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	Wicks, I.P., Wilkinson, D., Salvaris, E. and Boyd, A.W.
TITLE	(bases 1 to 3149)
JOURNAL	Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed by human lymphoid tumor cell lines
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 89 (5), 1611-1615 (1992)
FEATURES	92179233
source	location/Qualifiers
gene	1..3149
CDS	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/cell_line="LK63"
	/tissue_type="lymphoid tumor"
	101..3052
	/gene="HEK"
	101..3052
	/gene="HEK"
	/codon_start=1
	/product="receptor protein kinase"
	/protein_id="AA58633.1"
	/db_xref="GI:183932"
	/translation="MDCCSTLLILSSVLDSPFGLIPQSENVNLDSTKIQGLGCK LSDNSIPVLVGTCKETFNLYTMSDDHGVKFEKHQTKIDTIAADESTQMDLGD ILKNTLEIREVGNPKRGKGYLAFDVGCVALSVRYKRCPTVKNLAFPTVPV DSQGLVEVKGSCVANNKSEEDPPRMVCSGEGMLVPIGSCNAGIEEGKQACRCP FYKLDLNMKCAKCPPHSTQEDSMNCRNNFRADKDPNMACTPSPNNVYS NINRTSYLDMSWPLDVGKRDVFNITCRKGNINCKCEGCPVRLPPQGLTNT TVNTYDILAHNTNTPFEIDAVNGVSEISPPPOPAVSTTTQAAISPVLITTKRDT NSISLQNEPHEPHGIIIDYVKYTERQEDSTTILNARGTNTISLKTDTLYVE IRATLAGVGTGNSKRKEFEETSPDSFSISESSQVMAISAVALILTAVYLIG FCGKSRKHGADEKRLHFGNGHLKLPGLTAYVDPTVEDPTDAVHFAELDATNIS KVYGAEGHEVCGSRKLKPSKKEISVALIKLVGTEKRODFGEASIMGOFDHPN IRLGGVYTKSRKPMIVTEVYKMGSLDPLRKHDQFTVIOVGMLRGISGMKYLSD GVYRLDAARNILINSNLVCKVSGSLRYLDDPEAAYTRGKIPITRTSPALAI PKETSDVMSYGIYLEWMSYGERPTYEMKNQYIKAVDGYIRPPMDPALIYQI MLDCKQDRNRNRPKEQIVSTLDRKIRNPGSLKTIISAAAPSNLLDQSNVSDTE TTGWLGNLRTAHCKEIKFTGVGYSSCDTIARIISDDMKRGVTYVWGQIISIKIA ETOSKNGPVPV"
BASE COUNT	891 a 711 c 768 g 779 t

[illegible]

JOURNAL Submitted (01-SEP-1996) Cardiology, University of Pittsburgh, 200 Lothrop Street, Pittsburgh, PA 15213, USA
 COMMENT On Apr 18, 1997 this sequence version replaced gi:1698721.
 FEATURES Location/Qualifiers

source 1..3077
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /dev_stage="neonatal"
 /cell_type="cardiomyocytes"
 1..3077
 /gene="Rek4"
 35..2989
 /gene="Rek4"
 /codon_start=1
 /product="eph-related receptor tyrosine kinase homolog"
 /protein_id="AAC06273.1"
 /db_xref="GI:1698722"
 /translation="MDCHLSILILRGCCVLSGSELSPQSPNEVNILDSKTIGELGW
 IYPSHGWEISGVDEHYPIRTYQVNMDSQNNMLTNNVPRNSAKIYVELKFT
 LRDCNSIPLVLTGCKETENLYMESDDHGVLEHQFTIDTIADESPQMDLDR
 IRLNTEIREVPVNRKGYLAQDYGACVAVSVYRKCPETKYNLAMPDVTYPM
 DSQSLVEVSGCVNNSKEEDPPRMTCSTGEMLVPYIGKTCNAGYEREGFTQACDPS
 EYKALDGVAKCTCKPHSSTQEDGSMNCENNYFAEDPPSMACTRPPSPARNYIS
 NINETSVIDMSMPLDTGKRKIDITENIICKGMNVRQCEPSPNRYEPRQDGLTNT
 TYVTVDLHNTYFEIDAINGVELSPRQFAVSIITNNAAPSPVNTIKDRISR
 NSISLSMOEPREHNGIILDYEVKYEKOEOESYTLIRAGINVTISLSKPTTYVGR
 IARATNAGYGTNSRKREFENSPDSFISGENSHVVAISAVAIIVLVVTVYVGR
 FCGYHRSKHSDEKRLHFGNHLRLPLGTYYDPHYEDPTQAVHEFAELQATNAT
 DKRYAGGEVGEVSGSRKTPSKREISVALKTLYCTEQRDLCEASIMQFDPHPN
 ITRBSGVTKSRPMVITYTYMENGSIDSLRKHDQFTYIQLGMLNGTASGKIYSD
 MGYVHDLARNILINSNLVCVSDGSLVLEDDPEAVTTRGGKILPRMYSPEPTA
 YKRTTSASVMSGYIVLEWMSYGERPYWEMSNODYIKAVDGRPLPMDCPALYQ
 LMLDCQKDRNNRPKEQIYSLDKLIRNPGSKITTSAAARPSNLLDOSNDITF
 HTGDMLNAGRTAAHCKEIFTGVYEYSSCDTIAISTDDMKVGTVYVGPQKTIISIKIA
 LFTOSKNGVPV"

BASE COUNT 877 a 714 c 758 g 728 t
 ORIGIN

Query Match 85.5%; Score 564; DB 12; Length 3077;
 Best Local Similarity 90.9%; Pred. No. 7.6e-161;
 Matches 600; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 tgggaagaagatcagtggtggaatgaacattacacccatcaggacttaccagtgctgc 60
 Db 188 TGGGAAGAGATCAGTGTGATGAGCATTTACACACCAATCAGGACTTACAGATGTC 247
 QY 61 aatgcatggacacagtcacaaacaattggtcgaagaacaattggtcccgagaactca 120
 Db 248 AATGTCATGATGATCAGCCAAAATAATTGGCTGAGGACCAACTGGGCGAGAAACTCA 307
 QY 121 gtcagaagaattatgtgaggtcgaattacacttaccagagactgcaatagcattccatg 180
 Db 308 GCTCAGAAAGTCTATGTGGAGCTAAAGTTCACTGCGGAGCTGTACACACATTTCCATG 367
 QY 181 gttttaggaactctgcaagagagacattcaacctgtactactctggagctcgtatgatcat 240
 Db 368 GTTTGGGAGCTTGCAAGAGAGACCTTTAACCTGTACTACATGAGGCTGTGATGATGATCAC 427
 QY 241 ggggtggaattctcgagagatcagtttcaagaagattgacaccattgagctgataaagt 300
 Db 428 GGTGTCAAAATTCCTAGAGCATCAGTTTACAAAGATTGACACCACTTGGCGCTGATGAAGT 487
 QY 301 ttcaactcaatggatctctggagaccgtatctgaagctcaaacactggattagaagaagta 360
 Db 488 TTCACTCAATGGATCTCGGGGACCGCATTTCTAAATCTCAACACTGAGATTAGAGAGTG 547
 QY 361 ggtcctgctcaacaagaaggatttattcttggtcattcaagaatgttggtctgtctgc 420
 Db 548 GGACACAGTCAATAAAGGGGTTTATTGTGGCTTCAAGATGTGTGCTGTGCTGCC 607
 QY 421 ttggtgtctgtgagagctatcttcaaaaaagtgccecatcttcaagtgaagaactctgctatg 480

Db 608 TTGTTCTGTGTGAGATGTACTCAAAAAGTCCCATTTACAGTGAAGATCTGGCTAG 667
 QY 481 ttccagacacggttaccatcgtgactccagtcctctgtgaggttgaaggtctctgtgc 540
 Db 668 TTTCACAGACAGTGGCCCATGAGCTCCAGTCTTGTGTGAGGTGAGGGCTCTTGTGTC 727
 QY 541 aacaattctaaggaggaagatcctccaagatgtactcgaagtagtacaagaagcgaaatgctt 600
 Db 728 AATAATTCAGAGAGAGAGACCGCTCCAGAGATGACTGACAGTACAGAAAGTGAATGGCTG 787
 QY 601 gtaccattggcgaagtgcttcctcgaatgtcgtgctatgaagaagaaggtttatgtccaa 660
 Db 788 GTCCCATTTGGCAAGTACAGCTGCAATGCTGGGTATGAAGACGAGGCTTATGTC 847

RESULT 5
 MUSMEK4SE 2032 bp mRNA ROD 15-FEB-1994
 LOCUS Mouse eph-related receptor tyrosine kinase (Mek4) secreted mRNA,
 DEFINITION complete cds.
 ACCESSION M68515.1 GI:454828
 VERSION 68515
 KEYWORDS receptor tyrosine kinase.
 SOURCE Mus musculus (strain IRC x Swiss Webster) 11.5 day embryo embryo
 CDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCES
 1 (bases 1 to 2032)
 Sajjadi,F.G., Pasquale,E.B. and Subraman,I.S.
 Identification of a new eph-related receptor tyrosine kinase gene
 from mouse and chicken that is developmentally regulated and
 encodes at least two forms of the receptor
 New Biol. 3, 769-778 (1991)

JOURNAL 92031278
 MEDLINE On Feb 16, 1994 this sequence version replaced gi:199121.
 COMMENT Location/Qualifiers
 FEATURES 1..2032
 source /organism="Mus musculus"
 /strain="IRC x Swiss Webster"
 /db_xref="taxon:10090"
 /dev_stage="11.5 day embryo"
 /tissue_type="embryo"
 89..1702
 /codon_start=1
 /product="Mek4 secreted"
 /protein_id="AA39522.1"
 /db_xref="GI:454828"
 /translation="MDCHLSILVLGCCVLSGSELSPQSPNEVNILDSKTIGELGW
 IYPSHGWEISGVDEHYPIRTYQVNMDSQNNMLTNNVPRNSAKIYVELKFT
 LRDCNSIPLVLTGCKETENLYMESDDHGVLEHQFTIDTIADESPQMDLDR
 IRLNTEIREVPVNRKGYLAQDYGACVAVSVYRKCPETKYNLAMPDVTYPM
 DSQSLVEVSGCVNNSKEEDPPRMTCSTGEMLVPYIGKTCNAGYEREGFTQACDPS
 EYKALDGVAKCTCKPHSSTQEDGSMNCENNYFAEDPPSMACTRPPSPARNYIS
 NINETSVIDMSMPLDTGKRKIDITENIICKGMNVRQCEPSPNRYEPRQDGLTNT
 TYVTVDLHNTYFEIDAINGVELSPRQFAVSIITNNAAPSPVNTIKDRISR
 NSISLSMOEPREHNGIILDYEVKYEKOEOESYTLIRAGINVTISLSKPTTYVGR
 IARATNAGYGTNSRKREFENSPDSFISGENSHVVAISAVAIIVLVVTVYVGR
 FCGYHRSKHSDEKRLHFGNHLRLPLGTYYDPHYEDPTQAVHEFAELQATNAT
 DKRYAGGEVGEVSGSRKTPSKREISVALKTLYCTEQRDLCEASIMQFDPHPN
 ITRBSGVTKSRPMVITYTYMENGSIDSLRKHDQFTYIQLGMLNGTASGKIYSD
 MGYVHDLARNILINSNLVCVSDGSLVLEDDPEAVTTRGGKILPRMYSPEPTA
 YKRTTSASVMSGYIVLEWMSYGERPYWEMSNODYIKAVDGRPLPMDCPALYQ
 LMLDCQKDRNNRPKEQIYSLDKLIRNPGSKITTSAAARPSNLLDOSNDITF
 HTGDMLNAGRTAAHCKEIFTGVYEYSSCDTIAISTDDMKVGTVYVGPQKTIISIKIA
 LFTOSKNGVPV"

CDS
 polyA_signal
 polyA_site 2032
 BASE COUNT 578 a 473 c 460 g 521 t
 ORIGIN

Query Match 82.5%; Score 544.8; DB 12; Length 2032;
 Best Local Similarity 90.2%; Pred. No. 5.2e-155;
 Matches 595; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 tgggaagaagatcagtggtggaatgaacattacacccatcaggacttaccagtgctgc 60
 Db 242 TGGGAAGAGATCAGTGTGATGAGCATTTACACACCAATCAGGACTTACACAGTGTGTC 301

Oy	61	aatgctcagtcaggaccacagttcaaaaacaattggctcgagaagacaactgggtcccccaggaaacta	120
Dd	302	AATGCTCATGTGACACAGCCAAAATAATTGGCTGAGGACCAAACTGGGGTACCACGAAACTCA	361
Oy	121	gctcgaagatttatgttgagctccaagtccactctcagactcgcagactgcataagcatccatcy	180
Dd	362	GCTCAGAAGATCTAAGTGGAAGCTAAAGTTACACTTCGGGACTGTAAACAGCATTCATTG	421
Oy	181	gttctaagaaccttgcagaagagacatccaactgtlactacatayagtcgatgatgcat	240
Dd	422	GTTTTGGGACTTGCAGAGGAGACCTTTAACCTCGTACTACATGAGAGTC--TGATGATCAT	478
Oy	241	ggggfsgaaattcggagagatcagttttaaaaaagattgaacacattgcacatgatgaaat	300
Dd	479	GCGTCGAATTCGGAGAGCATGATCTCACGAAGATTGACACCATTCGCCCTGATGAAGT	538
Oy	301	tccactccaatgatccttggggaccgtatctctgaagctcaaacactgatataganaagta	360
Dd	539	TTCACCTCAGATGATCTCGGGATTCGCATCTTCGAACCTCAACACTAGATTAGANAAGTG	598
Oy	361	ggctctgtcaacaagaaggatttatttggacatttcaaagatgtytgcttgtgtgcc	420
Dd	599	GGACCAAGTCACAAMAAAGGGGTTTAATTATGGCCTTCAGANAGTTGGTCTGTGTGGCC	658
Oy	421	ttagtgctcgttagagtgtaacttcaaaaaagtgccccatttacagtgtaagaatctgtctatg	480
Dd	659	TTGGTGCTGTAGAGTGTACTTCAAAAAGTCCCTTTACAGTAGAAGATCTGGCTATAG	718
Oy	481	ttccagacacggttaccacttgagctccagctccctgtgtgaggttagagagctctgtgc	540
Dd	719	TTTCCAGACACAGTGGCCATGACATCTCCAGTCTTTGGTGGAGTTTAGGGCTCTTGTGTGC	778
Oy	541	aacaattctaaaggagaaagatccctccaagatgtactgcagtcagtcagagaagcgaatgctt	600
Dd	779	AATAATTCGAAGAGAGAGACCCTCCCGAGAGTACTGCAGACACANAAGGGAGATGCTG	838
Oy	601	gtaccacattggcgaagtgtctctcgtcgaatgctgtgctatgaaagaagggtttatgtycca	660
Dd	839	GTCCCATTGGCAAAATGCACTTGCAATGCTGGGTATGAGAACGAGGTTTCATATCCAA	898
<hr/>			
RESULT	6		
MUSMER4	LOCUS		
	3197 bp	mRNA	ROD
			15-FEB-1994
DEFINITION	Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.		
ACCESSION	M68513		
VERSION	M68513.1	GI:199119	
KEYWORDS	receptor tyrosine Kinase.		
SOURCE	Mus musculus (strain IRC x Swiss Webster) 11.5 day embryo embryocDNA to mRNA.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.		
AUTHORS	Sajjadi,F.G., Pasquale,E.B. and Subraman1,S.		
TITLE	Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor		
JOURNAL MEDLINE	New Biol. 3, 769-778 (1991)		
FEATURES	92031278		
SOURCE	Location/Qualifiers		
	1..3197		
	/organism="Mus musculus"		
	/strain="IRC x Swiss Webster"		
	/db_xref="taxon:10090"		
	/dev_stage="11.5 day embryo"		
	/tissue_type="embryo"		
	89..3040		
	/gene="Mek4"		
	89..3040		
	/gene="Mek4"		
CDS	/codon_start=1		

Query Match	Best Local Similarity	Score	DB	Length
Matches 595; Conservative 0; Mismatches 62; Indels 3; Gaps 1;	90.2%; Pred. No. 5.3e-155;	544.8;	12;	3197;
1	1	1	1	1
242	242	242	242	242
61	61	61	61	61
302	302	302	302	302
121	121	121	121	121
362	362	362	362	362
181	181	181	181	181
422	422	422	422	422
241	241	241	241	241
479	479	479	479	479
301	301	301	301	301
533	533	533	533	533
361	361	361	361	361
599	599	599	599	599
421	421	421	421	421
653	653	653	653	653
481	481	481	481	481
719	719	719	719	719
541	541	541	541	541
779	779	779	779	779
601	601	601	601	601
839	839	839	839	839

RESULT 7
CHICKEN 3241 bp mRNA VRT 15-FEB-1994
LOCUS CHICKEN eph-related receptor tyrosine kinase (Cek4) mRNA, complete
DEFINITION
ACCESSION M68514
VERSION M68514.1 GI:454809
KEYWORDS receptor tyrosine kinase.
SOURCE Gallus gallus 10 day embryo CDNA to mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE
AUTHORS Sajjadi, F.G., Pasquale, E.B. and Subramani, S.
TITLE Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor
JOURNAL New Biol. 3, 769-778 (1991)
COMMENT 92031278
FEATURES
source On Feb 16, 1994 this sequence version replaced gi:211446.
location/Qualifiers
1..3241
/organism="Gallus gallus"
/db_xref="taxon:9031"
/dev_stage="10 day embryo"
/tissue_type="embryo"
32..2983
/gene="Cek4"
32..2983
/gene="Cek4"
/codon_start=1
/product="receptor tyrosine kinase"
/protein_id="AA448666.1"
/db_xref="GI:211447"
translation="MDRRRLPLLLICAAISAGRSAPRGENVLLDSKTIOGELGVI
SYRSHGWEIGVDVBEHTPIPTIOESNMDSONKMLTNPNSAKITVELKFTL
RDCNSIPVLGTCETENLYTIMESDDHLAREHQFKIDITLADESEFTMDGRI
LKLNTAEVAVPSKSKFYLAFOGVAAVAVYKPKCPFYKPNAMPDVPMD
QSJLVEVSGVNSKEEPEKMACSTGEMLVPGICLNAEERFACQARPG
YKASAGNKCACPKPSHSTEDPASCENKCEPSEDPSPMACTRPSPAPRVISN
INETSVIDMSMPTIDTGRKDTFNITICKGSGSKTCEPCSDNVRPLPRTGLNT
VTVDLAHTNTPTEIDVNVSDTISRPPAASITTNNAASPTIVIRKDTSRN
SVLSMDPEHPNGILIDYEVKITEKQESTYILRAKSTNVITISGLKPTTYVFOI
RAATAARQTSRKEFEFTSPDSFSISENSQVMAIASAAVAILLVVYVIGRF
CGYKSKHGIDETKRLHFGNGLKLPGLRTYVDPHYEDPNOVAHEFAELDQNSID
KYVAGEGEVCSGRLKLPKKEISVAIKRTYAGTEKORDFGEAIGMOPHPNI
IRLGGVYTKSPVMIVTEYMENGLSDFLRHDOQFYIOIGWMLRGIAAGMKYLSM
GVYHDLAARNILINSNVCKYSDPGESRYLEDPEAATYTRGKIPTRMTSPETAIY
RKFTSASDAMSTGYLWEMVSTYGERPIYEMSFODYIKAVDGYRLPPMDCPALYOL
MLDCWQKDRNNRPFEOIYVSLDKLIRNPSSIKITNNAARPSNLLDQNSIDSAFR
TAGDWLNGFRTGQCKGIFTGYEYSSCDTIARIKISIDDMKVKVTVVGPKKIVSSIKTL
ETHTKNSFPVPV"
polyA_site 3241
BASE COUNT 916 a 735 c 794 g 796 t
ORIGIN

Query Match 70.4%: Score 464.8; DB 4; Length 3241;
Best Local Similarity 81.5%: Pred. No. 1.2e-130;
Matches 538; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 1 tgggaagagatcagtggtgtaaacattacacccatcaggactaccaggtgtgc 60
DB 182 TGGGAAGAGATTAGTGTGTGATGAGCATYTAATCCAAATGAGAAATGACAGAGAGC 241
QY 61 aatgcattgagaccacagttcaaacatttgctgtagagacaaactggttccccaagaacta 120
DB 242 AATGTTATGAGATCAGTCAAGTCAAAATTTGGCTGCGMAAAATGAGTTCCACGCAATTCA 301
QY 121 gctcgaagatttaattgtagctcaagttcactctacgagactgcaatagcatcattcatg 180
DB 302 GCGGCAAGATATATGTGAGAGCTCAAGTTTACCTTGAGGAGACTGCAATATGATCCCTCTA 361

QY 181 gtttaggaacttgcgaagagacattcaacctgtactacatgagtgctctgatgatcatcat 240
DB 362 GTTGTGGCACTTGCAGAGAGAGACTTCAATCTGTATTCATAGATGAAATCCGATGATGACAT 421
QY 241 ggggtgaaatttcgagagatcattgttcaaaagattgacaccattgcagctgtagaagtc 300
DB 422 TTGGCAAGATTTCAG 481
QY 301 ttcactcaaatgagatcttgaggagcgttctctgaagctcaacacacagatagagaagta 360
DB 482 TTCACCCAGATGAGATCTTGGGAGCGGATTTCTCAAGCTGAAATACCGAATCCCGAGGTG 541
QY 361 gttcctgcacaagaagagagatttatttggcatcttcaagaattgtgtgtgtgtgtgtcc 420
DB 542 GGACCTGTTAGTAAG 601
QY 421 ttggtgtctgtgagagtgcttacttcaaaaagtgcacatttaacagtgagaatctgtatg 480
DB 602 TTAGTCTGGTGGAGTGTACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 661
QY 481 ttccagagacagtgatccatgactccatccatccctggtgagaggttagagaggtctgtgc 540
DB 662 TTTCAGATATACAGTCTCATGAGACTCCAGTCCCTGCTGAGAGTCCGGGCTTCTTGTGTC 721
QY 541 aacattctaaagagagatctctccaaagtactgtcagtlacagaaagcgaaatgtgctt 600
DB 722 AATCATTCAG 781
QY 601 gtaccattgtcgaagtgcttctcgtcaatgctgtgctatgagaagaagagtttaattgtcca 660
DB 782 GTGCCATAGGAG 841

RESULT 8
LOCUS 115007 3254 bp DNA PAT 02-APR-1996
DEFINITION Sequence 15 from patent US 5457048.
ACCESSION 115007
VERSION 115007.1 GI:1249915
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3254)
AUTHORS Pasquale, E.B. and Sajjadi, F.G.
TITLE Eph-related tyrosine kinases, nucleotide sequences and methods of use
JOURNAL Patent: US 5457048-A 15 10-OCT-1995;
FEATURES
source Location/Qualifiers
1..3254
/organism="unknown"
BASE COUNT 926 a 737 c 796 g 795 t
ORIGIN

Query Match 70.2%: Score 463.2; DB 5; Length 3254;
Best Local Similarity 81.4%: Pred. No. 3.6e-130;
Matches 537; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 1 tgggaagagatcagtggtgtaaacattacacccatcaggactaccaggtgtgc 60
DB 182 TGGGAAGAGATTAGTGTGTGATGAGCATYTAATCCAAATGAGAAATGACAGAGAGC 241
QY 61 aatgcattgagaccacagttcaaacatttgctgtagagacaaactggttccccaagaacta 120
DB 242 AATGTTATGAGATCAGTCAAGTCAAAATTTGGCTGCGMAAAATGAGTTCCACGCAATTCA 301
QY 121 gctcgaagatttaattgtagctcaagttcactctacgagactgcaatagcatcattcatg 180
DB 302 GCGGCAAGATATATGTGAGAGCTCAAGTTTACCTTGAGGAGACTGCAATATGATCCCTCTA 361
QY 181 gtttaggaacttgcgaagagacattcaacctgtactacatgagtgctctgatgatcatcat 240

TITLE An Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain

JOURNAL Oncogene 8 (4), 1103 (1993)

MEDLINE 93205393

REMARK GenBank staff at the National Library of Medicine created this entry (NCBI g1bbsq 127779) from the original journal article.

COMMENT *ERRATUM* Gilaradi-Hebenstreit et al., Oncogene (1992) 7, 2499-2507. This sequence comes from Fig. 5.

FEATURES

source Location/Qualifiers

1..4242

/organism="Mus sp."

/db_xref="taxon:10095"

58..3018

/gene="Sek"

/note="Eph-related receptor protein tyrosine kinase"

58..3018

/protein_id="AAB25836.1"

/db_xref="GI:298688"

/translation="MAGIFFLFSLFGICDAYGSHVYPAHEVTLIDSRVQELG WIASPLEGMEVSIIMDEKNTPIRYQCNVMEASQNMRLRTDITREGAORYIEK FTLRDCNSLPGVGTCKETFMLYYESDNDEKRFRESQFGKTDIADSEFTQYDIDG DRIMKINTEIRVDGPIASKKGFYLAPODGAICAIYSVVFPKCLYRINLAQPPDT TGADPSSLYVRGSCVNNSEKDPKATCGADGELVYIGCLCNAGEEDGEOAC KIGYTKALSTQACAKCPHSISYWEAGTSCDDEFRANDKASMCCTPSPAPLN LISVNETSVNLEWSSPQNTGRODISYNNVCKGQADPCKRCGSGGVTRPDQNG LKTRVSTITDLAHTNYFEIIMAVGSKYKSPQSVSYVITTNKIPAPSSIALYQAK EVTRSVLAHLLEDPNGVILLEYEVKYEKQDNQSVYRTAARNMDIGLADPITS YFHVHARTAGYDGESEPLEVTNTVYPTLIGGANSCTLLVSSGVYVILLIAA FVIRBRKSKAKOADEKHNQVATYDPTPEPNNAVREFAEIMQFHPNT KVIYGEFGEVCSGRKATPKAREICVAITKTAGTDKORDFSEASITMOCFHPNT IHLGCVYTKCPVMIITEYEMENGLDAFLRNQDGFVYIQVGMIRGIGSOMKYLSDM SYVHDLAARNILVNSNLVCKVSDGSRVLEDDPEAYTRGGKIPJRYTAPALYAK RKTFSADSVSYGIVMEVMSYGERPYWDMNODVITKALEGRILRPPMDGPIALHOL MLDQMKRSDRPRKGOIYNNLDIRNPNLSKTRGSSSRPNTRALDPPSPERSVAY SVCDMLAKIKRDKRKNDNTAAGTYTTLLEVYHMSODDLAKIGITALTTHONKLLSSVOAM RTMOQOHGRVPPV"

BASE COUNT 1155 a 1034 c 1052 g 1001 t

ORIGIN

Query Match 50.0%; Score 330.2; DB 12; Length 4242;

Best Local Similarity 69.7%; Pred. No. 1.le-89;

Matches 462; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

OY 1 tgggaagagatcagtggtgataaacattacacccatcagatgagatgtgtgc 60

DB 217 TGGGAGGAGTAGTATGATGAGTGAAGAAAATACCCGATCGAAGCTTACCAAGGTGTC 276

OY 61 aatgcatcagacacagtcacaaatcagctgagagacaaatcagctggtcccgagaactca 120

DB 277 AACGATGATGAGAGCCAGCAGCAACTGCTGCGAATGACTGATGATCACCGCGAAGG 336

OY 121 gctcagaagattatgtgtgagctcaagttcactcagcagatgcaatagcatctccatgt 180

DB 337 GCGCAGAGGGTGTACTGTAATTAAGTTCACCTTAAGGAGCTGCAACAGTCTCCGGGC 396

OY 181 gtttaagaacttcgaagaagacattcaacctgtactatcagtgagctctgatgatcat 240

DB 397 GTCATGAGGGAGCTTGCAGAGAGACGTTTAACCTCTTACTACTATGAGTCCGACAAACGCAAG 456

OY 241 ggggtgaatttcgagaagatcagttacaaagattgacacacatcagcagctgatgaagt 300

DB 457 GAGCCCTTCATCATGAGAGAGCAGTTTGCGAAGACTGACACCATCGACACTGATGAGAC 516

OY 301 ttcactcaaatgagatcttggggacccgtatctcgaagctcaaacatcagatgagaagta 360

DB 517 TTCACGACAGTGTGATGTCGCAATCATCAACATCATGAGATCCGGGATGTA 576

OY 361 gttcctcgaacaagaagagattatttggcatcttcaagaatgtgtgtgtgtgtcc 420

DB 577 GGGCCACTGAGCAAGAAAGGTTTAACTGCTTTCAGAGATGTGGGTTCGATCGCC 636

OY 421 ttgtgtctgtgtgagatctacttcaaaaagtgcacatttaagttgaagaatcgtgtatg 480

DB 637 CTGGTGTCTGTGCTGCTGTGTGTACAAAGAGTGTCCACGACCGTTCGAATCTACCCAG 696

OY 481 ttccaagaagtgatcccatgt---gactccaagtcctcgtgtgaggtttagaaggtctgt 537

DB 697 TTTCTGTACACCATTTACGAGGCGCTGATACCTCTTCCCTGGTGGAGTTTCGAGGCTCTGT 756

OY 538 gtcacaacttcgaagaagagatcctcgaagatcgtatcctcagtaacagaagcggaatcg 597

DB 757 CTCACCAACTCGAAGAGAGAGATGTGCCAATAATGTCTGTGGGCGAGATGTAAATGG 816

OY 598 ctgtaccatctgcaagtgcttcctcgaatcgtgtcgtatgaagaagaaggtttatgtgc 657

DB 817 CTGTATCCCATTTGCAAGTGGCTATGCAACGCTGGCGACGAGACCAATATGCTAATGC 876

OY 658 caa 660

DB 877 CAA 879

RESULT 12

LOCUS MMU58332 3943 bp mRNA ROD 08-MAY-1997

DEFINITION Mus musculus receptor tyrosine kinase mRNA, complete cds.

ACCESSION U58332

VERSION U58332.1 GI:1457960

KEYWORDS house mouse.

SOURCE Mus musculus.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE Lee,A.M., Navaratnam,D., Ichimiya,S., Greene,M.I. and Davis,J.G. Cloning of m-ehx2 from the murine inner ear, an eph family receptor tyrosine kinase expressed in the developing and adult cochlea DNA Cell Biol. 15 (10), 817-825 (1996)

JOURNAL 97047913

MEDLINE 97047913

AUTHORS Lee,A.M., Ichimiya,S., Greene,M.I. and Davis,J.G.

AUTHORS Direct Submission

TITLE Submitted (14-MAY-1996) Pathology & Laboratory Medicine, University of Pennsylvania, 36th and Hamilton Walk, Philadelphia, PA 19104-6082, USA

FEATURES

source Location/Qualifiers

1..3943

/organism="Mus musculus"

/strain="Balb/c"

/db_xref="taxon:10090"

285..3392

/note="Eph-related tyrosine kinase; similar to Rattus norvegicus receptor-like tyrosine kinase Ehk-2, Swissprot Accession Number S51605"

/codon_start=1

/product="receptor tyrosine kinase"

/protein_id="AAB53836.1"

/db_xref="GI:1457961"

/translation="MGCEVREKFLQGFPLITANTGDCSHVSNQVILLDTTVNG ELGWKTYPLNGWCAITMDENHRPIHRYQCNVMEASQNMRLRTNLSRBAOKIYE MKFTLRDCNSLPGVLTGCKETFMLYYESDSHGTRKPSQYIKIDTIADEFTQYD LGDRIKLNTEIRVGVIERKGFYLAODIGACIALVSVYFVKCPFTYRSLAMFED TTPRVDSSLYVRGSCVNSAEEDPDKLYCGAGDMVLVPRGTCSTGYEELGSCG ACRCGFKAPAGNPKCKSCPHSTSYEATSYVCEGEGYRAEDPSSACTRPPSP RNVAFNINETALITMSPSPSDTGERKDLITVICKCGLDITQDCDGGGURFTPRH GLINNSVVLDEPVSHVNYTEIEMANGVSELSISPKPETAITVTDDAPSLIGMKRK DVAQNSLALSMQAPARSNGAILDYETKRYEKEEQLYSTRKASVYTGKLPAT TYFIHIRVATATGSGYSGOKFEFTGETGETGMAEQOIIYATAAVGGFLVITL FELITGCOMYIKAKMSEKRRHTLNGHLRFGIGITTYIDPDYEDPSLAVFEPAE IDPSRIENIENIAGGEFVCSGRKATPKREIPVATIKTLKGMDRORDFLEASI


```
repeat_region /rpt_family="Alu" .43816)
complement(42859.
/rpt_family="L1"
repeat_region complement(42946. .43193)
/rpt_family="Alu"
repeat_region 43874. .44564
/rpt_family="L1"
repeat_region 48397. .49774
/rpt_family="L1"
complement(55712.
/rpt_family="L1"
repeat_region complement(58953. .59284)
/rpt_family="THE1"
repeat_region 59425. .59770
/rpt_family="THE1"
repeat_region 63634. .63701
/rpt_family="L1"
repeat_region 64533. .64831
/rpt_family="Alu"
complement(69359.
/rpt_family="MIR"
repeat_region complement(75583. .75896)
/rpt_family="Alu"
repeat_region 77142. .77197
/rpt_family="Alu"

BASE COUNT 23370 a 13418 c 14087 g 26322 t
ORIGIN

Query Match 49.6% Score 327.6; DB 11; Length 77197;
Best Local Similarity 69.5% Pred. No. 7.9e-89;
Matches 460; Conservative 0; Mismatches 199; Indels 3; Gaps 1;

QY 1 tgggaagagatcagtggtggtgatacattacacacccatcagacttaccagttgtgc 60
|||||
DB 4625 TGGGATGCATCAGTGAATGATGATACATATAGCCCATTCACACATACCGATATGT 4684
61 aatctatgagccacagtcacaacacatgctgagacaacatggtcccccagagactca 120
|||||
DB 4685 AATGTAATGGAACCAACCAACCAACACAGTGGCTCTGTAACAACTGATATCCCGTATGCA 4744
121 gctcagaagattatggtgagctcaagttcaactctacagagactgcaatagcattccattg 180
|||||
DB 4745 GCTTGGAATAATTTATGTCGAATGAAATTCACACTAAGGATGTAACAGCATCCCATGG 4804
181 gtttaggaacttgcagaagagacattcaactgtctactcagtgagttcgtatgatcat 240
|||||
DB 4805 GCTTGGGACTTGCAGAAAGAAACATTTAATCTGTTTATATGGAATCAGATGAGCCAC 4864
241 ggggtgaattcgcagagcatcagatttacaagaattgacacacatgacagctgagtgaaat 300
|||||
DB 4865 GGAATTAATTCAGCCAAACCAACCAACCAACAGATACGACACAAATTCCTGCTGATAGAGT 4924
301 ttcactcaaatgatctctgggagccgtatcttgaagctcaacactgagattagagaagta 360
|||||
DB 4925 TTTACCCAGATGATTTGGTGTGATGTCCTCAAACTCAACACTGAATTCGTAGGTG 4984
361 ggtctgcacaagaagagatttatttgatcattcaagaattgtgtgtgtgtgtgtcc 420
|||||
DB 4985 GGGGCTATAGAAAGAAAGGATTTATATCGCTTTTCAAGACATGGGGCGTGCATTCGCC 5044
421 ttggtgtctgtagagatctacttcaaaagtggccattcagtgagtgagtgagta 480
|||||
DB 5045 CTGGTTTACGTCGGGTCTTTTACAAAGAAATGCCCTTCATCTGTCGTAACCTGGCCATG 5104
481 ttccagagacaggtaccca---tgagactccagtcctcctggtgagagttagagagttctgt 537
|||||
DB 5105 TTTCTCTGATACCATTCAGAGGTTGATTCCTCTCTTGTGTAAGTACGGGGTCTTGT 5164
538 gtcaacaatttaagagagagatctctcaagagatgtctcagtagacagaagcgcaatgg 597
|||||
DB 5165 GTGAAGAGTGTGGAAGCGTGACACTCTCTAAACTGATGTGTGAGCTGATGAGATGG 5224
```

```
QY 598 cttgaccattggcagaagtctctcgcgaatgctgctatgaagaagaaggtttatgtgc 657
|||||
DB 5225 CTGGTCTCTTGGAAAGGTGATCTGCACTACAGATATGAAGAAATGAGAGTCTCTGC 5284
QY 658 ca 659
DB 5285 CA 5286

RESULT 14
HMDRPTK
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
FEATURES
source
location/Qualifiers
1..3107
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="fetus, 17-18 weeks gestation"
/sex="female"
/clone_id="Stratagene premade library, cat #936206"
/tissue_type="brain"
1..3107
/gene="HER8"
/product="receptor protein-tyrosine kinase"
1..3107
/gene="HER8"
<1..33
/gene="HER8"
34..2994
/gene="HER8"
/codon_start=1
/product="receptor protein-tyrosine kinase"
/db_xref="GI:551614"
/translating="MAGI5FALFSCIFGICDAVTSGRVYPAVEVTLILDSRSVOGELG
WIASPLEGWEVSEINDEKNTPIRIYQCVAMPSPSONMWTIMITREGQORYIEIK
FTLRDNLSPGVGKTEFENLYEEDNDKEFIRENCKIDTIADESFQVODG
DRIMKLNTEIRDGPLSKGFEYAFQVAGCIALVRYRYKCPITVRMLAQEPDIT
TGADTSILVRSQVNNSEKXVPKATGCADEMLYPTICNCGNHERSSECCAC
KIYRYRLSDTADCAKCPHSISYVWEGATSCDTRGFADNDRAASPCTRPSPAPLN
LISNVEISVNLWSSPQNTGSRQDLSYNVCKKCGAGDSKCRPGSGVHYTPQNG
LKTTRYSITDLAHNTYFEIMAVNGSKXNPDOVSVTVTNQAAPSSIALYAK
EVRYSVALAMLEPDRPNQVILEYVYKEDQNEISYRIVTAARNTDICKNPLTS
YFHVHARRTAAGDSEPLEVTNTYPSRIIDGANSYTLVSVSGSVLVYVITLAA
FVTSRRSKYSKAKOEADDEKHNLNOCVRYVDPFTYEDPQAVREPAKEIDACIKIE
KYVGVEFGVCGRKLKVPKREITCAIKTLKAGYTDKQDRDLSEASLIGQDHPNI
IHLGVVTKCKPVMILITEYMENSLAEFLKNDGRRTVYDLYOMKIGSGMYLSDM
SYVHRDLAANILVNSLWCKVSDFGSKNLEDDPEAAYTTRGKIPIDMTAEALAY
RKFTSADSVSYIVMEVMSYGERPYMDNSQDYLKAIIEGYRLPDPMDCPALHOL
MLCQWOKERSDVRKFGQIYVMLKILRNPSLKRGTGESSRPTMTALIDPSSPFSAY
SVGDMLQATKMDRKYKDNFTAGATTLEAVYHVQEDLIARIGITAIITHOKITLSSVQAM
RTQMOMHGKMYV"
2995..3107
/gene="HER8"
BASE COUNT 850 a 720 c 812 g 725 t
ORIGIN
```

Query Match 49.5%; Score 327; DB 10; Length 3107;
Best Local Similarity 69.4%; Pred. No. 9.9e-89;
Matches 460; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 1 tgggaagatcaatggtgtgtgataacattacacccatcagaactaccaggtgtgc 60
DB 193 TGGGAGGAGTGAATGATCATGATAAATAATACCAATCGAATCCGAACTGCAAGAGTTC 252
QY 61 aatgtcatgagaccagatcaaaacattgctgagacaactgggtccccaagaaactca 120
DB 253 AATGTGATGGAACCCAGCAGATTAATCTGGCTACGAACTGATTTGATCCGAGAAAGG 312
QY 121 gctcagaagatttaatgtgagctcaagctcactcagagactgagactgacattccatg 180
DB 313 GCTCAGAGGCTTATATGATGATTAATTAATTCACCTTAGGAGACTGCAATAGTCTCCGGGC 372
QY 181 gtttaagaaacttgcaagaaagacattcaacctgtactataatgaggtctgatatcat 240
DB 373 GTCATGGGACTTGCAGAGAGACGTTTAACCTGTACTATGATTAATCAGAACACAA 432
QY 241 ggggtgaatttcgagagatcagtttacaagaattgacacattgacattgagatgaagt 300
DB 433 GAGCGTTTCATCAGAGAGAACCAAGTTTGTCAAAATTTGACACCTTCTCTGATGAGAC 492
QY 301 ttcaactcaaatgtatcttgggagaccgtatcttgaagctcaacactgagattagaagaatga 360
DB 493 TTCACCCAGTGGACATTTGTGTGACAGAAATCATGAACTGAACTGAAACACGAGATCCGGATGTA 552
QY 361 ggtcctgtcaacaagaaggatcttaattggcaattcaagaatgtgtgtctgtgtcc 420
DB 553 GGGCCATTAAAGCAAAAGGGGTTTACCTGGCTTTTACAGAGAGTGGGGCCCTGCATCGCC 612
QY 421 ttggtgtcgtgagagtaacttcaaaaagtgcacattcaagtgagaagatctggtcatg 480
DB 613 CTGGTATCAGTCCGTGTCTTATAAAAGTGTCCACTCAGACTCCGCAATCTGGCCCAAG 672
QY 481 ttccagacaagtgatcccatg--gactccagtcctgtgtgaggttagaaggtctgt 537
DB 673 TTTCCTGACACCATCAGAGGGGCTGATAGCTTCCCTGGTGAAGTTGAGGCTCCTGT 732
QY 538 gtcaacaattctaaaggaagaatctcctcaagagatgtactgtcagagaagcgaaatg 597
DB 733 GTCACAACTCAGAAAGAGAAAGATGTGCCAAAATATGTACTGTGGCAGATGTGTGATGG 792
QY 598 ctgttaaccatttggcaagtgcttcctgcaatgtcgtcgtatgaagaagaaggtttatgtgc 657
DB 793 CTGGTACCATTTGGCAACTGCTTATGCAACGCTGGGCAATGAGAGCGGAGCGAAGATGC 852
QY 658 caa 660
DB 853 CAA 855

RESULT 15
I44522
LOCUS I44522 3348 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 34 from patent US 5635177.
ACCESSION I44522
VERSION I44522.1 GI:2469235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3348)
AUTHORS Bennett,B.D., Goeddel,D. and Matthews,W.
TITLE Protein tyrosine kinase agonist antibodies
JOURNAL Patent: US 5635177-A 34 03-JUN-1997;
FEATURES
source 1. 3348
location/Qualifiers
1..3348 /organism="unknown"

BASE COUNT 924 a 769 c 855 g 800 t
ORIGIN

Query Match 49.5%; Score 327; DB 5; Length 3348;
Best Local Similarity 69.4%; Pred. No. 9.9e-89;
Matches 460; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 1 tgggaagatcaatggtgtgtgataacattacacccatcagaactaccaggtgtgc 60
DB 160 TGGGAGGAGTGAATGATCATGATAAATAATACCAATCCGAACTGCAAGTGTGC 219
QY 61 aatgtcatgagaccagatcaaaacattgctgagacaactgggtccccaagaaactca 120
DB 220 AATGTGATGGAACCCAGCAGATTAATCTGGCTACGAACTGATTTGATCCGAGAAAGG 279
QY 121 gctcagaagatttaatgtgagctcaagctcactcagagactgagactgacattccatg 180
DB 280 GCTCAGAGGCTTATATGATGATTAATTAATTCACCTTAGGAGACTGCAATAGTCTCCGGGC 339
QY 181 gtttaagaaacttgcaagaaagacattcaacctgtactataatgaggtctgatatcat 240
DB 340 GTCATGGGACTTGCAGAGAGACGTTTAACCTGTACTATGATTAATCAGAACACAA 399
QY 241 ggggtgaatttcgagagatcagtttacaagaattgacacattgacattgagatgaagt 300
DB 400 GAGCGTTTCATCAGAGAGAACCAAGTTTGTCAAAATTTGACACCTTCTCTGATGAGAC 459
QY 301 ttcaactcaaatgtatcttgggagaccgtatcttgaagctcaacactgagattagaagaatga 360
DB 460 TTCACCCAGTGGACATTTGTGTGACAGAAATCATGAACTGAACTGAAACACGAGATCCGGATGTA 519
QY 361 ggtcctgtcaacaagaaggatcttaattggcaattcaagaatgtgtgtctgtgtcc 420
DB 520 GGGCCATTAAAGCAAAAGGGGTTTACCTGGCTTTTACAGAGAGTGGGGCCCTGCATCGCC 579
QY 421 ttggtgtcgtgagagtaacttcaaaaagtgcacattcaagtgagaagatctggtcatg 480
DB 580 CTGGTATCAGTCCGTGTCTTATAAAAGTGTCCACTCAGACTCCGCAATCTGGCCCAAG 639
QY 481 ttccagacaagtgatcccatg--gactccagtcctgtgtgaggttagaaggtctgt 537
DB 640 TTTCCTGACACCATCAGAGGGGCTGATAGCTTCCCTGGTGAAGTTGAGGCTCCTGT 699
QY 538 gtcaacaattctaaaggaagaatctcctcaagagatgtactgtcagagaagcgaaatg 597
DB 700 GTCACAACTCAGAAAGAGAAAGATGTGCCAAAATATGTACTGTGGGCAAGATGTGTAATGG 759
QY 598 ctgttaaccatttggcaagtgcttcctgcaatgtcgtcgtatgaagaagaaggtttatgtgc 657
DB 760 CTGGTACCATTTGGCAACTGCTTATGCAACGCTGGGCAATGAGAGCGGAGCGAAGATGC 819
QY 658 caa 660
DB 820 CAA 822

Search completed: May 15, 2000, 11:43:49
Job time: 1656 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 21:16:51 ; Search time 44.2 Seconds
(without alignments)
71.991 Million cell updates/sec

Title: US-09-104-340-1
Perfect score: 1200
Sequence: 1 WEERISGVDEHYTPRIYQVC.....VPIKCSGNAGEERGFMCQ 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 143561 seqs, 14463640 residues
Total number of hits satisfying chosen parameters: 143561

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents, AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/Backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	983	1	US-08-167-919A-10
2	1200	100.0	983	2	US-08-449-645A-21
3	1200	100.0	983	2	US-08-702-367A-21
4	1200	100.0	983	3	US-08-715-106-10
5	1200	100.0	983	4	PCT-US95-04681-21
6	1136	94.7	983	1	US-08-162-809-16
7	1132	94.3	982	2	US-08-673-789-4
8	917.5	76.5	986	2	US-08-673-789-3
9	914.5	76.2	948	2	US-08-469-537A-101
10	905.5	75.5	986	2	US-08-449-645A-15
11	905.5	75.5	986	2	US-08-702-367A-15
12	905.5	75.5	986	4	PCT-US95-04681-15
13	905.5	75.5	1104	4	US-08-222-616-36
14	905.5	75.5	1104	4	PCT-US95-04228-36
15	866.5	72.2	877	2	US-08-673-789-2
16	866.5	72.2	1005	2	US-08-469-537A-103
17	865.5	72.1	928	1	US-08-442-248-2
18	865.5	72.1	928	1	US-08-440-815-2
19	860.5	71.7	967	2	US-08-449-645A-30
20	860.5	71.7	967	2	US-08-702-367A-30
21	860.5	71.7	991	2	US-08-449-645A-13
22	860.5	71.7	991	2	US-08-702-367A-13
23	860.5	71.7	991	4	PCT-US95-04681-13
24	857.5	71.5	610	4	PCT-US96-00419-3
25	857.5	71.5	626	4	PCT-US96-00419-5
26	857.5	71.5	998	4	PCT-US96-00419-2
27	856.5	71.4	998	2	US-08-449-645A-17
28	856.5	71.4	998	2	US-08-702-367A-17
29	856.5	71.4	998	4	PCT-US95-04681-17

30	715	59.6	995	2	US-08-673-789-5	Sequence 5, Appl
31	713	59.4	995	1	US-08-162-809-18	Sequence 18, Appl
32	713	59.4	1011	1	US-08-162-809-12	Sequence 12, Appl
33	708	59.0	970	2	US-08-449-645A-11	Sequence 11, Appl
34	708	59.0	970	2	US-08-702-367A-11	Sequence 11, Appl
35	708	59.0	970	4	PCT-US95-04681-11	Sequence 11, Appl
36	693.5	57.8	984	2	US-08-673-789-6	Sequence 6, Appl
37	681.5	56.8	710	1	US-08-162-809-22	Sequence 22, Appl
38	681.5	56.8	722	1	US-08-162-809-4	Sequence 4, Appl
39	681.5	56.8	744	1	US-08-162-809-20	Sequence 20, Appl
40	644	53.7	973	1	US-08-162-809-10	Sequence 10, Appl
41	644	53.7	988	1	US-08-162-809-14	Sequence 14, Appl
42	642	52.7	998	2	US-08-449-645A-20	Sequence 20, Appl
43	632	52.7	998	4	US-08-702-367A-20	Sequence 20, Appl
44	632	52.7	998	4	PCT-US95-04681-20	Sequence 20, Appl
45	627	52.2	976	2	US-08-449-645A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-167-919A-10
; Sequence 10, Application us/08167919A
; Patent No. 5674691
; GENERAL INFORMATION:
; APPLICANT: Boyd, Andrew W.
; APPLICANT: Simpson, Richard J.
; APPLICANT: Wicks, Ian
; APPLICANT: Ward, Larry D.
; APPLICANT: Wilkinson, David
; TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,919A
; FILING DATE: 18-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK6841 (AU)
; FILING DATE: 21-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK9992 (AU)
; FILING DATE: 12-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU92/00294
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-167-919A-10

Query Match 100.0%; Score 1200; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 3.7e-122;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEISGVDEHYPIRTYQVCNMDHSONNWLRTNWPNSAOKIYELKFTLRDCNSIPL 60
DB 52 WEISGVDEHYPIRTYQVCNMDHSONNWLRTNWPNSAOKIYELKFTLRDCNSIPL 111
QY 61 VGTCKETFNLYMESDDHGVKFRFHOFKIDTIAADESFTQMDLGRILKLNTEIREV 120
DB 112 VGTCKETFNLYMESDDHGVKFRFHOFKIDTIAADESFTQMDLGRILKLNTEIREV 171
QY 121 GPNKKGFLAFQDYGACVALSVRYFKKCPFTYKNLAMPDTPYPMDSQSLVEYRGSCV 180
DB 172 GPNKKGFLAFQDYGACVALSVRYFKKCPFTYKNLAMPDTPYPMDSQSLVEYRGSCV 231
QY 181 NNSKEDEPPRMVCSLEGEMLVPIGKSCNAGYEERGFMCQ 220
DB 232 NNSKEDEPPRMVCSLEGEMLVPIGKSCNAGYEERGFMCQ 271

RESULT 2

US-08-449-645A-21
; Sequence 21, Application US/08449645A
; Patent No. 5981245

; GENERAL INFORMATION:

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Patent Operations/RBW

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,645A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-287

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 983 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-449-645A-21

Query Match 100.0%; Score 1200; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 3.7e-122;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEISGVDEHYPIRTYQVCNMDHSONNWLRTNWPNSAOKIYELKFTLRDCNSIPL 60
DB 52 WEISGVDEHYPIRTYQVCNMDHSONNWLRTNWPNSAOKIYELKFTLRDCNSIPL 111
QY 61 VGTCKETFNLYMESDDHGVKFRFHOFKIDTIAADESFTQMDLGRILKLNTEIREV 120
DB 112 VGTCKETFNLYMESDDHGVKFRFHOFKIDTIAADESFTQMDLGRILKLNTEIREV 171

QY 121 GPNKKGFLAFQDYGACVALSVRYFKKCPFTYKNLAMPDTPYPMDSQSLVEYRGSCV 180
DB 172 GPNKKGFLAFQDYGACVALSVRYFKKCPFTYKNLAMPDTPYPMDSQSLVEYRGSCV 231
QY 181 NNSKEDEPPRMVCSLEGEMLVPIGKSCNAGYEERGFMCQ 220
DB 232 NNSKEDEPPRMVCSLEGEMLVPIGKSCNAGYEERGFMCQ 271

RESULT 3

US-08-702-367A-21
; Sequence 21, Application US/08702367A
; Patent No. 5981246

; GENERAL INFORMATION:

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Patent Operations/RBW

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/702,367A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-287

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 983 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-702-367A-21

Query Match 100.0%; Score 1200; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 3.7e-122;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEISGVDEHYPIRTYQVCNMDHSONNWLRTNWPNSAOKIYELKFTLRDCNSIPL 60
DB 52 WEISGVDEHYPIRTYQVCNMDHSONNWLRTNWPNSAOKIYELKFTLRDCNSIPL 111
QY 61 VGTCKETFNLYMESDDHGVKFRFHOFKIDTIAADESFTQMDLGRILKLNTEIREV 120
DB 112 VGTCKETFNLYMESDDHGVKFRFHOFKIDTIAADESFTQMDLGRILKLNTEIREV 171
QY 121 GPNKKGFLAFQDYGACVALSVRYFKKCPFTYKNLAMPDTPYPMDSQSLVEYRGSCV 180
DB 172 GPNKKGFLAFQDYGACVALSVRYFKKCPFTYKNLAMPDTPYPMDSQSLVEYRGSCV 231
QY 181 NNSKEDEPPRMVCSLEGEMLVPIGKSCNAGYEERGFMCQ 220
DB 232 NNSKEDEPPRMVCSLEGEMLVPIGKSCNAGYEERGFMCQ 271

RESULT 4

US-08-715-106-10
; Sequence 10, Application US/08715106
; Patent No. 6020306

GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-715-106-10

Query Match 100.0%; Score 1200; DB 3; Length 983;
Best Local Similarity 100.0%; Pred. No. 3,7e-122;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEISGVDEHYPIRTYQVCNMDHSQNNWLTNNVPRNSAKIYVELKFTLRDNCISPL 60
|||||
DB 52 WEISGVDEHYPIRTYQVCNMDHSQNNWLTNNVPRNSAKIYVELKFTLRDNCISPL 111
|||||
QY 61 VLGTCKEFTNLYMESDDHGKVFREHOFKIDITIADESFQMDLGRILKLTNTEIRREV 120
|||||
DB 112 VLGTCKEFTNLYMESDDHGKVFREHOFKIDITIADESFQMDLGRILKLTNTEIRREV 171
|||||
QY 121 GPVNNKGFYLAQDVGACALYSVRVYFKKCFYTKNLAMPDTPVPMDSQSLVEYRGSCV 180
|||||
DB 172 GPVNNKGFYLAQDVGACALYSVRVYFKKCFYTKNLAMPDTPVPMDSQSLVEYRGSCV 231
|||||
QY 181 NNSKEEDPPRMATCSTEGEMLVPIGKSCNAGYEERGFMCQ 220
|||||
DB 232 NNSKEEDPPRMATCSTEGEMLVPIGKSCNAGYEERGFMCQ 271
|||||

RESULT 5
PCT-US95-04681-21
Sequence 21, Application PC/TUS9504681
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-21

Query Match 100.0%; Score 1200; DB 4; Length 983;
Best Local Similarity 100.0%; Pred. No. 3,7e-122;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEISGVDEHYPIRTYQVCNMDHSQNNWLTNNVPRNSAKIYVELKFTLRDNCISPL 60
|||||
DB 52 WEISGVDEHYPIRTYQVCNMDHSQNNWLTNNVPRNSAKIYVELKFTLRDNCISPL 111
|||||
QY 61 VLGTCKEFTNLYMESDDHGKVFREHOFKIDITIADESFQMDLGRILKLTNTEIRREV 120
|||||
DB 112 VLGTCKEFTNLYMESDDHGKVFREHOFKIDITIADESFQMDLGRILKLTNTEIRREV 171
|||||
QY 121 GPVNNKGFYLAQDVGACALYSVRVYFKKCFYTKNLAMPDTPVPMDSQSLVEYRGSCV 180
|||||
DB 172 GPVNNKGFYLAQDVGACALYSVRVYFKKCFYTKNLAMPDTPVPMDSQSLVEYRGSCV 231
|||||
QY 181 NNSKEEDPPRMATCSTEGEMLVPIGKSCNAGYEERGFMCQ 220
|||||
DB 232 NNSKEEDPPRMATCSTEGEMLVPIGKSCNAGYEERGFMCQ 271
|||||

RESULT 6
US-08-162-809-16
Sequence 16, Application US/08162809
Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego

STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-809-16

Query Match 94.7%; Score 1136; DB 1; Length 983;
Best Local Similarity 94.1%; Pred. No. 3.5e-115;

Matches 207; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEISGVDEHYTPIRTYQCVNVDHSONNWLRTNWPVPRNSAOKIYVELKFTLRDCNSIPL 60
DB 51 WEISGVDEHYTPIRTYQCVNVDHSONNWLRTNWPVPRNSAOKIYVELKFTLRDCNSIPL 110
QY 61 VLGTCKETFMLYMESDDHGVKFRHQFTKIDITIADESFQMDGLDRILKLTETREY 120
DB 111 VLGTCKETFMLYMESDDHGVKFRHQFTKIDITIADESFQMDGLDRILKLTETREY 170
QY 121 GPVNRKGFTYLAFOVGCALVSVRYVFKKCPFTVKNLAFPTVPMDQSLSVEVRGSCV 180
DB 171 GPVNRKGFTYLAFOVGCALVSVRYVFKKCPFTVKNLAFPTVPMDQSLSVEVRGSCV 230
QY 181 NNSKEEDPPRMKSTEGEWLVPIGKCSNAGYERGFMCQ 220
DB 231 NNSKEEDPPRMKSTEGEWLVPIGKCSNAGYERGFMCQ 270

RESULT 7
US-08-673-789-4
Sequence 4, Application US/08673789
Patent No. 5814479

GENERAL INFORMATION:
APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 982
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
US-08-673-789-4

Query Match 94.3%; Score 1132; DB 2; Length 982;
Best Local Similarity 94.1%; Pred. No. 9.5e-115;
Matches 207; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEISGVDEHYTPIRTYQCVNVDHSONNWLRTNWPVPRNSAOKIYVELKFTLRDCNSIPL 60
DB 51 WEISGVDEHYTPIRTYQCVNVDHSONNWLRTNWPVPRNSAOKIYVELKFTLRDCNSIPL 110
QY 61 VLGTCKETFMLYMESDDHGVKFRHQFTKIDITIADESFQMDGLDRILKLTETREY 120
DB 111 VLGTCKETFMLYMESDDHGVKFRHQFTKIDITIADESFQMDGLDRILKLTETREY 170
QY 121 GPVNRKGFTYLAFOVGCALVSVRYVFKKCPFTVKNLAFPTVPMDQSLSVEVRGSCV 180
DB 171 GPVNRKGFTYLAFOVGCALVSVRYVFKKCPFTVKNLAFPTVPMDQSLSVEVRGSCV 230
QY 181 NNSKEEDPPRMKSTEGEWLVPIGKCSNAGYERGFMCQ 220
DB 231 NNSKEEDPPRMKSTEGEWLVPIGKCSNAGYERGFMCQ 270

RESULT 8
US-08-673-789-3
Sequence 3, Application US/08673789
Patent No. 5814479

GENERAL INFORMATION:
APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-15

Query Match 75.5%; Score 905.5; DB 2; Length 986;
Best Local Similarity 73.3%; Pred. No. 4.5e-90;
Matches 162; Conservative 30; Mismatches 28; Indels 1; Gaps 1;

QY 1 WEISGVDEHYTPRTYOVCMNDHSONNMLRTNVPNRSQAKIYVELKFTLRDCNSIPL 60
DB 54 WEVSINDEKNTPIRTYOVCMNDHSONNMLRTNVPNRSQAKIYVELKFTLRDCNSIPL 113
DB 61 VLGTCKETFNLYMESDDHGVKREHOFTKIDTIADESFQVMDLGRILKLTETREY 120
DB 114 VMGTCKETFNLYYESDNDKERFIRENQFKIDTIADESFQVMDLGRILKLTETREY 173
QY 121 GPNVKKGFYLAFOVGCALVALSVRYFKKCPFTVKNLAMPDTPV-MDSQSLVEVRGSC 179
DB 174 GPLSKKGFYLAFOVGCALVALSVRYFKKCPFTVKNLAMPDTPV-MDSQSLVEVRGSC 233
QY 180 VNNSKEDEPPRMVSTEGEWLPIGKSCNAGYERGFMCQ 220
DB 234 VNNSKEDEPPRMVSTEGEWLPIGKSCNAGYERGFMCQ 274

RESULT 11
US-08-702-367A-15
Sequence 15, Application US/08702367A
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Denavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702.367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 986 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367A-15

Query Match 75.5%; Score 905.5; DB 2; Length 986;
Best Local Similarity 73.3%; Pred. No. 4.5e-90;
Matches 162; Conservative 30; Mismatches 28; Indels 1; Gaps 1;

QY 1 WEISGVDEHYTPRTYOVCMNDHSONNMLRTNVPNRSQAKIYVELKFTLRDCNSIPL 60
DB 54 WEVSINDEKNTPIRTYOVCMNDHSONNMLRTNVPNRSQAKIYVELKFTLRDCNSIPL 113
QY 61 VLGTCKETFNLYMESDDHGVKREHOFTKIDTIADESFQVMDLGRILKLTETREY 120

DB 114 VMGTCKETFNLYYESDNDKERFIRENQFKIDTIADESFQVMDLGRILKLTETREY 173
QY 121 GPNVKKGFYLAFOVGCALVALSVRYFKKCPFTVKNLAMPDTPV-MDSQSLVEVRGSC 179
DB 174 GPLSKKGFYLAFOVGCALVALSVRYFKKCPFTVKNLAMPDTPV-MDSQSLVEVRGSC 233
QY 180 VNNSKEDEPPRMVSTEGEWLPIGKSCNAGYERGFMCQ 220
DB 234 VNNSKEDEPPRMVSTEGEWLPIGKSCNAGYERGFMCQ 274

RESULT 12
PCT-US95-04681-15
Sequence 15, Application PC/TUS9504681
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Denavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 986 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-15

Query Match 75.5%; Score 905.5; DB 4; Length 986;
Best Local Similarity 73.3%; Pred. No. 4.5e-90;
Matches 162; Conservative 30; Mismatches 28; Indels 1; Gaps 1;

QY 1 WEISGVDEHYTPRTYOVCMNDHSONNMLRTNVPNRSQAKIYVELKFTLRDCNSIPL 60
DB 54 WEVSINDEKNTPIRTYOVCMNDHSONNMLRTNVPNRSQAKIYVELKFTLRDCNSIPL 113
QY 61 VLGTCKETFNLYMESDDHGVKREHOFTKIDTIADESFQVMDLGRILKLTETREY 120
DB 114 VMGTCKETFNLYYESDNDKERFIRENQFKIDTIADESFQVMDLGRILKLTETREY 173
QY 121 GPNVKKGFYLAFOVGCALVALSVRYFKKCPFTVKNLAMPDTPV-MDSQSLVEVRGSC 179
DB 174 GPLSKKGFYLAFOVGCALVALSVRYFKKCPFTVKNLAMPDTPV-MDSQSLVEVRGSC 233
QY 180 VNNSKEDEPPRMVSTEGEWLPIGKSCNAGYERGFMCQ 220
DB 234 VNNSKEDEPPRMVSTEGEWLPIGKSCNAGYERGFMCQ 274

RESULT 13
US-08-222-616-36
Sequence 36, Application US/08222616
Patent No. 5635177
GENERAL INFORMATION:

APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,616
FILING DATE: 4-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 821P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-222-616-36

Query Match 75.5%; Score 905.5; DB 1; Length 1104;
Best Local Similarity 73.3%; Pred. No. 5.2e-90;
Matches 162; Conservative 30; Mismatches 28; Indels 1; Gaps 1;
QY 1 WEISGVDEHTPIRTYOVGNMDSNNWLTNNVPRNSAKIYVELKFTLRDCNSIPL 60
DB 54 WEESVIMDEKNTPIRTYOVGNMDSNNWLTNNVPRNSAKIYVELKFTLRDCNSIPL 113
QY 61 VLGTKEFTNLYYMSDDHGVKFRHOFTKIDITIADESFQMDLGRILKLNTEIREV 120
DB 114 VMGTKEFTNLYYMSDDHGVKFRHOFTKIDITIADESFQMDLGRILKLNTEIREV 173
QY 121 GPNVKKGYFLAFQDVACALVSVAFFKCCPFTYKNTLAMPDTPV-MDSQSLVEVRGSC 179
DB 174 GPLSKRGYFLAFQDVACALVSVAFFKCCPFTYKNTLAMPDTPV-MDSQSLVEVRGSC 233
QY 180 VNSKEEDPPRYKSTEGEMLVPIGKCSNAGYEERGFMCQ 220
DB 234 VNSSEKDVPRMYCGADEMLVPIGNCICNAGHEERSGECQ 274

RESULT 14
PCT-US95-04228-36
Sequence 36, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.

APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-04228-36

Query Match 75.5%; Score 905.5; DB 4; Length 1104;
Best Local Similarity 73.3%; Pred. No. 5.2e-90;
Matches 162; Conservative 30; Mismatches 28; Indels 1; Gaps 1;
QY 1 WEISGVDEHTPIRTYOVGNMDSNNWLTNNVPRNSAKIYVELKFTLRDCNSIPL 60
DB 54 WEESVIMDEKNTPIRTYOVGNMDSNNWLTNNVPRNSAKIYVELKFTLRDCNSIPL 113
QY 61 VLGTKEFTNLYYMSDDHGVKFRHOFTKIDITIADESFQMDLGRILKLNTEIREV 120
DB 114 VMGTKEFTNLYYMSDDHGVKFRHOFTKIDITIADESFQMDLGRILKLNTEIREV 173
QY 121 GPNVKKGYFLAFQDVACALVSVAFFKCCPFTYKNTLAMPDTPV-MDSQSLVEVRGSC 179
DB 174 GPLSKRGYFLAFQDVACALVSVAFFKCCPFTYKNTLAMPDTPV-MDSQSLVEVRGSC 233
QY 180 VNSKEEDPPRYKSTEGEMLVPIGKCSNAGYEERGFMCQ 220
DB 234 VNSSEKDVPRMYCGADEMLVPIGNCICNAGHEERSGECQ 274

RESULT 15
US-08-673-789-2
Sequence 2, Application US/08673789
Patent No. 5814479
GENERAL INFORMATION:
APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE

;; TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
;; TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
;; TITLE OF INVENTION: METHODS
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/673,789
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/177,812
;; FILING DATE: 04-JAN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPE
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4105
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELE: 421/92
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 877
;; TYPE: AMINO ACID
;; STRANDEDNESS: UNKNOWN
;; TOPOLOGY: UNKNOWN
;;
US-08-673-789-2

Query Match 72.2%; Score 866.5; DB 2; Length 877;
Best Local Similarity 68.3%; Pred. No. 6.7e-86;
Matches 151; Conservative 35; Mismatches 34; Indels 1; Gaps 1;

QY 1 WEISGVDEHYTPRTYQVCNVMADHSQNMWLRNWPVRSQAKIYVELKFTLRDCNSIPL 60
||| |||:| ||||| ||: ||||| ||: ||||| |||||:|
DB 85 WEIGEVDEHYAPRIHYQVCKVMEQNMNMLTWSINEGASRIETELKFTLRDCNSLPG 144
||| |||:| ||||| ||: ||||| ||: ||||| |||||:|
QY 61 VLGCTKETNLVYMESDDHGVKFRHQFTKIDTIADESFQMDLGDRLKLNTEIREV 120
||||| |||:| ||||| ||: ||||| ||: ||||| |||||:|
DB 145 GLGTCKETNNMYFEESDDEGRSIRKENQYKIDTIADESFTELDGDRYMKLNTEVRYD 204
||||| |||:| ||||| ||: ||||| ||: ||||| |||||:|
QY 121 GPVNRKGFYLPQDVACVALVSVRYRFFKCPFTYKLNLMFPPTVP-MDSQSLVEYRGSC 179
||| |||:| ||||| ||: ||||| ||: ||||| |||||:|
DB 205 GPLSKGFTYLPQDVACIALVSVRYRFFKCPVVRHLAIFPDTIGADSSQLLEVSGSC 264
||| |||:| ||||| ||: ||||| ||: ||||| |||||:|
QY 180 VNSKKEDEPPRMVCSGTEGELVPIGKSCNAGYEERGFMCQ 220
||:| |||:| ||||| ||: ||||| ||: ||||| |||||:|
DB 265 VNHSTVDPPKMHCSAEGELVPIGKCMKAGYEERKNGTCQ 305
||:| |||:| ||||| ||: ||||| ||: ||||| |||||:|

Search completed: May 9, 2000, 22:25:58
Job time: 4147 sec